

GenCore version 5.1.6  
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MM protein - protein search, using sw model

Run on: February 9, 2004, 09:56:08 ; Search time 18.2838 Seconds  
(without alignments)  
646.953 Million cell updates/sec

Title: US-09-981-876-200  
Perfect score: 657  
Sequence: 1 MACRCFLMGLTFLSVSQT.....PVPEDDADYGVGVGSP 123

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:.\*  
1: PIR1:.\*  
2: PIR2:.\*  
3: PIR3:.\*  
4: PIR4:.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Query Length	DB ID	Description
1	430	65.4	123	2 S35302	B-cell protein 8HS
2	233.5	35.5	142	2 B28344	VpreB protein prec
3	229.5	34.9	142	2 A28344	VpreB protein prec
4	217.5	33.1	120	2 PS0055	Ig lambda chain pr
5	215.5	32.8	139	2 S00258	VpreB protein - hu
6	215.5	32.8	145	2 I57832	Vpre-B protein - h
7	213.5	32.5	232	2 S17399	Ig lambda chain pr
8	210.5	32.0	120	2 PS0056	Ig lambda chain pr
9	208.5	31.7	133	2 A28565	Ig lambda chain pr
10	207.5	31.6	243	2 S25755	Ig lambda chain -
11	202	30.7	111	1 L6HUST	Ig lambda chain V-
12	200.5	30.5	118	2 A32529	Ig lambda chain pr
13	199	30.3	112	1 L6HUAR	Ig lambda chain V-
14	197	30.0	117	2 S04525	Ig lambda chain pr
15	196	29.8	136	2 S16848	Ig lambda chain V-
16	193.5	29.5	98	2 S36068	Ig lambda chain -
17	191.5	29.1	99	2 S36058	Ig lambda chain -
18	191.5	29.1	132	2 A55410	Ig light chain V r
19	191	29.1	235	2 S25758	Ig lambda chain -
20	190.5	29.0	216	2 S69130	Ig lambda chain (D
21	189.5	28.8	234	2 A39956	Ig lambda chain pr
22	186.5	28.4	99	2 S36057	Ig lambda chain -
23	186.5	28.4	111	1 L2HUMC	Ig lambda chain V-
24	185	28.2	111	1 L6HULT	Ig lambda chain pr
25	185	28.2	111	1 L6HUEB	Ig lambda chain pr
26	184.5	28.1	111	1 L2HUBO	Ig lambda chain V-
27	184.5	28.1	233	2 S25744	Ig lambda chain -
28	183.5	27.9	130	1 L1HUBL	Ig lambda chain pr
29	182.5	27.8	99	2 S36051	Ig lambda chain -

Ig lambda chain -  
Ig lambda chain pr  
Ig lambda chain -  
Ig lambda chain -  
Ig lambda chain V  
Ig lambda chain V  
Ig lambda chain pr  
Ig lambda chain pr  
Ig lambda chain pr  
Ig lambda chain V-  
Ig lambda chain V-  
Ig lambda chain pr  
Ig lambda chain pr  
Ig lambda chain pr  
Ig lambda chain -

30 182.5 27.8 99 2 S36053  
31 182.5 27.8 117 2 S23627  
32 182.5 27.8 233 2 S25752  
33 182.5 27.8 235 2 S25750  
34 181.5 27.6 111 2 S46397  
35 181.5 27.6 112 2 S31515  
36 181.5 27.6 117 2 S04526  
37 181.5 27.6 118 2 S12627  
38 181.5 27.6 234 2 S25757  
39 180.5 27.5 107 2 B4516  
40 180.5 27.5 111 1 L1HUNG  
41 180.5 27.5 112 1 L2HUNG  
42 180.5 27.5 117 1 LVHU2  
43 180.5 27.5 132 2 PL0114  
44 180.5 27.5 132 2 S04937  
45 180 27.4 108 2 S38498

ALIGNMENTS

RESULT 1  
S35302  
B-cell protein 8HS-20 precursor - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 31-Dec-1993 #sequence\_revision 02-Jun-1994 #text\_change 20-Jun-2000  
C/Accession: S35302  
R/Shirasawa, T.; Ohnishi, K.; Hagiwara, S.; Shigenoto, K.; Takebe, Y.; Rajewsky, K.; Te  
EMBO J. 12, 1827-1834, 1993  
A>Title: A novel gene product associated with mu chains in immature B cells.  
A/Reference number: S35302; MUID:93259124; PMID:8491176  
A/Accession: S35302  
A/Molecule type: DNA  
A/Residues: 1-123 <SHI>  
A/Cross-references: EMBL:DJ3208; NID:g286064; PIDN:BAA02495.1; PID:g286065  
C/Genetics:  
A/Gene: 8HS-20  
A/Introns: 18/1  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: B-cell  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-123/Product: B-cell protein 8HS-20 #status predicted <MAT>  
Query Match 65.4%; Score 430; DB 2; Length 123;  
Best Local Similarity 66.1%; Pred. No. 2.9e-36;  
Matches 82; Conservative 14; Mismatches 26; Indels 2; Gaps 2;  
QY 1 MACRCFLMGLTFLSVSQTVAQLDALLVFFQVLAQLSCTLSPOKVTIRDYGVSWYQQ 59  
Db 1 MACPCCLPLLIGTFVAVFQPTLPDPAFVSFPGQDAHLSCITNSCHATAGDIGVSWYQQ 60  
QY 60 RAGSAPRVLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISPVPQEDDADYGVSVGY 119  
Db 61 QPGSAP-RLLYYABEEHYRPADIPDRFSATVDAAHNACILITISVLPEDDADYFCSIAH 119  
QY 120 GFSP 123  
Db 120 TREP 123  
RESULT 2  
B28344  
VpreB protein precursor - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 05-Nov-1999  
C/Accession: B28344  
R/Kudo, A.; Melchers, F.  
EMBO J. 6, 2267-2272, 1987  
A>Title: A second gene, VpreB in the lambda-5 locus of the mouse, which appears to be s  
A/Reference number: A91077; MUID:88029315; PMID:3117530  
A/Accession: B28344  
A/Molecule type: DNA  
A/Residues: 1-142 <KUD>

A;Cross-references: GB:X05563; GB:Y00079; NID:G55415; PIDN:CAA29077.1; PID:G55416  
A;Note: the authors translated the codon GAG for residue 110 as Gln  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;20-142/Product: VpreB protein #status predicted <Mar>

Query Match 35.5%; Score 233.5; DB 2; Length 142;

Best Local Similarity 54.7%; Pred. No. 2.2e-16;  
Matches 47; Conservative 9; Mismatches 29; Indels 1; Gaps 1;

QY 33 GQVQLSCTLSFQVHTIRDYGVSVYQORAGSAPRYLLYRSEEDHRRPADIPDRFSAKD 92  
DB 34 GATIRLSCTLSNDH-NIGIYIYVYQORPGHPRFLRYFSDHSDXKQGPDIIPRSGSKD 92

QY 93 EAHNACVLTISPVEDDADYCSVG 118

DB 93 TARNLGYLSISELQFEDEAVYICAVG 118

## RESULT 3

A28344

VpreB protein precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 21-Jul-2000

C;Accession: A28344

R;Kudo, A.; Melchers, F.

EMBO J. 6, 2267-2272, 1987

A;Title: A second gene, VpreB in the lambda-5 locus of the mouse, which appears to be se

A;Reference number: A31077; MUID:88029315; PID:3117330

A;Accession: A28344

A;Molecule type: DNA

A;Residues: 1-142 <KUD>

A;Cross-references: GB:X05556; GB:Y00079; NID:G55409; PIDN:CAA29077.1; PID:G55410

A;Note: the authors translated the codon GAG for residue 110 as Gln

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;20-142/Product: VpreB1 protein #status predicted <MAT>

Query Match 34.9%; Score 229.5; DB 2; Length 142;

Best Local Similarity 53.5%; Pred. No. 5.6e-16;  
Matches 46; Conservative 9; Mismatches 30; Indels 1; Gaps 1;

QY 33 GQVQLSCTLSFQVHTIRDYGVSVYQORAGSAPRYLLYRSEEDHRRPADIPDRFSAKD 92

DB 34 GATIRLSCTLSNDH-NIGIYIYVYQORPGHPRFLRYFSDHSDXKQGPDIIPRSGSKD 92

QY 93 EAHNACVLTISPVEDDADYCSVG 118

DB 93 TTRNLGYLSISELQFEDEAVYICAVG 118

## RESULT 4

PS0055

IG lambda chain precursor V-II region - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 23-Jul-1999

C;Accession: PS0055

R;Hayzer, D.J.; Jaton, J.C.

Gene 80, 185-191, 1989

A;Title: Cloning and sequencing of two functional rabbit germ-line immunoglobulin V lamb

A;Reference number: A31614; MUID:9006781; PMID:2507399

A;Accession: PS0055

A;Molecule type: DNA

A;Residues: 1-120 <HAY>

A;Cross-references: GB:M27840; NID:G341760; PIDN:AAA31363.1; PID:G552407

A;Note: the authors translated the codon TTG for residue 97 as Trp

C;Genetics:

A;Introns: 17/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-120/Product: Ig lambda chain V-II region #status predicted <MAT>

Query Match

Best Local Similarity 33.1%; Score 217.5; DB 2; Length 120;

Matches 41.2%; Pred. No. 7.5e-15;

Matches 49; Conservative 17; Mismatches 44; Indels 9; Gaps 3;  
QY 5 CLSFLIMCTFL----SVSTVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSVYQOR 60  
DB 3 CYPLELLTLTLOCTGSUSQPVLTQSPSVSAALGASAKLTCTLSSAHT---YTIWYQQQ 59  
QY 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAAKDBAHNACVLTISPVEDDADYCSVG 119  
DB 60 QQEAPRYLMQLKSGSYTKGTGVDRFSGSSGADR--YLLIPSVQADDEADYICGADY 116

## RESULT 5

S00258

VpreB protein - human

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 05-Nov-1999

C;Accession: S00258

R;Bauer, S.R.; Kudo, A.; Melchers, F.

EMBO J. 7, 111-116, 1988

A;Title: Structure and pre-B lymphocyte restricted expression of the VpreB gene in hum

A;Reference number: S00258; MUID:88196069; PMID:3258819

A;Accession: S00258

A;Molecule type: DNA

A;Residues: 1-139 <BAU>

A;Cross-references: ENBL:M34927; NID:G340304; PIDN:AAA61292.1; PID:G340305

C;Genetics:

A;Gene: GDB:VPREB1

A;Cross-references: GDB:120493; OMIM:146770

A;Map position: 22q11.2-22q11.2

A;Introns: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match

Best Local Similarity 32.8%; Score 215.5; DB 2; Length 139;

Matches 47; Conservative 13; Mismatches 39; Indels 1; Gaps 1;

QY 19 QTVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSVYQORAGSAPRYLLYRSEEDH 78

DB 20 QPVLPQPPAMSSALGTTRITLCTLRNDH-DIGYISYVYQORCHPRFLRYFSQSDKS 78

QY 79 RPADIPDRFSAAKDBAHNACVLTISPVEDDADYCSVG 118

DB 79 QQPVPVPRFSGSKDVARNRGYLSISELQFEDEAMYICAMG 118

## RESULT 6

IS7832

Vpre-B protein - human

C;Species: Homo sapiens (man)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999

C;Accession: IS7832

R;Guelpa-Ponlupt, V.; Bossy, D.; Alzati, P.; Fumoux, P.; Fougereau, M.; Schiff, C.

Mol. Immunol. 31, 1099-1108, 1994

A;Title: The human pre-B cell receptor: structural constraints for a tentative model of

A;Reference number: IS7832; MUID:95021319; PMID:7935499

A;Accession: IS7832

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-145 <RES>

A;Cross-references: GB:S74019; NID:G693810; PIDN:AA321118.1; PID:G693811

C;Genetics:

A;Gene: Vpre-B

A;Introns: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 32.8%; Score 215.5; DB 2; Length 145;

Best Local Similarity 47.0%; Pred. No. 1.5e-14;  
Matches 47; Conservative 13; Mismatches 39; Indels 1; Gaps 1;

QY 19 QTVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSVYQORAGSAPRYLLYRSEEDH 78

DB 20 QPVLPQPPAMSSALGTTRITLCTLRNDH-DIGYISYVYQORCHPRFLRYFSQSDKS 78



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Y 79 RPADIDPERSAAKDEAHNACVLTISFVQPEDDADYYCSVG 118
b 79 QGPQVPRFSGSKDVARNRGYLSISELOPEDDADYYCANG 118

RESULT 7
117399
Ig lambda chain precursor - rabbit (fragment)
:Species: Oryctolagus cuniculus (domestic rabbit)
:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
:Accession: S17399
:Hayzer, D.J.; Young-Cooper, G.O.; Mage, R.G.; Jaton, J.C.
Eur. J. Immunol. 20, 2707-2712, 1990
A:Title: cDNA clones encoding immunoglobulin lambda chains from rabbit expressing the ph
A:Reference number: S17399; MUID:91099420; PMID:2125274
A:Keywords: heterotetramer; immunoglobulin
F:147-215/Domain: immunoglobulin homology <IMM>

Query Match 32.5%; Score 213.5; DB 2; Length 232;
Best Local Similarity 41.7%; Pred. No. 4e-14;
Matches 48; Conservative 18; Mismatches 40; Indels 9; Gaps 3;

QY 9 LLMGTFL---SVSQTVLAQLDALLVFPQVAQLSCTLSPQHVIRDYGVSWYQORAGSA 64
D 2 LLLTLTLLQCTGSLSQPVLTQSPSASALGASARLCTLSSAKT---YTDWQQQGEA 58
QY 65 PRLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISFVQPEDDADYYCSVG 119
D 59 PRVLMHKSDGTYKGTGVPDRFSGSSGADR--YLIIPSVQADDEADYYCGADY 111

RESULT 8
PS0056
Ig lambda chain precursor V-III region - rabbit
:Species: Oryctolagus cuniculus (domestic rabbit)
:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 23-Jul-1999
:Accession: PS0056
:Hayzer, D.J.; Jaton, J.C.
Gene 80, 185-191, 1989
A:Title: Cloning and sequencing of two functional rabbit germ-line immunoglobulin V lam
A:Reference number: A91614; MUID:90006781; PMID:2507399
A:Accession: PS0056
A:Molecule type: DNA
A:Residues: 1-120 <HAY>
A:Cross-references: GB:M27841; NID:G341761; PIDN:AAA31364.1; PID:G552408
A:Note: the authors translated the codon TTA for residue 97 as Trp
C:Genetics:
A:Introns: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:121-120/Product: Ig lambda chain V-III region #status predicted <SIG>

Query Match 32.0%; Score 210.5; DB 2; Length 120;
Best Local Similarity 41.9%; Pred. No. 3.8e-14;
Matches 49; Conservative 16; Mismatches 43; Indels 9; Gaps 3;

QY 5 CLSFLMGTEL---SVSQTVLAQLDALLVFPQVAQLSCTLSPQHVIRDYGVSWYQOR 60
D 3 CTPLLLTLTLLQCTGSLSQPVLTQSPSASALGASAKUTCTLSSAKT---YYIEWYQQQ 59
QY 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISFVQPEDDADYYCSV 117
D 60 QGEAPRYLMQLKSDGTYKGTGVPDRFSGSSGADR--YLIISVQADDEADYYICGV 114

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Biochem. J. 195, 561-572, 1981  
A:Title: The complete amino acid sequence of a prototype immunoglobulin-lambda light-c  
A:Reference number: A01987; MUID:82091000; PMID:6797401  
A:Molecule type: protein  
A:Accession: A01987  
A:Genetics:  
A:Gene: GDB:IGLV@  
A:Cross-references: GDB:119342; OMIM:147240  
A:Map position: 22q11.2-22q11.2  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds.  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: amyloid; heterotetramer; immunoglobulin  
F:15-93/Domain: immunoglobulin homology <IMM>  
F:22-91/Disulfide bonds: #status predicted

Query Match 30.3%; Score 199; DB 1; Length 112;  
Best Local Similarity 44.2%; Pred. No. 5.1e-13;  
Matches 42; Conservative 18; Mismatches 29; Indels 6; Gaps 2;

QY 21 VLAQDALLVFPQVQALSTLSPQHVITRDYGVSWYQVQAGSAPRYLLYRSEEDHRRP 80  
DB 3 MLTQHSVSESPGKTVIFCTSGSG--SIADSFVQWYQVQPGSAPTIVY---DDNQRP 56  
QY 81 ADIPRFSAAKDEAHNACVLTISVPQEDDADYYC 115  
DB 57 SGVPRFSGSIDNSANSASLTISGLKTEDEADYYC 91

RESULT 14  
S04525  
Ig lambda chain precursor V region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 21-Jan-2000  
C:Accession: S04525  
R:Alexandre, D.; Chuchana, P.; Brockly, F.; Blancher, A.; Lefranc, G.; Lefranc, M.P.  
Nucleic Acids Res. 17, 3975, 1989  
A:Title: First genomic sequence of a human Ig variable lambda gene belonging to subgroup 1  
A:Reference number: S04525; MUID:89282401; PMID:2499871  
A:Molecule type: DNA  
A:Residues: 1-117 <ALE>  
A:Cross-references: EMBL:X14615; NID:933397; PIDN:CAA32769.1; PID:9736246  
C:Genetics:  
A:Introns: 16/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-110/Domain: immunoglobulin homology <IMM>

Query Match 30.0%; Score 197; DB 2; Length 117;  
Best Local Similarity 40.3%; Pred. No. 8.6e-13;  
Matches 50; Conservative 23; Mismatches 41; Indels 10; Gaps 5;

QY 1 MACR-CLSFLLMGTFLSVQTVLAQDALLVFPQVQALSTLSPQHVITRDYGVSWYQ 59  
DB 1 MTCSPILLTLLHCTGSAQSVLTQPPSVSAAPQGVKVTISCGSS--DMGNVAVSWYQ 58  
QY 60 RAGSAPRYLLYRSEEDHRRPADIPRFSAAKDEAHNACVLTISVPQEDDADYYCSVG 119  
DB 59 LPGTAPKLLIY----ENNKRPSPGIDPRFSGSK--SGTSATLIGTLWPEDEADYYC-LAW 111  
QY 120 GFSP 123  
DB 112 DTSP 115

RESULT 15  
S16848  
Ig lambda chain V-II region precursor - human

A:Reference number: A01988  
A:Accession: A01988  
A:Molecule type: protein  
A:Residues: 1-111 <SOL>  
A:Genetics:  
A:Gene: GDB:IGLV@  
A:Cross-references: GDB:119342; OMIM:147240  
A:Map position: 22q11.2-22q11.2  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds.  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-93/Domain: immunoglobulin homology <IMM>  
F:22-91/Disulfide bonds: #status predicted

Query Match 30.7%; Score 202; DB 1; Length 111;  
Best Local Similarity 45.3%; Pred. No. 2.5e-13;  
Matches 43; Conservative 15; Mismatches 31; Indels 5; Gaps 2;

QY 21 VLAQDALLVFPQVQALSTLSPQHVITRDYGVSWYQVQAGSAPRYLLYRSEEDHRRP 80  
DB 3 MLTQHSVSESPGKTVIFCTSGSG--TIAGYVQWYQVQPGSAPTIVY---EDTQRP 56  
QY 81 ADIPRFSAAKDEAHNACVLTISVPQEDDADYYC 115  
DB 57 SGVPRFSGSIDNSANSASLTISGLQTEDEADYYC 91

RESULT 12  
A32529  
Ig lambda chain precursor V region (clone pD8) - rabbit (fragment)  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 07-Jun-1990 #sequence\_revision 23-Nov-1991 #text\_change 16-Aug-1996  
C:Accession: A32529  
R:Hayzer, D.J.; Duvoisin, R.M.; Jaton, J.C.  
Biochem. J. 245, 691-697, 1987  
A:Title: cDNA clones encoding rabbit immunoglobulin lambda chains. Evidence for length variation in the variable region  
A:Reference number: A90339; MUID:88024122; PMID:3117050  
A:Accession: A32529  
A:Molecule type: mRNA  
A:Residues: 1-118 <RAY>  
A:Cross-references: GB:M25617  
A:Note: the authors translated the codon TTG for residue 37 as Phe  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 30.5%; Score 200.5; DB 2; Length 118;  
Best Local Similarity 42.3%; Pred. No. 3.8e-13;  
Matches 44; Conservative 14; Mismatches 41; Indels 5; Gaps 2;

QY 16 SVSQTVLAQDALLVFPQVQALSTLSPQHVITRDYGVSWYQVQAGSAPRYLLYRSE 75  
DB 3 SLSPQVLTQPSAAAALGASAKLTCTLSAHTSL---VENYQKQGEAPRYLLMWLRKDG 59  
QY 76 DHRPADIPRFSAAKDEAHNACVLTISVPQEDDADYYCSVG 119  
DB 60 SYTKGTGVDRFSGSSGGADR--YLLISVQADDEADYYCGVDY 101

RESULT 13  
L6HUAR  
Ig lambda chain V-VI region (AR) - human (tentative sequence)  
C:Species: Homo sapiens (man)  
C:Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 31-Mar-2000  
A:Accession: A01987





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 CC EMBL; AB050772; BAB83034.1; -  
 CC EMBL; BC020666; AAH20666.1; -  
 CC HSSP; P01709; 2MCG  
 CC Genew; HGNC.12710; VPREB3.  
 CC MIM; 605017.  
 CC InterPro; IPR007110; Ig-like.  
 CC InterPro; IPR003006; Ig\_MHC.  
 CC InterPro; IPR003596; Ig\_V.  
 CC Pfam; PF00047; Ig; 1.  
 CC SMART; SM00406; IGV; 1.  
 CC PROSITE; PSS0835; IG LIKE; 1.  
 CC Immunoglobulin domain; B-cell; Signal.  
 CC SIGNAL 1 20 POTENTIAL.  
 CC CHAIN 21 123 PRE-B LYMPHOCYTE PROTEIN 3.  
 CC DOMAIN 21 123 IG-LIKE.  
 CC DISULFID 40 115 BY SIMILARITY.  
 CC SEQUENCE 123 AA; 13710 MW; BF09AC5196059E85 CRC64;

Query Match 100.0%; Score 657; DB 1; Length 123;  
 Best Local Similarity 100.0%; Pred. No. 2,1e-62;  
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MACRCLSFLMGFTLSVQTVLAQDALLVPPGVAQLSCTLSPOHVTIRDYGVSWYQQR 60  
 DB 1 MACRCLSFLMGFTLSVQTVLAQDALLVPPGVAQLSCTLSPOHVTIRDYGVSWYQQR 60  
 QY 61 AGSAPRYLLYRSEEDHRRPADIPRFSAAKDEAHNACVLIISVPQEDDADYCVSGYG 120  
 DB 61 AGSAPRYLLYRSEEDHRRPADIPRFSAAKDEAHNACVLIISVPQEDDADYCVSGYG 120  
 QY 121 FSP 123  
 DB 121 FSP 123

RESULT 2  
 ID\_VPRE2\_MOUSE STANDARD; PRT; 142 AA.  
 AC P13373;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Immunoglobulin omega chain precursor (VpreB2 protein).  
 GN VPREB2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6 X DBA/2J;  
 RX MEDLINE=88029315; PubMed=3117530;  
 RA Kudo A., Melchers F.;  
 RT "A second gene, VpreB in the lambda 5 locus of the mouse, which  
 RT appears to be selectively expressed in pre-B lymphocytes.";  
 RL EMO J. 6:2267-2272(1987).  
 CC -!- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR  
 CC COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS. THIS  
 CC COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE EARLY  
 CC STEPS OF B-CELL DIFFERENTIATION.  
 CC -!- TISSUE SPECIFICITY: ONLY EXPRESSED BY PRE-B-CELLS.  
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
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CC EMBL; X05563; CAA29077.1; -  
 CC PIR; B28344; B28344.  
 CC HSSP; P01607; IREI.  
 CC MGD; MGI-98937; VpreB2.  
 CC InterPro; IPR007110; Ig-like.  
 CC InterPro; IPR003006; Ig\_MHC.  
 CC InterPro; IPR003596; Ig\_V.  
 CC Pfam; PF00047; Ig; 1.  
 CC SMART; SM00406; IGV; 1.  
 CC PROSITE; PSS0835; IG LIKE; 1.  
 CC Immunoglobulin domain; B-cell; Signal.  
 CC SIGNAL 1 19 POTENTIAL.  
 CC CHAIN 20 142 IMMUNOGLOBULIN OMEGA CHAIN.  
 CC DOMAIN 20 41 FRAMEWORK-1.  
 CC DOMAIN 42 56 COMPLEMENTARITY-DETERMINING-1.  
 CC DOMAIN 57 70 FRAMEWORK-2.  
 CC DOMAIN 71 81 COMPLEMENTARITY-DETERMINING-2.  
 CC DOMAIN 82 115 FRAMEWORK-3.  
 CC DISULFID 41 115 BY SIMILARITY.  
 CC SEQUENCE 142 AA; 16052 MW; 7EA7128A4E63D920 CRC64;

Query Match 35.5%; Score 233.5; DB 1; Length 142;  
 Best Local Similarity 54.7%; Pred. No. 1.1e-17;  
 Matches 47; Conservative 9; Mismatches 29; Indels 1; Gaps 1;  
 QY 33 GQVAQLSCTLSPOHVTIRDYGVSWYQQRAGSAPRYLLYRSEEDHRRPADIPRFSAAK 92  
 DB 34 GATRLSCTLSNDH-NIGYISYVYQQRPGHPRFLLYFHSKQGPDPFRFSGSKD 92  
 QY 93 EAHNACVLIISVPQEDDADYCVSG 118  
 DB 93 TARNLGVLSISELQPEDEAVYICAVG 118

RESULT 3  
 ID\_VPRE1\_MOUSE STANDARD; PRT; 142 AA.  
 AC P13372;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Immunoglobulin iota chain precursor (VpreB1 protein).  
 GN VPREB1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6 X DBA/2J;  
 RX MEDLINE=88029315; PubMed=3117530;  
 RA Kudo A., Melchers F.;  
 RT "A second gene, VpreB in the lambda 5 locus of the mouse, which  
 RT appears to be selectively expressed in pre-B lymphocytes.";  
 RL EMO J. 6:2267-2272(1987).  
 CC -!- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR  
 CC COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS. THIS  
 CC COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE EARLY  
 CC STEPS OF B-CELL DIFFERENTIATION.  
 CC -!- TISSUE SPECIFICITY: ONLY EXPRESSED BY PRE-B-CELLS.  
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
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 R R EMBL; X05556; CAA29071.1; -;  
 R R EMBL; X05557; CAA29072.1; -;  
 R R PIR; A28344; A28344.  
 R R HSSP; P01607; IREI.  
 R R MGD; MG1:98936; Vpreb1.  
 R R GO; GO:0005886; Cytoplasmic membrane; IPI.  
 R R GO; GO:0004872; Receptor activity; IPI.  
 R R GO; GO:0030097; P:hemopoiesis; IMP.  
 R R GO; GO:0006955; P:immune response; IPI.  
 R R InterPro; IPR007110; IG-like.  
 R R InterPro; IPR003006; IG\_MHC.  
 R R InterPro; IPR003596; IG\_V.  
 R R Pfam; PF00047; ig; 1.  
 R R SMART; SM00406; IGV; 1.  
 R R PROSITE; PS00835; IG\_LIKE; 1.  
 R W Immunoglobulin domain; B-cell; Signal.  
 T T SIGNAL 1 19 POTENTIAL.  
 T T CHAIN 20 142 IMMUNOGLOBULIN IOTA CHAIN.  
 T T DOMAIN 40 41 FRAMEWORK-1.  
 T T DOMAIN 42 56 COMPLEMENTARITY-DETERMINING-1.  
 T T DOMAIN 57 70 FRAMEWORK-2.  
 T T DOMAIN 71 81 COMPLEMENTARITY-DETERMINING-2.  
 T T DOMAIN 82 115 FRAMEWORK-3.  
 T T DISULFID 41 115 BY SIMILARITY.  
 T T SEQUENCE 142 AA; 16125 MW; 2518BF963A0F48C CRC64;  
 T T  
 T T Query Match 34.9%; Score 229.5; DB 1; Length 142;  
 T T Best Local Similarity 53.5%; Pred. No. 2.9e-17;  
 T T Matches 46; Conservative 9; Mismatches 30; Indels 1; Gaps 1;  
 T T  
 Y Y 33 QVLAQLDALLVFPQVLAQLSPTQVTRIDYGVSWYQORAGSAPRYLLYRSEDHRRPADIPDRSAKD 92  
 Y Y 34 GATIRLSCTLSNDH-NIGIYIYQORPGHPPRFLRYFSHSDKHQGEDIPRFSGSKD 92  
 Y Y 93 EAHNACVLITSPVQEDDADYCVSG 118  
 Y Y 93 TTRNLGLSISLQEDAEVYCVAG 118  
 Y Y  
 RESULT 4  
 VPRE\_HUMAN STANDARD; PRT; 145 AA.  
 ID VPRE\_HUMAN  
 AC P12018;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Immunoglobulin iota chain precursor (V(pre)B protein) (VpreB protein)  
 DE (CD179a antigen).  
 DE VPRED1 OR VPRED.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 OX [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95021318; PubMed=7935499;  
 RA Guelpa-Fonlupt V., Bossy D., Alzari P., Fumoux F., Fougereau M.,  
 RA Schiff C.;  
 RT "The human pre-B cell receptor: structural constraints for a tentative  
 RT model of the pseudo-light (psi L) chain.";  
 RT Mol. Immunol. 31:1099-1108 (1994).  
 RT [2].  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9728902; PubMed=9074928;  
 RA Kawaaki K., Minoshima S., Mine E., Shibuya K., Shintani A.,  
 RA Schmeits J.L., Wang J., Shimizu N.;  
 RT "One-megabase sequence analysis of the human immunoglobulin lambda  
 RT gene locus.";  
 RL Genome Res. 7:250-261 (1997).

[3]  
 RN RP SEQUENCE OF 1-139 FROM N.A.  
 RX MEDLINE=88196069; PubMed=3258819;  
 RA Bauer S.R., Kudo A., Melchers F.;  
 RT "Structure and pre-B lymphocyte restricted expression of the VpreB in  
 RT humans and conservation of its structure in other mammalian  
 RT species";  
 RL EMBO J. 7:111-116 (1988).  
 CC -1- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR  
 CC COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS. THIS  
 CC COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE EARLY  
 CC STEPS OF B-CELL DIFFERENTIATION.  
 CC -1- SUBUNIT: Associates non-covalently with IGLL1.  
 CC -1- TISSUE SPECIFICITY: ONLY EXPRESSED BY PRE-B-CELLS.  
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
 CC -1- DATABASE: NAME=PROM; NOTE=PROM 1:59-63 (2000).  
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/guide/574153212\_g.htm".  
 CC  
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 DR EMBL; D86992; BAAL9987.1; -;  
 DR EMBL; D86270; BAA20030.1; -;  
 DR EMBL; S74019; AAB32118.1; -;  
 DR EMBL; M34927; AAA61292.1; -;  
 DR PIR; I57832; I57832.  
 DR PIR; S00258; S00258.  
 DR HSSP; P80748; 2LOI.  
 DR Genew; HGNC:12709; VPREB1.  
 DR MIM; 605141; -;  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR Immunoglobulin domain; B-cell; Signal; Antigen.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 145 IMMUNOGLOBULIN IOTA CHAIN.  
 FT DOMAIN 20 41 FRAMEWORK-1.  
 FT DOMAIN 42 56 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 57 70 FRAMEWORK-2.  
 FT DOMAIN 71 81 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 82 115 FRAMEWORK-3.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT CONFLICT 10 10 L -> H (IN REF. 3).  
 SQ SEQUENCE 145 AA; 16605 MW; 197665B13AF64D46 CRC64;  
 SQ  
 Query Match 32.8%; Score 215.5; DB 1; Length 145;  
 Best Local Similarity 47.0%; Pred. No. 9e-16;  
 Matches 47; Conservative 13; Mismatches 39; Indels 1; Gaps 1;  
 QY 19 QTVLAQLDALLVFPQVLAQLSPTQVTRIDYGVSWYQORAGSAPRYLLYRSEDH 78  
 Db 20 QPVTHQPPAMSSALGTITRLTCTLRNDH-DIGVSVYVYQORPGHPPRFLRYFSOSDKS 78  
 QY 79 RPADIPDRSAKDAHNAACVLITSPVQEDDADYCVSG 118  
 Db 79 QGPQVPRFSGSKDVARNRGYLSISLQEDAEVYCVAG 118  
 Db  
 RESULT 5  
 ID LV6C\_HUMAN  
 ID LV6C\_HUMAN STANDARD; PRT; 111 AA.  
 AC P06317;

DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-VI region ANT.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RA Solomon A., Kyle R.A., Frangione B.;  
RT "Light chain variable region subgroups of monoclonal immunoglobulins  
in amyloidosis AL."  
RL (in) Glenner G.G., Cessman E.P., Benditt E.P., Calkins E.,  
Cohen A.S., Zucker-Franklin D. (eds.); New York (1986).  
RL Amyloidosis, pp.449-462, Plenum Press, New York (1986).  
DR PIR; A01988; L6HUST.  
DR PDB; 1CD0; 06-MAR-00.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
KW Immunoglobulin V region; 3D-structure.  
FT DOMAIN 1 22  
FT DOMAIN 23 35  
FT DOMAIN 36 50  
FT DOMAIN 51 57  
FT DOMAIN 58 91  
FT DOMAIN 92 100  
FT DOMAIN 101 111  
FT DISULFID 22 91  
FT NON TER 111 111  
SQ SEQUENCE 111 AA; 12247 MW; 0941DD547D983598 CRC64;  
  
Query Match 30.7%; Score 202; DB 1; Length 111;  
Best Local Similarity 45.3%; Pred. No. 1.8e-14;  
Matches 43; Conservative 15; Mismatches 31; Indels 6; Gaps 2;  
  
QY 21 VLAQDALLVFPQVQAQLSCTLSFQHVTRDYGVSQYQQRAGSAPRYLLYRSEEDHHRP 80  
Db 3 MLTQPHSVESFGKTVISCTSDG--FIAGYVQVQYQQRGAPTTVIF----EDTQRP 56  
  
QY 81 ADIPDRFSAKDEAHNACVLTISFQVPEDDADYYC 115  
Db 57 SGVDPDRFSGSIDRSSNSASLTISGLKTEDEADYYC 91  
  
RESULT 6  
LV6A HUMAN STANDARD; PRT; 112 AA.  
AC P01721;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-VI region AR.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE (AMYLID PROTEIN AR).  
RA Sletten K., Natvig J.B., Husby G., Juul J.;  
RT "The complete amino acid sequence of a prototype  
immunoglobulin-lambda light-chain-type amyloid-fibril protein AR."  
RL Biochem. J. 195:561-572(1981).  
CC -1- MISCELLANEOUS: ABOUT HALF OF THE LAMBDA CHAIN C REGION IS MISSING  
FROM THIS PROTEIN.  
CC -1- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE SPLEEN OF A  
PATIENT WITH AMYLOIDOSIS.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR PIR; A01987; L6HUA6.  
DR HSP; P01709; 2MCG.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; P:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
KW Immunoglobulin V region; Amyloid.  
FT DOMAIN 1 107  
FT NON TER 112 112  
SQ SEQUENCE 112 AA; 11918 MW; 570BCD9A368EF1FE CRC64;  
  
Query Match 30.3%; Score 199; DB 1; Length 112;  
Best Local Similarity 44.2%; Pred. No. 3.7e-14;  
Matches 42; Conservative 18; Mismatches 29; Indels 6; Gaps 2;  
  
QY 21 VLAQDALLVFPQVQAQLSCTLSFQHVTRDYGVSQYQQRAGSAPRYLLYRSEEDHHRP 80  
Db 3 MLTQPHSVESFGKTVISCTSDG--SIADSFVQVQYQQRGAPTTVIF----DDNQRP 56  
  
QY 81 ADIPDRFSAKDEAHNACVLTISFQVPEDDADYYC 115  
Db 57 SGVDPDRFSGSIDRSSNSASLTISGLKTEDEADYYC 91  
  
RESULT 7  
LV2F HUMAN STANDARD; PRT; 111 AA.  
AC P01709;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-II region MGC.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RA Felt J.W., Deutsch H.F.;  
RT "Primary structure of the MCG lambda chain."  
RL Biochemistry 13:4102-4114(1974).  
RN [2]  
RP LAMBDA CHAIN GENES.  
RX MEDLINE=76093781; PubMed=812801;  
RA Felt J.W., Deutsch H.F.;  
RT "A new lambda-chain gene."  
RL Immunochimistry 12:643-652(1975).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
RA Edmundson A.B., Ely K.R., Abola E.E., Schiffer M.,  
Panagiotopoulos N.;  
RT "Rotational allomerism and divergent evolution of domains in  
immunoglobulin light chains."  
RL Biochemistry 14:3953-3961(1975).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY.  
RX MEDLINE=90133913; PubMed=2515285;  
RA Ely K.R., Herron J.N., Harker M., Edmundson A.B.;  
RT "Three-dimensional structure of a light chain dimer crystallized in  
water. Conformational flexibility of a molecule in two crystal  
forms."  
RL J. Mol. Biol. 210:601-615(1989).  
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
CC -1- MISCELLANEOUS: THE MCG-TYPE C REGION APPEARS TO BE CORRELATED WITH  
A VERY UNUSUAL V-REGION SUBSTITUTION, 103-THR ABOVE FOR GLY,  
SUGGESTING THAT THE V-C JOINING MECHANISM IS NOT ALWAYS RANDOM.  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+

MARKERS.  
-1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
PIR: A90381; L2HUMC.  
PDB: 2MCG; 15-JUL-92.  
PDB: 1A8J; 17-JUN-98.  
PDB: 1DCU; 15-MAY-97.  
GO: GO:0005576; C:extracellular; NAS.  
GO: GO:0003823; F:antigen binding activity; NAS.  
GO: GO:0006955; P:immune response; NAS.  
InterPro: IPR007110; IG-like.  
InterPro: IPR003006; Ig\_MHC.  
InterPro: IPR003596; Ig\_V.  
Pfam: PF00047; Ig; 1.  
SMART: SM00406; IGV; 1.  
PROSITE: PS00835; IG-LIKE; 1.  
Immunoglobulin V region; Bence-Jones protein; 3D-structure;  
Pyroglutamate carboxylic acid.  
DOMAIN 1 108  
MOD RES 1 1  
DISULFID 22 90  
STRAND 5 5  
STRAND 10 12  
STRAND 18 23  
TURN 26 32  
STRAND 36 40  
TURN 42 43  
TURN 50 51  
STRAND 52 54  
TURN 55 55  
STRAND 62 63  
STRAND 66 68  
STRAND 72 77  
HELIX 82 84  
STRAND 86 93  
STRAND 99 101  
STRAND 105 109  
STRAND 111 111  
NON TER 111  
SEQUENCE 111 AA; 11558 MW; 70CID6E2FA3377BA CRC64;  
Query Match 28.4%; Score 186.5; DB 1; Length 111;  
Best Local Similarity 43.9%; Pred. No. 7.6e-13;  
Matches 43; Conservative 16; Mismatches 32; Indels 7; Gaps 3;  
DY 19 QTVLAQLDALLVFPQVAQSLSPQHVTIRYGVSWYQQRAGSAPRYLLYRSEEDHH 78  
DB 1 QSALTQPSASGSLGSLQSVTISCTGTSSDVGYNV-VSWYQQHAGKPKVIY----EVNK 55  
QY 79 PADIPRFSAAKDEAHNACVLTISPQPEDDADYCS 116  
DB 56 RPSGVNFRFSKSK--SGNTASLTVSGLQAEADYCS 91  
RESULT 8  
LV2L\_HUMAN STANDARD; PRT; 111 AA.  
AC P80422;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig gamma lambda chain V-II region DOT.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RS SEQUENCE.  
RP MEDLINE=95255298; PubMed=7737190;  
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;  
RT "Characterization of the two unique human anti-flavin mononuclear  
immunoglobulins".  
RL Eur. J. Biochem. 228:886-893(1995).  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
HSSP: P01709; 2MCG.

DR GO: GO:0005576; C:extracellular; NAS.  
DR GO: GO:0003823; F:antigen binding activity; NAS.  
DR GO: GO:0006955; P:immune response; NAS.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PS00835; IG-LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 106  
FT DISULFID 22 90  
FT NON TER 111  
FT NON TER 111  
SQ SEQUENCE 111 AA; 11787 MW; F358B1EA2CD7109A CRC64;  
Query Match 28.2%; Score 185.5; DB 1; Length 111;  
Best Local Similarity 44.8%; Pred. No. 9.7e-13;  
Matches 43; Conservative 14; Mismatches 32; Indels 7; Gaps 3;  
QY 20 TVLAQLDALLVFPQVAQSLSPQHVTIRYGVSWYQQRAGSAPRYLLYRSEEDHH 79  
DB 2 SALTQPSLSGSGFGQAVTISCTGLPS-VVDDNFSVWYQQTGPRAPRLIY---DDSLR 56  
QY 80 PADIPRFSAAKDEAHNACVLTISPQPEDDADYCS 115  
DB 57 PSGVNPFRFSKSKSDTKAA--LTISGLQPDDEATYFC 90  
RESULT 9  
LV6D\_HUMAN STANDARD; PRT; 111 AA.  
AC P06318;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig lambda chain V-VI region WLT.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RS SEQUENCE.  
RP MEDLINE=86122667; PubMed=4089539;  
RA Dwulet F.B., Szrako K., Benson M.D.;  
RT "Amino acid sequence of a lambda VI primary (AL) amyloid protein  
(WLT)".  
RL Scand. J. Immunol. 22:653-660(1985).  
DR PIR: A01989; L6HULT.  
DR HSSP: P01709; 2MCG.  
DR GO: GO:0005576; C:extracellular; NAS.  
DR GO: GO:0003823; F:antigen binding activity; NAS.  
DR GO: GO:0006955; P:immune response; NAS.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PS00835; IG-LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 22  
FT DOMAIN 23 35  
FT DOMAIN 36 50  
FT DOMAIN 51 57  
FT DOMAIN 58 91  
FT DOMAIN 92 101  
FT DOMAIN 102 111  
FT DISULFID 22 91  
FT NON TER 111  
FT NON TER 111  
SQ SEQUENCE 111 AA; 11966 MW; 0C88B2FE37BCE24F CRC64;  
Query Match 28.2%; Score 185; DB 1; Length 111;  
Best Local Similarity 45.2%; Pred. No. 1.1e-12;  
Matches 38; Conservative 16; Mismatches 24; Indels 6; Gaps 2;



```

2Y 32 PCQVAQLSCTLSPOHVTIRYGVSWYQORAGSAPRYLLYRSEEDHRRPADIPRFSAAK 91
2D 14 PEKVTITSCGSSG--SIGSNYYQVQORPGSAPTIVII--ENNQRPEVDRFSGSI 67
2Y 92 DEAHNACVLTISPQVEDDADYYC 115
2D 68 DSSSNSASLTISGLKTEDEADYYC 91

RESULT 10
LV6E_HUMAN STANDARD; PRT; 131 AA.
AC LV6E_HUMAN 1
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-VI region EB4 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. PubMed=3923440;
RX MEDLINE=85215660; PubMed=3923440;
RA Anderson M.L.M., Brown L., McKenzie E., Kellow J.E., Young B.D.;
RT "Cloning and sequence analysis of an Ig lambda light chain mRNA
expressed in the Burkitt's lymphoma cell line EB4."
RL Nucleic Acids Res. 13:2931-2941(1985).
DR PIR; A01930; L6HUEB.
DR HSSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 20 131 IG LAMBDA CHAIN V-VI REGION EB4.
FT DOMAIN 20 41 FRAMEWORK-1.
FT DOMAIN 42 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 110 FRAMEWORK-3.
FT DOMAIN 111 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 131 FRAMEWORK-4.
FT DISULFID 41 110 BY SIMILARITY.
FT NON TER 131
SQ SEQUENCE 131 AA; 14147 MW; 02A9179C8C05C2CD CRC64;

Query Match 28.2%; Score 185; DB 1; Length 131;
Best Local Similarity 42.1%; Pred. No. 1.3e-12;
Matches 40; Conservative 16; Mismatches 33; Indels 6; Gaps 2;

QY 21 VLAQLDALLVFPQVAQLSCTLSPOHVTIRYGVSWYQORAGSAPRYLLYRSEEDHRRP 80
DB 22 MLTQPHSVESFGKVTITSC--GNSGSIASNYQVQORVSAPTIVY----EDNQR 75
QY 81 ADIPRFSAAKDEAHNACVLTISPQVEDDADYYC 115
DB 76 LGVDRFSGSIDSSNSASLTISGLKTEDEADYYC 110

RESULT 11
LV2G_HUMAN STANDARD; PRT; 111 AA.
AC LV2G_HUMAN 1
DT 01-JAN-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)

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DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-II region BO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71103825; PubMed=5532228;
RA Wikler M., Putnam F.W.;
RT "Amino acid sequence of human lambda chains. 3. Tryptic peptides,
chymotryptic peptides, and sequence of protein Bo.";
RL J. Biol. Chem. 245:4488-4507(1970).
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01976; L2HUBO.
DR HSSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein;
KW Pyroglutamate carboxylic acid. IG-LIKE
FT DOMAIN 1 106 PYROGLUTAMATE CARBOXYLIC ACID.
FT MOD RES 1 1 BY SIMILARITY.
FT DISULFID 22 90
FT NON TER 111
SQ SEQUENCE 111 AA; 11785 MW; 92F5A1BF72421BAC CRC64;

Query Match 28.1%; Score 184.5; DB 1; Length 111;
Best Local Similarity 41.8%; Pred. No. 1.2e-12;
Matches 41; Conservative 16; Mismatches 34; Indels 7; Gaps 3;

QY 19 QTVLAQLDALLVFPQVAQLSCTLSPOHVTIRYGVSWYQORAGSAPRYLLYRSEEDHH 78
DB 1 QSALTQPPSASGSGQSVTISCTSDVDGNKY-VSWYQCHFGRAPKLVIF----EVSQ 55
QY 79 RPADIPRFSAAKDEAHNACVLTISPQVEDDADYYCS 116
DB 56 RPSGVDRFSGSKSD--NTASLTVSGLRADDEADYYCS 91

RESULT 12
LV1G_HUMAN STANDARD; PRT; 130 AA.
AC LV1G_HUMAN 1
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-I region BL2 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85062823; PubMed=6095199;
RA Tsujimoto Y., Croce C.M.;
RT "Molecular cloning of a human immunoglobulin lambda chain variable
sequence.";
RL Nucleic Acids Res. 12:8407-8414(1984).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/

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or send an email to license@lsb-sib.ch).

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C  ENEL; X01147; CAA25598.1; -.
R  PIR; A01966; L1HUBU.
R  HSP; P01703; 7FAB.
R  GO; GO:0005576; C:extracellular; NAS.
R  GO; GO:0003823; F:antigen binding activity; NAS.
R  GO; GO:0006955; P:immune response; NAS.
R  InterPro; IPR007110; Ig-like.
R  InterPro; IPR003006; Ig_MHC.
R  InterPro; IPR003596; Ig_v.
R  Pfam; PF00047; Ig; 1.
R  SMART; SM00406; IGV; 1.
R  PROSITE; PS00835; IG_LIKE; 1.
R  Immunoglobulin V region; Signal.
C  SIGNAL 1 19
C  CHAIN 20 130 IG LAMBDA CHAIN V-I REGION BL2.
C  DOMAIN 20 115 V SEGMENT.
C  DOMAIN 116 130 J SEGMENT.
C  DISULFID 41 108 BY SIMILARITY.
C  NON_TER 130 130
C  SEQUENCE 130 AA; 13564 MW; FA44BB17D3A55EBF CRC64;
Query Match 27.9%; Score 183.5; DB 1; Length 130;
Best Local Similarity 40.5%; Pred. No. 1.9e-12;
Matches 47; Conservative 22; Mismatches 38; Indels 9; Gaps 5;
Y 1 MACR-CLISFLMGTFVSVQTVLAQLDALLVFPQVAQLSCTLSFQHVIRDYGVSWYQQ 59
D 1 MTCSPLLLTLLHCTGSAQSVLTQPPSVSAAPGQKVITSCGSSNIG-NDY-VSWYQQ 58
Y 60 RAGSAPRYLYYSEEDHHPADIPRFSNAKDEAHNACVLITSPVQEDDADYVC 115
D 59 VFGTAPKLLIY----DNKRPSGIPDRFGSK--SGTSATLGLTGLTGDEADYVC 108
RESULT 13
LV2D HUMAN STANDARD; PRT; 111 AA.
AC P01702;
Y 21-JUL-1986 (Rel. 01, Created)
Y 21-JUL-1986 (Rel. 01, Last sequence update)
Y 15-SEP-2003 (Rel. 42, Last annotation update)
Y IG lambda chain V-I region NIG-64.
Y Homo sapiens (Human).
Y Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Y Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Y NCBI_TaxID=9606;
[1]
SEQUENCE.
MEDLINE=83186114; PubMed=6404900;
Kametani T., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
Shimizu A.;
"Comparative studies on the structure of the light chains of human
immunoglobulins. IV. Assignment of a subgroup.",
J. Biochem. 93:421-429(1983).
-1- SIMILARITY: Contains 1 immunoglobulin-like domain.
Y PIR; A01965; L1HUNG.
Y HSP; P01703; 7FAB.
Y GO; GO:0005576; C:extracellular; NAS.
Y GO; GO:0003823; F:antigen binding activity; NAS.
Y GO; GO:0006955; P:immune response; NAS.
Y InterPro; IPR007110; Ig-like.
Y InterPro; IPR003006; Ig_MHC.
Y InterPro; IPR003596; Ig_v.
Y Pfam; PF00047; Ig; 1.
Y SMART; SM00406; IGV; 1.
Y PROSITE; PS00835; IG_LIKE; 1.
Y Immunoglobulin V region; Pyroglutamate carboxylic acid.
Y DOMAIN 1 105 IG-LIKE.
Y MOD RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.
Y DISULFID 22 89 BY SIMILARITY.
Y NON_TER 111 111

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SQ SEQUENCE 111 AA; 11454 MW; A21C6121C18A61E0 CRC64;
Query Match 27.5%; Score 180.5; DB 1; Length 111;
Best Local Similarity 41.1%; Pred. No. 3.3e-12;
Matches 44; Conservative 19; Mismatches 29; Indels 15; Gaps 4;
Y 19 QTVLAQLDALLVFPQVAQLSCTLSFQHVIRDYGVSWYQQRAGSAPRYLYYSEEDH 78
D 1 QSVLTQPPSVSAAPGQKVITSCGSSN--IGDNFVSWYQQLPGTAPKLLIY----DNK 54
Y 79 READIPDRFSAKDEAHNACVLITSPVQEDDADYVC-----SVG 118
D 55 RPSGIPDRFGSK--SGTSATLGLTGLTGDEADYVCCTWDSSLSVG 99
RESULT 14
LV2K HUMAN STANDARD; PRT; 112 AA.
AC P04209;
Y 20-MAR-1987 (Rel. 04, Created)
Y 20-MAR-1987 (Rel. 04, Last sequence update)
Y 15-SEP-2003 (Rel. 42, Last annotation update)
Y IG lambda chain V-II region NIG-84.
Y Homo sapiens (Human).
Y Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Y Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Y NCBI_TaxID=9606;
[1]
SEQUENCE.
MEDLINE=85204383; PubMed=3922791;
Tonoike H., Kametani T., Hoshi A., Shinoda T., Isobe T.;
"Amino acid sequence of an amyloidogenic Bence Jones protein in
myeloma-associated systemic amyloidosis.",
FEBS Lett. 185:139-141(1985).
-1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN ISOLATED FROM AN
INDIVIDUAL WITH MYELOMA-ASSOCIATED SYSTEMIC AMYLOIDOSIS.
-1- SIMILARITY: Contains 1 immunoglobulin-like domain.
Y PIR; A01971; L2HUNG.
Y HSP; P01709; 2MCG.
Y GO; GO:0005576; C:extracellular; NAS.
Y GO; GO:0003823; F:antigen binding activity; NAS.
Y GO; GO:0006955; P:immune response; NAS.
Y InterPro; IPR007110; Ig-like.
Y InterPro; IPR003006; Ig_MHC.
Y InterPro; IPR003596; Ig_v.
Y Pfam; PF00047; Ig; 1.
Y SMART; SM00406; IGV; 1.
Y PROSITE; PS00835; IG_LIKE; 1.
Y Immunoglobulin V region; Amyloid; Bence-Jones protein.
Y DOMAIN 1 102 IG-LIKE.
Y DISULFID 22 90 BY SIMILARITY.
Y NON_TER 112 112
Y SEQUENCE 112 AA; 11581 MW; 989FEF363AE1B4F3 CRC64;
Query Match 27.5%; Score 180.5; DB 1; Length 112;
Best Local Similarity 43.9%; Pred. No. 3.3e-12;
Matches 43; Conservative 16; Mismatches 32; Indels 7; Gaps 3;
Y 19 QTVLAQLDALLVFPQVAQLSCTLSFQHVIRDYGVSWYQQRAGSAPRYLYYSEEDH 78
D 1 QSALTQPSVSGSFGQSITISCTGTTSDVGGYDF-VSWYQQHPGKAPKLLIY----DVNS 55
Y 79 RPADIPDRFSAKDEAHNACVLITSPVQEDDADYVC 116
D 56 RPSGISNRFSGK--SGNTASLTISGLQAEADYVC 91
RESULT 15
LV0A HUMAN STANDARD; PRT; 117 AA.
ID LV0A_HUMAN
AC P04211;
Y 20-MAR-1987 (Rel. 04, Created)
Y 20-MAR-1987 (Rel. 04, Last sequence update)

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Search completed: February 9, 2004, 12:47:04  
Job time : 11.6351 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

M protein - protein search, using sw model

run on: February 9, 2004, 12:38:06 ; Search time 38.7838 seconds  
(without alignments)  
818.395 Million cell updates/sec

Title: US-09-981-876-200

Perfect score: 657

Sequence: 1 MACRCLSLFMGTFLSVST.....PVQPEDDADYCVSGVGFSP 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:\*

1: sp\_arChea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mbc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_virus:\*

16: sp\_bacteriap:\*

17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	430	65.4	123	11	Q61243	Q61243 mus musculus
2	199	30.3	112	4	Q96JD1	Q96JD1 homo sapien
3	199	30.3	135	4	Q9H5Z4	Q9H5Z4 homo sapien
4	194	29.5	112	4	Q96JD2	Q96JD2 homo sapien
5	191.5	29.1	116	4	Q96JD0	Q96JD0 homo sapien
6	190.5	29.0	236	4	Q96E61	Q96E61 homo sapien
7	187	28.5	237	4	Q9WTU6	Q9WTU6 homo sapien
8	184.5	28.1	237	4	Q9WUK4	Q9WUK4 homo sapien
9	182	27.7	240	4	Q9WUK3	Q9WUK3 homo sapien
10	178	27.1	234	4	Q9N355	Q9N355 homo sapien
11	174	26.5	235	11	Q99M11	Q99M11 mus musculus
12	171	26.0	107	4	Q9NSD6	Q9NSD6 homo sapien
13	170	25.9	233	4	Q9TBC9	Q9TBC9 homo sapien
14	169.5	25.8	236	4	Q9NEJ1	Q9NEJ1 homo sapien
15	168	25.6	108	4	Q9G5B0	Q9G5B0 homo sapien
16	167.5	25.5	109	4	Q9UL86	Q9UL86 homo sapien

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17 166 25.3 100 6 077624
18 166 25.3 110 4 08TE63
19 164 25.0 233 4 096I69
20 164 25.0 233 4 08N5F4
21 159.5 24.3 109 4 08UL78
22 158.5 24.1 105 4 08RVJ6
23 154.5 23.5 132 4 08TBD0
24 154 23.4 107 4 09UL82
25 151 23.0 101 4 08IZD8
26 140.5 21.4 108 4 09UL83
27 140.5 21.4 234 4 08NEK1
28 136.5 20.7 484 11 08VEA0
29 136 20.8 129 11 08VDE2
30 135.5 20.6 109 4 09UL85
31 135.5 20.6 113 11 08CGS1
32 134 20.4 97 4 043234
33 134 20.4 107 11 09ER29
34 134 20.4 235 11 091WI2
35 133.5 20.3 93 4 09UL76
36 131 19.9 239 4 08NEK0
37 130.5 19.9 99 11 09UL74
38 130.5 19.9 108 4 09UL79
39 129 19.6 134 11 08VDD0
40 128 19.5 107 4 096SA9
41 128 19.5 108 4 09UL77
42 126.5 19.3 521 4 08N4Y9
43 126 19.2 278 11 0921K1
44 126 19.2 468 11 099L31
45 125.5 19.1 111 11 0920E9

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#### ALIGNMENTS

#### RESULT 1

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ID Q61243 PRELIMINARY; PRT; 123 AA.
AC Q61243;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE SHS20 protein precursor (Pre-B lymphocyte gene 3).
GN VPRES3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_taxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=93259124; PubMed=8491176;
RA Shirasawa T., Ohnishi K., Hagiwara S., Shigemoto K., Takebe Y.,
RA Rajewsky K., Takemori T.;
RT "A novel gene product associated with mu chains in immature B cells.";
RL EMBL J. 12:1827-1834(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Stomach;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okfeli D., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

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RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weiss C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kotsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; D13208; BAA02495.1; -.
DR EMBL; AK008794; BAB25899.1; -.
DR HSSP; P01709; 2MCG.
DR MGD; MGI:98938; Vprb3.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT CHAIN 20..123
FT PROTEIN 8HS20 PROTEIN.
SQ SEQUENCE 123 AA; 13400 MW; 2A1AD371D1CEE98F CRC64;

Query Match 65.4%; Score 430; DB 11; Length 123;
Best Local Similarity 66.1%; Pred. No. 5.7e-41;
Matches 82; Conservative 14; Mismatches 26; Indels 2; Gaps 2;

QY 1 MAC-RCLFLLMGFLSVQVQLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQQ 59
DB 1 MACPGCLPFLLLTGTFVAVFQPTLTQPDASFVPGQDAHLSTINSQATAGDIGVSWYQQ 60
QY 60 RAGSAPRYLLYRSBEDHRRPADIPDRFSAKDAHNACVLTISPVQEDDADYICVGY 119
DB 61 QGSSAP-HLLYYABEHRPADIPDRFSATVDAHNACILITISVLPEDDADYFCGSI 119
QY 120 GFSP 123
DB 120 TREP 123

RESULT 2
Q96JD1 PRELIMINARY; PRT; 112 AA.
ID Q96JD1
AC Q96JD1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Amyloid lambda 6 light chain variable region PIP (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Bone marrow;
RC Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;
RT "Amyloid lambda 6 light chain variable region PIP";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF267874; AAK58586.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 112
SQ SEQUENCE 112 AA; 12047 MW; 0D3885AC23567B9F CRC64;

Query Match 30.3%; Score 199; DB 4; Length 112;
Best Local Similarity 44.2%; Pred. No. 8.5e-15;
Matches 42; Conservative 17; Mismatches 30; Indels 6; Gaps 2;

QY 21 VLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQAGSAPRYLLYRSBEDHRRP 80
DB 3 MLTQFVSVPSPGKLTITISCTRSSG--SIASNYVQVQORPGSAPTIVY----EDNQRP 56
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QY 81 ADIPDRFSAKDAHNACVLTISPVQPEDDADYIC 115
DB 57 SGVDFRFGSSIDSSNSASLTISGLKTEADYIC 91

RESULT 3
Q9HSZ4 PRELIMINARY; PRT; 135 AA.
ID Q9HSZ4
AC Q9HSZ4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ22755.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Ileal mucosa;
RC Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
RA Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
RA Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y.,
RA Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,
RA Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK026408; BAB15473.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 135 AA; 14780 MW; 652492DED930F401 CRC64;

Query Match 30.3%; Score 199; DB 4; Length 135;
Best Local Similarity 45.3%; Pred. No. 1.1e-14;
Matches 34; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

QY 48 TIRDYGVSWYQORAGSAPRYLLYRSBEDHRRPADIPDRFSAKDAHNACVLTISPVQ 107
DB 7 SVGDFTIRWYQKFGNPRVLYHSDSNKQSGVPSRFGSGNSANAGILIRISGLQ 66
QY 108 EDDADYICVGVGYFS 122
DB 67 EDEADYICGTWHSNS 81

RESULT 4
Q96JD2 PRELIMINARY; PRT; 112 AA.
ID Q96JD2
AC Q96JD2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Amyloid lambda 6 light chain variable region NEG (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Bone marrow;
RC Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;
RT "Amyloid lambda 6 light chain variable region NEG";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF267873; AAK58585.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
```

```
R PROSITE; PS50835; IG LIKE; 1.
T NON_TER 1
Q SEQUENCE 112 112
Q SEQUENCE 112 AA; 11906 MW; 080B4B37E2360B06 CRC64;

Query Match
Best Local Similarity 29.5%; Score 194; DB 4; Length 112;
Matches 41; Conservative 16; Mismatches 32; Indels 6; Gaps 2;

Y 21 VLAQDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYYRSEE 80
b 3 MLTQPHSVSESGKVTITISCTGSSGR--IASNSVQWYQORAGSAPRYLLYYRSEE 56
Y 81 ADIPRFSNAKDEAHNACVLTISPQVEDDADYYC 115
b 57 SGVPRFSGSIDSSNSASLTISGLMTEDEADYYC 91

RESULT 5
96JDU0 PRELIMINARY; PRT; 116 AA.
D Q96JDU0
C Q96JDU0;
T 01-DEC-2001 (TrEMBLrel. 19, Created)
T 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
T 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
E Amyloid lambda 6 light chain variable region SAR (Fragment).
S Homo sapiens (Human).
X Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
X Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
X NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
T TISSUE=Bone marrow;
T Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;
T "Amyloid lambda 6 light chain variable region SAR.";
T Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
R EMBL; AF267875; AKS58587.1;
R InterPro; IPR007110; IG LIKE.
R InterPro; IPR003006; IG MHC.
R Pfam; PF00047; IG 1.
R SMART; SM00406; IG 1.
R PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 116 AA; 12284 MW; F7B0B9F49FAB369E CRC64;

Query Match
Best Local Similarity 29.1%; Score 191.5; DB 4; Length 116;
Matches 43; Conservative 19; Mismatches 30; Indels 11; Gaps 4;

Y 21 VLAQDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYYRSEE 80
b 3 MLTQPHSVSESGKVTITISCTGSSGSA-TNY-VQWYQLRPSGAPTIVY----EDNQEP 56
Y 81 ADIPRFSNAKDEAHNACVLTISPQVEDDADYYC-----SVG 118
b 57 SGVPRFSGSIDSSNSASLTISGLMTEDEADYYCQSYDSSIG 99

RESULT 6
96E61 PRELIMINARY; PRT; 236 AA.
D Q96E61
C Q96E61;
T 01-DEC-2001 (TrEMBLrel. 19, Created)
T 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
T 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
X Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
X Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
X NCBI_TaxID=9606;
[1]
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RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012876; AAH12876.1;
DR InterPro; IPR007110; IG LIKE.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG V.
DR Pfam; PF00047; IG 2.
DR SMART; SM00406; IG 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 24712 MW; 7EC9FB3622FED957 CRC64;

Query Match
Best Local Similarity 29.0%; Score 190.5; DB 4; Length 236;
Matches 42; Conservative 21; Mismatches 30; Indels 7; Gaps 3;

QY 16 SVSOTVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYYRSEE 75
Db 17 SWAQSVLAQPPSVGAPGQVTITISCTGSSNIG-AGYAVHWYQOPGAPKVLIIY----G 71
QY 76 DHRPADIPRFSNAKDEAHNACVLTISPQVEDDADYYC 115
Db 72 NYNRPSGVDPFRSGSK--SGTSASLAITGLQAEDEADYYC 109

RESULT 7
Q8WTU6 PRELIMINARY; PRT; 237 AA.
D Q8WTU6
AC Q8WTU6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
X Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
X Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
X NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RC TISSUE=Tonsil;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022098; AAH22098.1;
DR InterPro; IPR007110; IG LIKE.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG V.
DR Pfam; PF00047; IG 2.
DR SMART; SM00406; IG 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 237 AA; 24884 MW; B6CF371E75396E88 CRC64;

Query Match
Best Local Similarity 41.1%; Score 187; DB 4; Length 237;
Matches 44; Conservative 20; Mismatches 35; Indels 8; Gaps 4;

QY 16 SVSOTVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYYRSEE 75
Db 17 SWAQSVLTQPPSVGAPGQVTITISCTGSSNIG-AGYDVHWYQOLPGTAPKLIYGN-- 73
QY 76 DHRPADIPRFSNAKDEAHNACVLTISPQVEDDADYYC 122
Db 74 --NRPSGVDPFRSGSK--SGTSASLAITGLQAEDEADYYCQ--SYDYS 115

RESULT 8
Q8WUK4 PRELIMINARY; PRT; 237 AA.
D Q8WUK4
AC Q8WUK4;
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01-MAR-2002 (TreeBrel. 20, Created)  
01-MAR-2002 (TreeBrel. 20, Last sequence update)  
01-MAR-2003 (TreeBrel. 23, Last annotation update)  
DE Hypothetical protein.  
DE Homo sapiens (Human).  
DC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
DC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
DN NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Tonsil;  
RA Strausberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC020233; AAH20233.1; -  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; ig; 2; -  
DR Pfam; PF00047; ig; 2; -  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00290; IG\_MHC; 1.  
DR Hypothetical protein.  
KW Hypothetical protein.  
SQ SEQUENCE 237 AA; 24897 MW; 73C7D70B8039D186 CRC64;  
  
Query Match 28.1%; Score 184.5; DB 4; Length 237;  
Best Local Similarity 42.0%; Pred. No. 9.4e-13;  
Matches 42; Conservative 19; Mismatches 32; Indels 7; Gaps 3;  
  
QY 16 SVSQTVAQLDALLVFGQVAQLSCTLSPOHVTIRYGVSWYQQRAGSAPRYLLVYSEE 75  
DB 17 SWAQSGLVTPSPVSGAPQQRVTISCTGSSNIG-AGYDVHWYQQLPGTAPKLLIYGN-- 73  
  
QY 76 DHRHPADIPDRFSAKDGAHNACVLTISPVPQPEDDADYYC 115  
DB 74 --NRPSGVDFRFGSK--SGTFSASLAITGLQAEDADYYC 109  
  
RESULT 9  
Q8WUK3 PRELIMINARY; PRT; 240 AA.  
ID OSWUK3  
AC OSWUK3;  
DT 01-MAR-2002 (TreeBrel. 20, Created)  
DT 01-MAR-2002 (TreeBrel. 20, Last sequence update)  
DT 01-MAR-2003 (TreeBrel. 23, Last annotation update)  
DE Hypothetical protein.  
DE Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
CN NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Tonsil;  
RA Strausberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC020236; AAH20236.1; -  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; ig; 2;  
DR Pfam; PF00047; ig; 2;  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG-LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; 1.  
DR Hypothetical protein.  
KW Hypothetical protein.  
SQ SEQUENCE 240 AA; 25977 MW; 921E47DDCA7259F0 CRC64;  
  
Query Match 27.7%; Score 182; DB 4; Length 240;  
Best Local Similarity 33.9%; Pred. No. 1.8e-12;  
Matches 43; Conservative 24; Mismatches 44; Indels 16; Gaps 4  
  
QY 6 LSFLLMGTFLSV---SQTVLAQLDALLVFGQVAQLSCTLSPOHVTIRYGVSWYQQRAG 62  
DB 4 VSFYLLPFITSTGLCALPVLTPFPASAFGLASIKLTKTCSRHH---SSTIWIYQQRFG 60  
  
QY 63 SAPRYLLYVRSEDHRRPADIPDRFSAKDGAHNACVLTISPVPQPEDDADYYC----- 115

```
R SMART; SM00406; IGV; 1.
R PROSITE; PS00290; IG_MHC; 1.
W Hypothetical protein.
Q SEQUENCE 235 AA; 25403 MW; 39807BFE6782A3FB CRC64;

Query Match
  26.5%; Score 174; DB 11; Length 235;
Best Local Similarity 40.0%; Pred. No. 1.4e-11;
Matches 40; Conservative 16; Mismatches 38; Indels 6; Gaps 2;

Y 16 SVSQTVLAQLDALLVFPQVQAQLSCTLSPPQHVITRDYGVSWYQORAGSAPRYLLYRSEEDHH 75
b 17 SCAQLVLTQSSVSTSLGTAKLPKASTGN--IGDSVYNNYQVMGRSPINMIY-----G 70
Y 76 DHRPADIPDRFSAKDEAHNACVLTISPVPQEDDADYYC 115
b 71 DDLRPSGVSDRFGSIDSSNSAFLTIQNVQADDEADYYC 110

RESULT 12
Q8NEJ1 PRELIMINARY; PRT; 107 AA.
ID Q8NEJ1
AC Q8NEJ1
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Hypothetical protein (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=Lymphocytes;
LA Hohmann A.;
IL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
JR EMBL; I43092; AAA69746.2; --
JR HSP; P01709; 2MCG.
JR InterPro; IPR007110; IG-like.
JR InterPro; IPR003006; IG_MHC.
JR InterPro; IPR003596; IG_v.
JR Pfam; PF00047; IG; 1.
JR SMART; SM00406; IGV; 1.
JR PROSITE; PS50835; IG_LIKE; 1.
JT NON_TER
FT NON_TER 107
SQ SEQUENCE 107 AA; 11306 MW; A2B04B37187A5F00 CRC64;

Query Match
  26.0%; Score 171; DB 4; Length 107;
Best Local Similarity 40.0%; Pred. No. 1.2e-11;
Matches 38; Conservative 18; Mismatches 29; Indels 10; Gaps 3;

Y 22 LAQLDALLVFPQVQAQLSCTLSPPQHVITRDYGVSWYQORAGSAPRYLLYRSEEDHHPA 81
b 2 LTQDPVSWVALGQVTRITC-----QGSLSRYASWYQKPGQAPVLVIYK-----NNRPS 53
Y 82 DIPRFSAAKDEAHNACVLTISPVPQEDDADYYCS 116
b 54 GIPDRFGS--SSGNWASLTITGAQADEADYYCN 86

RESULT 13
Q8TBC9 PRELIMINARY; PRT; 233 AA.
ID Q8TBC9
AC Q8TBC9
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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SEQUENCE FROM N.A.
RP TISSUE=B-Cell;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; SC022823; AAH22823.1; --
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 233 AA; 24867 MW; 367411BD6F4DF92 CRC64;

Query Match
  25.9%; Score 170; DB 4; Length 233;
Best Local Similarity 40.2%; Pred. No. 4.1e-11;
Matches 39; Conservative 17; Mismatches 25; Indels 16; Gaps 4;

Y 22 LAQLDALLVFPQVQAQLSCT--LSPQHVITRDYGVSWYQORAGSAPRYLLYRSEEDHH 78
b 23 LTQPPSVSVSPQTRITCSGDALPKQY-----AYWYQKPGQAPVLVIY---KDN 71
Y 79 RPADIPDRFSAKDEAHNACVLTISPVPQEDDADYYC 115
b 72 RPSGIPERFGS--SSGTTVTITISGVQAEDEADYYC 106

RESULT 14
Q8NEJ1 PRELIMINARY; PRT; 236 AA.
ID Q8NEJ1
AC Q8NEJ1;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RP TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030984; AAH30984.1; --
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25024 MW; 1703B77942630E08 CRC64;

Query Match
  25.8%; Score 169.5; DB 4; Length 236;
Best Local Similarity 40.4%; Pred. No. 4.7e-11;
Matches 46; Conservative 23; Mismatches 32; Indels 13; Gaps 6;

Y 8 FLLMGTEL-----SVSQTVLAQLDALLVFPQVQAQLSCTLSPPQHVITRDYGVSWYQORAG 62
b 4 FPLLTLTLTTCAGSNAQSVLTQPPSAGSGPQGRVTITSCGSRNIG-SNY-VYVYQVPG 61
Y 63 SAPRYLLYRSEEDHHPADIPDRFSAKDEAHNACVLTISPVPQEDDADYYCS 116
b 62 TAPK-LIYRNDQ---RPSGVDRFGSK--SGTSASLAISGLRSEADYYTCA 109

RESULT 15
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Q96SBO  
ID Q96SBO PRELIMINARY; PRT; 108 AA.  
AC Q96SBO;  
DT 01-DEC-2001 (TReMBLrel. 19, Created)  
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
DE Anti-streptococcal/anti-myosin immunoglobulin lambda light chain  
DE variable region (fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. PubMed=9712075;  
RX MEDLINE=98375893; Shikman A.R., Ward K.E., Cunningham M.W.;  
RA "Molecular analysis of polyreactive monoclonal antibodies from  
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin  
RT antibody V region genes.";  
RL J. Immunol. 161:2020-2031(1998).  
DR EMBL; U96394; AAB68783.1; -  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
FT NON\_TER 1  
SQ SEQUENCE 108 AA; 11594 MW; F4B5DC478A043F48 CRC64;  
Query Match 25.6%; Score 168; DB 4; Length 108;  
Best Local Similarity 39.8%; Pred. No. 2.7e-11;  
Matches 39; Conservative 21; Mismatches 30; Indels 8; Gaps 4;  
QY 19 QTVLAQLDALLVPPGVAQLSCTISPOHVTIRDYGVSWYQORAGSAPRYLLYYRSEEDHH 78  
Db 1 QSVLTQPPSASGTGQRTVISCSSSSNIG-SNY-VWYQQLPGTAPKLLIY---RNNQ 54  
QY 79 RPADIPDRPSAAKDEAHNACVLTISPVOPEDDADYVCS 116  
Db 55 RPSGVDPDRFSGK--SGTSASLAISGLRSEDEADYCA 90

Search completed: February 9, 2004, 12:48:28  
Job time : 41.7838 secs

GenCore version 5.1.6  
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M protein - protein search, using sw model

un on: February 9, 2004, 08:36:32 ; Search time 38.2297 Seconds  
(without alignments)  
510.685 Million cell updates/sec

file: US-09-981-876-200

effect score: 657

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searched: 1107863 seqs, 158726573 residues

total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Query No.	Score	Match	Length	DB ID	Description
1	657	100.0	123	19	AAW75123	Human secreted pro
2	657	100.0	123	21	AA824061	Human PRO619 prote
3	657	100.0	123	21	AA166855	Membrane-bound pro
4	657	100.0	123	22	AAU12372	Human PRO619 polyp
5	657	100.0	123	22	AA865178	Human PRO619 (UNQ3
6	657	100.0	123	24	ABU56770	Human PRO polypept
7	657	100.0	123	24	ABU57046	Human secreted/tra
8	657	100.0	123	24	ABU59851	Novel secreted and
9	657	100.0	123	24	ABU59071	Novel human secret

10	657	100.0	123	24	ABU59218	Human secreted/tra
11	657	100.0	123	24	ABU59367	Novel human secret
12	657	100.0	123	24	ABU60502	Human secreted/tra
13	657	100.0	123	24	ABU57993	Human PRO polypept
14	657	100.0	123	24	ABU58924	Human secreted/tr
15	657	100.0	123	24	ABU13884	Human PRO619 polyp
16	657	100.0	123	24	ABU10839	Human PRO polypept
17	634	96.5	141	22	AA39690	Human polypeptide
18	582	88.6	113	22	AA41476	Human polypeptide
19	251.5	38.3	182	22	ABG19759	Novel human diagno
20	244.5	37.2	185	22	ABG29426	Novel human diagno
21	236	35.9	256	23	ABP45219	Human Blys binding
22	234	35.6	259	23	ABP45474	Human Blys binding
23	233.5	35.5	237	22	ABG19300	Novel human diagno
24	233.5	35.5	250	22	ABG19303	Novel human diagno
25	232.5	35.4	277	22	ABG19760	Novel human diagno
26	231.5	35.2	142	9	AA83001	V preB-1 protein.
27	227.5	34.6	142	9	AA80288	V preB-1 protein.
28	227	34.6	259	23	ABP45541	Human Blys binding
29	225	34.2	263	23	ABP45267	Human Blys binding
30	217.5	33.1	105	22	ABG22849	Novel human diagno
31	208.5	31.7	542	22	ABG23085	Novel human diagno
32	207.5	31.6	244	22	ABG19289	Novel human diagno
33	206.5	31.4	137	19	AAW57597	Chimeric antibody
34	206.5	31.4	137	20	AAW89641	Human antibody hMB
35	206.5	31.4	137	21	AAW77525	Peptide encoded by
36	206.5	31.4	137	22	AAW67106	Amino acid sequenc
37	206.5	31.4	137	22	AAW63404	Amino acid sequenc
38	206.5	31.4	137	22	AAW63405	Humanised anti-PTH
39	206.5	31.4	137	22	AAW64787	Human joint diseas
40	206.5	31.4	137	23	ABJ95214	Arginogenesis inhib
41	206.5	31.4	138	24	ABJ36673	Human Vpre-B prote
42	205	31.2	125	9	AA80289	Human VSGF-2 relat
43	204	31.1	248	24	ABJ19832	Chimeric antibody
44	203.5	31.0	137	19	AAW57598	Chimeric antibody
45	203.5	31.0	137	19	AAW57595	Chimeric antibody

ALIGNMENTS

RESULT 1  
AAW75123  
ID AAW75123 standard; Protein; 123 AA.  
XX AC AAW75123;  
XX AC AAW75123;  
XX DT 25-MAR-2003 (updated)  
XX DT 28-JAN-1999 (first entry)  
XX DE Human secreted protein encoded by gene 67 clone HRGDF73.  
XX KW Human; secreted protein; fusion protein; gene therapy; protein therapy;  
XX KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
XX KW developmental abnormality; foetal deficiency; blood; allergy; renal;  
XX KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
XX KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
XX KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
XX KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
XX KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
XX OS Homo sapiens.  
XX FN WO9839446-A2.  
XX PD 11-SEP-1998.  
XX PF 06-MAR-1998; 98WO-US04482.  
XX PR 07-MAR-1997; 97US-0038621.  
XX PR 07-MAR-1997; 97US-0040161.  
XX PR 07-MAR-1997; 97US-0040162.  
XX PR 07-MAR-1997; 97US-0040163.



C AAB24061;  
 X 29-JAN-2001 (first entry)  
 X Human PRO619 protein sequence SEQ ID NO:16.  
 X  
 W Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;  
 W proliferation; tumorigenesis; identification; cancer; cytostatic;  
 W neotropic; neuroprotective; anti-inflammatory; immunosuppressive;  
 W immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;  
 W neuronal disorder; glial disorder; astrocytal disorder; angiogenic;  
 W hypothalamic disorder; glandular disorder; macrophagal disorder;  
 W epithelial disorder; stromal disorder; blastocoeleic disorder;  
 W inflammatory disorder; immunologic disorder.  
 X Homo sapiens.  
 X  
 X AAY66655  
 X WO2000053755-A2.  
 X  
 X 14-SEP-2000.  
 X  
 X 06-JAN-2000; 2000WO-US00376.  
 X  
 X 08-MAR-1999; 99WO-US05028.  
 X 02-JUN-1999; 99WO-US12252.  
 X 23-JUN-1999; 99US-0141037.  
 X 07-JUL-1999; 99US-0143048.  
 X 26-JUL-1999; 99US-0145698.  
 X 30-NOV-1999; 99WO-US28313.  
 X 20-DEC-1999; 99WO-US30911.  
 X 05-JAN-2000; 2000WO-US00219.  
 X (GETH ) GENENTECH INC.  
 X  
 X Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;  
 X Watanabe CK, Wood WI;  
 X WPI: 2000-572270/53.  
 X N-PSDB; AAC58371.  
 X  
 X Thirty PRO polynucleotides encoding PRO polypeptides, useful in the  
 X treatment, diagnosis and prevention of cancer -  
 X  
 X Claim 61; Fig 10; 286pp; English.  
 X  
 X The present invention describes an isolated antibody that binds to  
 X one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,  
 X PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,  
 X PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1133, PRO1182, PRO1184,  
 X PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094,  
 X PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell  
 X growth. The PRO polypeptides and nucleotides are useful in the  
 X treatment, diagnosis and prevention of cancer. The antibodies and other  
 X anti-tumour compounds may be used to treat various conditions, including  
 X those characterised by overexpression and/or activation of the amplified  
 X PRO genes. Exemplary conditions or disorders to be treated with such  
 X antibodies and other compounds include benign or malignant tumours  
 X (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,  
 X colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic  
 X carcinomas, sarcomas, glioblastomas, and various head and neck tumours),  
 X leukaemias and lymphoid malignancies, other disorders such as neuronal,  
 X glial, astrocytal, hypothalamic and other glandular, macrophagal,  
 X epithelial, stromal and blastocoeleic disorders, and inflammatory,  
 X angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR  
 X primers and hybridisation probes used in the isolation of the human PRO  
 X sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human  
 X PRO polynucleotide and protein sequences given in the exemplification of  
 X the present invention.  
 X  
 X Sequence 123 AA;  
 X  
 X Query Match 100.0%; Score 657; DB 21; Length 123;  
 X Best Local Similarity 100.0%; Pred. No. 5.9e-65;

Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MACRCISFLMGTSLVSQTVLAQLDALLVPPGVAQLSCTLSPOHVITRDYGVSWYQQR 60  
 DB 1 MACRCISFLMGTSLVSQTVLAQLDALLVPPGVAQLSCTLSPOHVITRDYGVSWYQQR 60  
 QY 61 AGSAPRYLLYRSSEDDHRRPADIDPFRSAKDEAHNACVLTISPVOEDDADYYCSVGYG 120  
 DB 61 AGSAPRYLLYRSSEDDHRRPADIDPFRSAKDEAHNACVLTISPVOEDDADYYCSVGYG 120  
 QY 121 FSP 123  
 DB 121 FSP 123  
 RESULT 3  
 AAY66655  
 ID AAY66655 standard; protein; 123 AA.  
 XX  
 AC AAY66655;  
 XX  
 DT 05-APR-2000 (first entry)  
 XX  
 DE Membrane-bound protein PRO619.  
 XX  
 KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
 KW pharmaceutical; receptor immunoadhesin; gene mapping.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9963088-A2.  
 XX  
 PD 09-DEC-1999.  
 XX  
 PF 02-JUN-1999; 99WO-US12252.  
 XX  
 PR 02-JUN-1998; 98US-0087607.  
 PR 02-JUN-1998; 98US-0087609.  
 PR 02-JUN-1998; 98US-0087759.  
 PR 03-JUN-1998; 98US-0087827.  
 PR 04-JUN-1998; 98US-0088021.  
 PR 04-JUN-1998; 98US-0088025.  
 PR 04-JUN-1998; 98US-0088028.  
 PR 04-JUN-1998; 98US-0088029.  
 PR 04-JUN-1998; 98US-0088030.  
 PR 04-JUN-1998; 98US-0088033.  
 PR 04-JUN-1998; 98US-0088326.  
 PR 05-JUN-1998; 98US-0088167.  
 PR 05-JUN-1998; 98US-0088202.  
 PR 05-JUN-1998; 98US-0088212.  
 PR 05-JUN-1998; 98US-0088217.  
 PR 09-JUN-1998; 98US-0088655.  
 PR 10-JUN-1998; 98US-0088722.  
 PR 10-JUN-1998; 98US-0088730.  
 PR 10-JUN-1998; 98US-0088734.  
 PR 10-JUN-1998; 98US-0088738.  
 PR 10-JUN-1998; 98US-0088740.  
 PR 10-JUN-1998; 98US-0088741.  
 PR 10-JUN-1998; 98US-0088742.  
 PR 10-JUN-1998; 98US-0088810.  
 PR 10-JUN-1998; 98US-0088811.  
 PR 10-JUN-1998; 98US-0088824.  
 PR 10-JUN-1998; 98US-0088825.  
 PR 10-JUN-1998; 98US-0088826.  
 PR 11-JUN-1998; 98US-0088858.  
 PR 11-JUN-1998; 98US-0088861.  
 PR 11-JUN-1998; 98US-0088863.  
 PR 11-JUN-1998; 98US-0088876.  
 PR 12-JUN-1998; 98US-0089090.  
 PR 12-JUN-1998; 98US-0089105.  
 PR 16-JUN-1998; 98US-0089440.  
 PR 16-JUN-1998; 98US-0089512.  
 PR 16-JUN-1998; 98US-0089514.

PR 17-JUN-1998; 98US-0089532.  
PR 17-JUN-1998; 98US-0089536.  
PR 17-JUN-1998; 98US-0089598.  
PR 17-JUN-1998; 98US-0089599.  
PR 17-JUN-1998; 98US-0089600.  
PR 17-JUN-1998; 98US-0089653.  
PR 18-JUN-1998; 98US-0089801.  
PR 18-JUN-1998; 98US-0089907.  
PR 18-JUN-1998; 98US-0089908.  
PR 19-JUN-1998; 98US-0089947.  
PR 19-JUN-1998; 98US-0089948.  
PR 19-JUN-1998; 98US-0089952.  
PR 22-JUN-1998; 98US-0090246.  
PR 22-JUN-1998; 98US-0090252.  
PR 22-JUN-1998; 98US-0090254.  
PR 23-JUN-1998; 98US-0090349.  
PR 23-JUN-1998; 98US-0090355.  
PR 24-JUN-1998; 98US-0090429.  
PR 24-JUN-1998; 98US-0090431.  
PR 24-JUN-1998; 98US-0090435.  
PR 24-JUN-1998; 98US-0090444.  
PR 24-JUN-1998; 98US-0090445.  
PR 24-JUN-1998; 98US-0090461.  
PR 24-JUN-1998; 98US-0090472.  
PR 24-JUN-1998; 98US-0090535.  
PR 24-JUN-1998; 98US-0090538.  
PR 24-JUN-1998; 98US-0090540.  
PR 24-JUN-1998; 98US-0090557.  
PR 25-JUN-1998; 98US-0090676.  
PR 25-JUN-1998; 98US-0090678.  
PR 25-JUN-1998; 98US-0090688.  
PR 25-JUN-1998; 98US-0090690.  
PR 25-JUN-1998; 98US-0090691.  
PR 25-JUN-1998; 98US-0090694.  
PR 25-JUN-1998; 98US-0090695.  
PR 25-JUN-1998; 98US-0090696.  
PR 26-JUN-1998; 98US-0090862.  
PR 26-JUN-1998; 98US-0090863.  
PR 01-JUL-1998; 98US-0091358.  
PR 01-JUL-1998; 98US-0091360.  
PR 01-JUL-1998; 98US-0091544.  
PR 02-JUL-1998; 98US-0091478.  
PR 02-JUL-1998; 98US-0091486.  
PR 02-JUL-1998; 98US-0091519.  
PR 02-JUL-1998; 98US-0091626.  
PR 02-JUL-1998; 98US-0091628.  
PR 02-JUL-1998; 98US-0091633.  
PR 02-JUL-1998; 98US-0091646.  
PR 02-JUL-1998; 98US-0091673.  
PR 07-JUL-1998; 98US-0091978.  
PR 07-JUL-1998; 98US-0091982.  
PR 09-JUL-1998; 98US-0092182.  
PR 10-JUL-1998; 98US-0092472.  
PR 20-JUL-1998; 98US-0093339.  
PR 30-JUL-1998; 98US-0094651.  
PR 04-AUG-1998; 98US-0095282.  
PR 04-AUG-1998; 98US-0095285.  
PR 04-AUG-1998; 98US-0095301.  
PR 04-AUG-1998; 98US-0095302.  
PR 04-AUG-1998; 98US-0095318.  
PR 04-AUG-1998; 98US-0095321.  
PR 04-AUG-1998; 98US-0095325.  
PR 10-AUG-1998; 98US-0095916.  
PR 10-AUG-1998; 98US-0095929.  
PR 10-AUG-1998; 98US-0096012.  
PR 11-AUG-1998; 98US-0096143.  
PR 11-AUG-1998; 98US-0096146.  
PR 12-AUG-1998; 98US-0096329.  
PR 17-AUG-1998; 98US-0096757.  
PR 17-AUG-1998; 98US-0096766.  
PR 17-AUG-1998; 98US-0096768.  
PR 17-AUG-1998; 98US-0096773.  
PR 17-AUG-1998; 98US-0096791.

PR 17-AUG-1998; 98US-0096867.  
PR 17-AUG-1998; 98US-0096891.  
PR 17-AUG-1998; 98US-0096894.  
PR 17-AUG-1998; 98US-0096895.  
PR 17-AUG-1998; 98US-0096897.  
PR 18-AUG-1998; 98US-0096949.  
PR 18-AUG-1998; 98US-0096950.  
PR 18-AUG-1998; 98US-0096959.  
PR 18-AUG-1998; 98US-0096960.  
PR 18-AUG-1998; 98US-0097022.  
PR 19-AUG-1998; 98US-0097141.  
PR 20-AUG-1998; 98US-0097218.  
PR 24-AUG-1998; 98US-0097661.  
PR 26-AUG-1998; 98US-0097951.  
PR 26-AUG-1998; 98US-0097952.  
PR 26-AUG-1998; 98US-0097954.  
PR 26-AUG-1998; 98US-0097955.  
PR 26-AUG-1998; 98US-0097971.  
PR 26-AUG-1998; 98US-0097974.  
PR 26-AUG-1998; 98US-0097978.  
PR 26-AUG-1998; 98US-0097979.  
PR 26-AUG-1998; 98US-0097986.  
PR 26-AUG-1998; 98US-0098014.  
PR 31-AUG-1998; 98US-0098525.  
PR 16-SEP-1998; 98US-0100634.  
PR 12-JAN-1999; 99US-0115565.  
XX (GETH ) GENENTECH INC.  
PA Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
PI Wood WI, Yuan J;  
XX WPI; 2000-072883/06.  
DR N-PSDB; AAZ64983.  
XX  
PT Membrane-bound proteins and related nucleotide sequences  
PS claim 12; Fig 68; 822pp; English.  
XX  
CC The invention provides membrane-bound PRO polypeptides and  
CC polynucleotides encoding them. The PRO sequences of the invention were  
CC identified based on extracellular domain homology screening. The PRO  
CC sequences have homology with proteins including LDL receptors, TIE  
CC ligands and various enzymes. The membrane-bound proteins and receptor  
CC molecules are useful as pharmaceutical and diagnostic agents to block  
CC immunoadhesins, for instance, can be used as therapeutic agents to block  
CC receptor-ligand interactions. The membrane-bound proteins can also be  
CC employed for screening of potential peptide or small molecule inhibitors  
CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
CC are useful as hybridization probes in chromosome and gene mapping and in  
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences  
CC will also be useful for the preparation of PRO polypeptides, especially  
CC by recombinant techniques.  
XX  
SQ Sequence 123 AA;  
Query Match 100.0%; Score 657; DB 21; Length 123;  
Best Local Similarity 100.0%; Pred. No. 5,9e+65;  
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MACRCLSFLLMGTFSLVSQTVLAQLDALLVFPQVQAQLSCTLSPOHVTIRDYGVSYQQR 60  
DB 1 MACRCLSFLLMGTFSLVSQTVLAQLDALLVFPQVQAQLSCTLSPOHVTIRDYGVSYQQR 60  
QY 61 AGSAPRYLLYRSEEDHHRPADIDRFSAKDEAHNAACVLTISPQVEDDADYYCSVGYG 120  
DB 61 AGSAPRYLLYRSEEDHHRPADIDRFSAKDEAHNAACVLTISPQVEDDADYYCSVGYG 120  
QY 121 FSP 123  
DB 121 FSP 123

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RESULT 4
ID AAU12372 standard; Protein; 123 AA.
CX
AC AAU12372;
CX
JT 24-OCT-2001 (first entry)
CX
DE Human PRO619 polypeptide sequence.
CX
CW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
CW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
CW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
CX adipocyte; A-peptide; factor VIIA; gene therapy.
CX
DS Homo sapiens.
CX
EN WO2000140466-A2.
CX
PD 07-JUN-2001.
CX
PF 01-DEC-2000; 2000WO-US32678.
CX
PR 01-DEC-1999; 99WO-US28301.
CX
PR 01-DEC-1999; 99WO-US28634.
CX
PR 02-DEC-1999; 99WO-US28531.
CX
PR 02-DEC-1999; 99WO-US28564.
CX
PR 02-DEC-1999; 99WO-US28565.
CX
PR 09-DEC-1999; 99US-0170262.
CX
PR 16-DEC-1999; 99WO-US30095.
CX
PR 20-DEC-1999; 99WO-US30911.
CX
PR 20-DEC-1999; 99WO-US30999.
CX
PR 30-DEC-1999; 99WO-US31243.
CX
PR 06-JAN-2000; 2000WO-US00277.
CX
PR 06-JAN-2000; 2000WO-US00376.
CX
PR 11-FEB-2000; 2000WO-US03565.
CX
PR 18-FEB-2000; 2000WO-US04341.
CX
PR 18-FEB-2000; 2000WO-US04342.
CX
PR 22-FEB-2000; 2000WO-US04414.
CX
PR 24-FEB-2000; 2000WO-US04914.
CX
PR 24-FEB-2000; 2000WO-US05004.
CX
PR 01-MAR-2000; 2000WO-US05601.
CX
PR 20-MAR-2000; 2000WO-US07377.
CX
PR 21-MAR-2000; 2000WO-US07532.
CX
PR 30-MAR-2000; 2000WO-US08439.
CX
PR 17-MAY-2000; 2000WO-US13705.
CX
PR 22-MAY-2000; 2000WO-US14042.
CX
PR 30-MAY-2000; 2000WO-US14941.
CX
PR 02-JUN-2000; 2000WO-US15264.
CX
PR 10-NOV-2000; 2000WO-US30873.
CX
PA (GETH) GENENTECH INC.
CX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
CX
DR WPI; 2001-408281/43.
DR N-PSDB; AAS21444.
CX
PT Isolated, secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing
PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT lung, breast, prostate, cervical.
CX
PS Claim 12; Fig 402; 813pp; English.
CX
AAU12172-AAU12446 represent novel human secretory and transmembrane
CX PRO polypeptides. The PRO polypeptides are useful to detect other
CX PRO polypeptides, to link bioactive molecules to cells expressing
CX PRO polypeptides, to modulate biological activities of cells expressing
CX PRO polypeptides, and to detect the presence of mammalian lung, colon,
CX breast, prostate, rectal, cervical or liver tumours by comparing PRO
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CC polypeptide expression in a cell sample to that in a control sample.
CC Some of the 275 sequences are thus useful to stimulate the release of
CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
CC proliferation or differentiation of chondrocytes, the proliferation or
CC gene expression in pericyte cells, the release of proteoglycans from
CC cartilage, the proliferation of inner ear utricular supporting cells or
CC of T-lymphocytes, the release of a cytokine from peripheral blood
CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
CC to factor VIIA. The PRO polypeptides can be used in assays to identify
CC molecules involved in binding interactions. The polynucleotides encoding
CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CX transgenic or knock out animals and can be used in gene therapy.
CX
SQ Sequence 123 AA;
Query Match 100.0%; Score 657; DB 22; Length 123;
Best Local Similarity 100.0%; Pred. No. 5.9e-65;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MACRCLSFLLMGTFLLSVQTVLAQLDALLVFPQVAQLSCTLSPOHVTIRYGVSWYQQR 60
DB 1 MACRCLSFLLMGTFLLSVQTVLAQLDALLVFPQVAQLSCTLSPOHVTIRYGVSWYQQR 60
QY 61 AGSAPRYLLYRSEEDHHRPADIPORFSAKDEAHNACVLTISPQPEDDADYCVGVG 120
DB 61 AGSAPRYLLYRSEEDHHRPADIPORFSAKDEAHNACVLTISPQPEDDADYCVGVG 120
QY 121 FSP 123
DB 121 FSP 123
RESULT 5
AAB65178
ID AAB65178 standard; Protein; 123 AA.
CX
AC AAB65178;
CX
DT 02-APR-2001 (first entry)
CX
DE Human PRO619 (UNQ355) protein sequence SEQ ID NO:117.
CX
KW Human; secreted and transmembrane protein; PRO; cytostatic;
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay.
CX
OS Homo sapiens.
CX
FN WO200073454-A1.
CX
PD 07-DEC-2000.
CX
PF 30-MAR-2000; 2000WO-US08439.
CX
PR 02-JUN-1999; 99WO-US12252.
CX
PR 23-JUN-1999; 99US-0141037.
CX
PR 07-JUL-1999; 99US-0143048.
CX
PR 20-JUL-1999; 99US-0144758.
CX
PR 26-JUL-1999; 99US-0145698.
CX
PR 28-JUL-1999; 99US-0146222.
CX
PR 17-AUG-1999; 99US-0149396.
CX
PR 15-SEP-1999; 99WO-US21090.
CX
PR 08-OCT-1999; 99US-0158663.
CX
PR 30-NOV-1999; 99WO-US28313.
CX
PR 01-DEC-1999; 99WO-US28301.
CX
PR 16-DEC-1999; 99WO-US30095.
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PR 20-DEC-1999; 99WO-US30911.
CX
PR 05-JAN-2000; 2000WO-US00219.
CX
PR 06-JAN-2000; 2000WO-US00376.
CX
PR 11-FEB-2000; 2000WO-US03565.
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PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 02-MAR-2000; 2000WO-US05004.  
PR 15-MAR-2000; 2000WO-US05841.  
PR 20-MAR-2000; 2000WO-US07377.  
XX (GETH ) GENENTECH INC.  
PA  
XX PI Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL,  
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,  
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF,  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
PI Zhang Z;  
XX WPI; 2001-032160/04.  
DR N-PSDB; AAF44129.  
XX  
XX PRO polynucleotides used to produce polypeptides used to target  
PT bioactive molecules such as toxins, radiolabels or antibodies, to  
PT specific cells, to cause targeted cell death -  
PT  
PS Claim 12; Fig 68; 935pp; English.  
XX  
CC The present invention describes human secreted and transmembrane PRO  
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins  
CC can be used for targeted delivery of bioactive molecules, such as  
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
CC sequences, and their fragments, can be used as hybridisation probes, in  
CC chromosomal and gene mapping, and in the generation of anti-sense RNA  
CC and DNA. They may also be used to produce transgenic animals which are  
CC used to develop and screen therapeutically useful reagents. The PRO  
CC nucleotide and protein sequence can be used for tissue typing and in  
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used  
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
CC AAB55154 to AAB65300 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.  
XX  
SQ Sequence 123 AA;  
Query Match 100.0%; Score 657; DB 22; Length 123;  
Best Local Similarity 100.0%; Pred. No. 5,9e-65;  
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MACRCLSFLLMGTFLVSQTVLAQLDALLVFPQVQVQLSCTLSPOHVTIRDYGVSNYQQR 60  
DB 1 MACRCLSFLLMGTFLVSQTVLAQLDALLVFPQVQVQLSCTLSPOHVTIRDYGVSNYQQR 60  
QY 61 AGSAPRYLLYRSEEDHRRPADIPRFSAAKDEAHNACVLTISPVQEDDADYYCVSYG 120  
DB 61 AGSAPRYLLYRSEEDHRRPADIPRFSAAKDEAHNACVLTISPVQEDDADYYCVSYG 120  
QY 121 FSP 123  
DB 121 FSP 123  
RESULT 6  
ABU66770  
ID ABU66770 standard; Protein; 123 AA.  
XX  
XX AC ABU66770;  
XX  
XX 23-MAY-2003 (first entry)  
XX Human PRO polypeptide #201.  
XX Human; PRO polypeptide; secreted and transmembrane protein;  
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;  
KW differentiation; chondrocyte; tumour; genetic disorder;  
KW cytostatic.

XX OS Homo sapiens.  
XX PN US2003036180-A1.  
XX PD 20-FEB-2003.  
XX  
XX 09-MAY-2002; 2002US-0143114.  
XX  
XX 31-MAR-1997; 97WO-US05230.  
XX 12-JUN-1998; 98WO-US12456.  
XX 14-JUL-1998; 98WO-US14552.  
XX 28-AUG-1998; 98WO-US17888.  
XX 10-SEP-1998; 98WO-US18824.  
XX 14-SEP-1998; 98WO-US19093.  
XX 14-SEP-1998; 98WO-US19094.  
XX 14-SEP-1998; 98WO-US19177.  
XX 16-SEP-1998; 98WO-US19330.  
XX 17-SEP-1998; 98WO-US19437.  
XX 07-OCT-1998; 98WO-US21141.  
XX 29-OCT-1998; 98WO-US22991.  
XX 29-OCT-1998; 98WO-US22992.  
XX 20-NOV-1998; 98WO-US24855.  
XX 01-DEC-1998; 98WO-US25108.  
XX 05-JAN-1999; 99WO-US00106.  
XX 08-MAR-1999; 99WO-US05028.  
XX 10-MAR-1999; 99WO-US05190.  
XX 20-APR-1999; 99WO-US08615.  
XX 14-MAY-1999; 99WO-US10733.  
XX 02-JUN-1999; 99WO-US12252.  
XX 01-SEP-1999; 99WO-US20111.  
XX 08-SEP-1999; 99WO-US20594.  
XX 13-SEP-1999; 99WO-US20944.  
XX 15-SEP-1999; 99WO-US21090.  
XX 15-SEP-1999; 99WO-US21547.  
XX 05-OCT-1999; 99WO-US23089.  
XX 29-NOV-1999; 99WO-US28214.  
XX 30-NOV-1999; 99WO-US28313.  
XX 30-NOV-1999; 99WO-US28409.  
XX 01-DEC-1999; 99WO-US28301.  
XX 01-DEC-1999; 99WO-US28624.  
XX 02-DEC-1999; 99WO-US28551.  
XX 02-DEC-1999; 99WO-US28564.  
XX 16-DEC-1999; 99WO-US30095.  
XX 20-DEC-1999; 99WO-US30911.  
XX 20-DEC-1999; 99WO-US30959.  
XX 22-DEC-1999; 99WO-US30720.  
XX 30-DEC-1999; 99WO-US31243.  
XX 30-DEC-1999; 99WO-US31274.  
XX 05-JAN-2000; 2000WO-US00219.  
XX 06-JAN-2000; 2000WO-US00277.  
XX 11-FEB-2000; 2000WO-US00376.  
XX 18-FEB-2000; 2000WO-US03565.  
XX 18-FEB-2000; 2000WO-US04341.  
XX 22-FEB-2000; 2000WO-US04342.  
XX 24-FEB-2000; 2000WO-US04414.  
XX 24-FEB-2000; 2000WO-US04914.  
XX 01-MAR-2000; 2000WO-US05601.  
XX 02-MAR-2000; 2000WO-US05746.  
XX 02-MAR-2000; 2000WO-US05841.  
XX 10-MAR-2000; 2000WO-US06319.  
XX 15-MAR-2000; 2000WO-US06884.  
XX 20-MAR-2000; 2000WO-US07377.  
XX 21-MAR-2000; 2000WO-US07532.  
XX 30-MAR-2000; 2000WO-US08439.  
XX 17-MAY-2000; 2000WO-US13705.  
XX 22-MAY-2000; 2000WO-US14042.  
XX 30-MAY-2000; 2000WO-US14941.  
XX 02-JUN-2000; 2000WO-US15264.  
XX 28-JUL-2000; 2000WO-US20710.  
XX 11-AUG-2000; 2000WO-US22031.

23-AUG-2000; 2000WO-US23522.  
24-AUG-2000; 2000WO-US23328.  
08-NOV-2000; 2000WO-US30952.  
10-NOV-2000; 2000WO-US30873.  
01-DEC-2000; 2000WO-US32678.  
20-DEC-2000; 2000WO-US34956.  
28-FEB-2001; 2001WO-US06520.  
01-MAR-2001; 2001WO-US06666.  
25-MAY-2001; 2001WO-US17092.  
01-JUN-2001; 2001WO-US17800.  
20-JUN-2001; 2001WO-US19692.  
22-JUN-2001; 2001WO-US20116.  
29-JUN-2001; 2001WO-US21066.  
09-JUL-2001; 2001WO-US21735.  
20-DEC-2000; 2000US-074259.  
28-FEB-2001; 2001US-0796498.  
09-MAR-2001; 2001US-0802706.  
14-MAR-2001; 2001US-0808689.  
05-APR-2001; 2001US-0816744.  
22-MAR-2001; 2001US-0828366.  
10-MAY-2001; 2001US-0854208.  
10-MAY-2001; 2001US-0854280.  
18-MAY-2001; 2001US-0860216.  
25-MAY-2001; 2001US-0866028.  
01-JUN-2001; 2001US-0872035.  
05-JUN-2001; 2001US-0874503.  
14-JUN-2001; 2001US-0882636.  
19-JUN-2001; 2001US-0886342.  
21-JUN-2001; 2001US-0887897.  
18-JUL-2001; 2001US-0908827.  
06-AUG-2001; 2001US-0924419.  
09-AUG-2001; 2001US-0927796.  
16-AUG-2001; 2001US-0931836.  
19-DEC-2001; 2001US-0028072.

(GETH ) GENENTECH INC.

Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
Smith V, Stewart TA, Tamas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-332040/31.

N-PSDB; ACA03803.

New secreted and transmembrane PRO nucleic acids, useful for gene  
therapy, in chromosome and gene mapping, as chromosome markers, in  
tissue typing, and in chromosome identification

Claim 12; Fig 402; 560pp; English.

The present invention relates to the isolation of novel human PRO  
polypeptides, and the polynucleotide sequences encoding them. The  
PRO polypeptides are secreted and transmembrane proteins. The PRO  
polypeptides are useful for detecting other PRO polypeptides, for  
linking bioactive molecules to cells expressing PRO polypeptides,  
for modulating biological activities of cells expressing PRO  
polypeptides, and for identifying agonists or antagonists.  
The PRO polypeptides are useful for stimulating the release of  
tumour necrosis factor (TNF)-alpha from human blood, for stimulating the  
proliferation or differentiation of chondrocytes, and detecting the  
presence of tumours. The polynucleotide sequences encoding PRO  
polypeptides are useful as hybridisation probes, in chromosome and  
gene mapping, in the generation of antisense RNA and DNA, in the  
preparation of PRO polypeptides, for generating transgenic animals or  
knockout animals, for the genetic analysis of individuals with genetic  
disorders, and in gene therapy. ABU6570-ABU66844 represent the human  
PRO polypeptides of the invention.

Note: The sequence data for this patent was obtained in electronic  
format directly from the USPTO web site at  
seqdata.uspto.gov/psipdsIDentry.html.

Sequence 123 AA;

Query Match 100.0%; Score 657; DB 24; Length 123;  
Best Local Similarity 100.0%; Pred. No. 5.9e-65; Indels 0; Gaps 0;  
Matches 123; Conservative 0; Mismatches 0;  
QY 1 MACRCISFLLMGTFLSVSQTVLALQDLALLVFPQVQAQLSCTLSPQHVTIRDYGVSWYQQR 60  
|||  
Db 1 MACRCISFLLMGTFLSVSQTVLALQDLALLVFPQVQAQLSCTLSPQHVTIRDYGVSWYQQR 60  
|||  
QY 61 AGSAPRYLLYRSBEDHHRPADIPDRFSAADKAHNAACVLTISPQVEDDADYCVSVGYG 120  
|||  
Db 61 AGSAPRYLLYRSBEDHHRPADIPDRFSAADKAHNAACVLTISPQVEDDADYCVSVGYG 120  
|||  
QY 121 FSP 123  
|||  
Db 121 FSP 123  
|||

#### RESULT 7

ABU67046

ID ABU67046 standard; Protein; 123 AA.

XX AC ABU67046;

XX DT 27-MAY-2003 (first entry)

XX DE Human secreted/transmembrane, PRO, protein SEQ ID 402.

XX KW Human, secreted protein; transmembrane protein; PRO;  
XX KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;  
XX KW infertility; birth defects; premature aging; AIDS; biosensor;  
XX KW acquired immunodeficiency syndrome; cancer; diabetic complication;  
XX KW bioreactor; tumour.

XX OS Homo sapiens.

XX PN US2003032155-A1.

XX PD 13-FEB-2003.

XX PF 03-MAY-2002; 2002US-0137865.

XX PR 31-MAR-1997; 97WO-US05230.

XX PR 12-JUN-1998; 98WO-US12456.

XX PR 14-JUL-1998; 98WO-US14552.

XX PR 28-AUG-1998; 98WO-US17888.

XX PR 10-SEP-1998; 98WO-US18824.

XX PR 14-SEP-1998; 98WO-US19093.

XX PR 14-SEP-1998; 98WO-US19094.

XX PR 16-SEP-1998; 98WO-US19177.

XX PR 17-SEP-1998; 98WO-US19330.

XX PR 07-OCT-1998; 98WO-US21141.

XX PR 29-OCT-1998; 98WO-US22991.

XX PR 29-OCT-1998; 98WO-US22992.

XX PR 20-NOV-1998; 98WO-US24855.

XX PR 01-DEC-1998; 98WO-US25108.

XX PR 05-JAN-1999; 99WO-US00106.

XX PR 08-MAR-1999; 99WO-US05028.

XX PR 10-MAR-1999; 99WO-US05190.

XX PR 20-APR-1999; 99WO-US08615.

XX PR 14-MAY-1999; 99WO-US10733.

XX PR 02-JUN-1999; 99WO-US12252.

XX PR 01-SEP-1999; 99WO-US20111.

XX PR 08-SEP-1999; 99WO-US20594.

XX PR 13-SEP-1999; 99WO-US20944.

XX PR 15-SEP-1999; 99WO-US21090.

XX PR 15-SEP-1999; 99WO-US21547.

XX PR 05-OCT-1999; 99WO-US23089.

XX PR 29-NOV-1999; 99WO-US28214.

XX PR 30-NOV-1999; 99WO-US28313.

XX PR 30-NOV-1999; 99WO-US28409.

XX PR 01-DEC-1999; 99WO-US28301.



PR 01-DEC-1999; 99WO-US28634.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 20-DEC-1999; 99WO-US30999.  
 PR 22-DEC-1999; 99WO-US30720.  
 PR 30-DEC-1999; 99WO-US31243.  
 PR 30-DEC-1999; 99WO-US31274.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04344.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 01-MAR-2000; 2000WO-US05601.  
 PR 02-MAR-2000; 2000WO-US05745.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 10-MAR-2000; 2000WO-US06319.  
 PR 15-MAR-2000; 2000WO-US06684.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 11-AUG-2000; 2000WO-US22031.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23528.  
 PR 10-NOV-2000; 2000WO-US30952.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001WO-US06666.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 22-JUN-2001; 2001WO-US20116.  
 PR 29-JUN-2001; 2001WO-US21066.  
 PR 09-JUL-2001; 2001WO-US21735.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0808689.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 18-MAY-2001; 2001US-0860216.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 01-JUN-2001; 2001US-0872035.  
 PR 05-JUN-2001; 2001US-0874503.  
 PR 14-JUN-2001; 2001US-0882636.  
 PR 19-JUN-2001; 2001US-0886342.  
 PR 21-JUN-2001; 2001US-0887879.  
 PR 18-JUL-2001; 2001US-0908827.  
 PR 06-AUG-2001; 2001US-0924419.  
 PR 09-AUG-2001; 2001US-0927796.  
 PR 16-AUG-2001; 2001US-0931836.  
 PR 19-DEC-2001; 2001US-0028072.

(GETH ) GENENTECH INC.

PA Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;

PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;  
 XX WPI; 2003-331925/31.  
 DR N-PSDB; ACA04224.  
 XX  
 PT New secreted and transmembrane nucleic acids and polypeptides,  
 designated as PRO, useful for treating inflammation, organ failure,  
 PT atherosclerosis, cardiac injury, infertility, birth defects, premature  
 PT aging, AIDS, or cancer  
 XX  
 PS Claim 12; Fig 402; 659pp; English.

XX The invention relates to an isolated nucleic acid comprising, or which is  
 CC at least 80% identical to, or the full-length coding sequence of, any of  
 CC the 275 nucleotide sequences encoding the corresponding PRO polypeptide  
 CC (one of 275 secreted or transmembrane proteins). The nucleic acid  
 CC further comprises the full-length coding sequence of the DNA deposited  
 CC under American Type Culture Collection (ATCC) accession number in a list  
 CC given in the specification. Also included are vectors and host  
 CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO  
 CC antibodies, PRO extracellular domains and mature sequences, methods  
 CC of detecting PRO proteins, methods for stimulating the release of  
 CC TNF-alpha (tumour necrosis factor alpha) from human blood,  
 CC (and the proliferation of differentiation of chondrocyte cells, the  
 CC proliferation of, or gene expression in pericyte cells, the release or  
 CC proteoglycans from cartilage, proliferation of inner ear utricular  
 CC supporting cells, the proliferation of T-lymphocyte cells, the release  
 CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the  
 CC proliferation of endothelial cells), a method for modulating the uptake  
 CC of glucose or free fatty acid (FFA) by skeletal muscle cells.  
 CC a method for inhibiting the binding of A-peptide to factor VIIA,  
 CC or the differentiation of adipocyte cells, a method for detecting the  
 CC presence of a tumour in a mammal and an oligonucleotide probe derived  
 CC from any of the nucleotide sequences cited above. The nucleic acids and  
 CC polypeptides are useful for treating inflammatory diseases, organ  
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,  
 CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or  
 CC diabetic complications. The nucleic acids are useful as hybridisation  
 CC probes, in chromosome and gene mapping, and in generating antisense RNA  
 CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,  
 CC biosensors or bioreactors. Both are useful in tissue typing.  
 CC The present sequence represents a PRO protein of the invention.

SQ Sequence 123 AA;

Query Match 100.0%; Score 657; DB 24; Length 123;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-65;  
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MACRLSFLLMGTFLSVSQTVLAQLDALLVFPQVLAQLSCTLSPOHVTIRDYGVSWYQQR 60  
 DB 1 MACRLSFLLMGTFLSVSQTVLAQLDALLVFPQVLAQLSCTLSPOHVTIRDYGVSWYQQR 60  
 QY 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISFVQPEDDADYCVSVG 120  
 DB 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISFVQPEDDADYCVSVG 120  
 QY 121 FSP 123  
 DB 121 FSP 123

RESULT 8

ABUS9851  
 ID ABUS9851 standard; Protein; 123 AA.  
 XX AC ABUS9851;  
 XX DT 13-MAY-2003 (first entry)  
 XX DE Novel secreted and transmembrane protein PRO619.

Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;

cardiac insufficiency disorder; cancer; tumour; immune response;  
adrenal cortical capillary endothelial growth; c-fos induction;  
vascular endothelial growth factor inhibition; VEGF inhibition;  
endothelial cell growth inhibitor; T-lymphocytes stimulation;  
retinal neurons cell survival; rod photoreceptor cell survival;  
retinal disorder; retinitis pigmentosa; kidney disease;  
mamalian kidney mesangial cell proliferation; Berger disease;  
dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
chondrocyte redifferentiation; sports injury; arthritis.  
Homo sapiens.  
US2003017563-A1.  
23-JAN-2003.  
07-MAY-2002; 2002US-0140808.  
31-MAR-1997; 97WO-US05230.  
12-JUN-1998; 98WO-US12456.  
14-JUL-1998; 98WO-US14552.  
28-AUG-1998; 98WO-US17888.  
10-SEP-1998; 98WO-US18824.  
14-SEP-1998; 98WO-US19093.  
14-SEP-1998; 98WO-US19094.  
14-SEP-1998; 98WO-US19177.  
16-SEP-1998; 98WO-US19330.  
17-SEP-1998; 98WO-US19437.  
29-OCT-1998; 98WO-US21141.  
29-OCT-1998; 98WO-US22991.  
29-OCT-1998; 98WO-US22992.  
20-NOV-1998; 98WO-US24855.  
01-DEC-1998; 98WO-US25108.  
05-JAN-1999; 99WO-US00106.  
08-MAR-1999; 99WO-US05028.  
10-MAR-1999; 99WO-US05130.  
20-APR-1999; 99WO-US08615.  
14-MAY-1999; 99WO-US10733.  
02-JUN-1999; 99WO-US12252.  
01-SEP-1999; 99WO-US20111.  
08-SEP-1999; 99WO-US20594.  
13-SEP-1999; 99WO-US20944.  
15-SEP-1999; 99WO-US21090.  
15-SEP-1999; 99WO-US21547.  
05-OCT-1999; 99WO-US23089.  
29-NOV-1999; 99WO-US28214.  
30-NOV-1999; 99WO-US28313.  
30-NOV-1999; 99WO-US28409.  
01-DEC-1999; 99WO-US28301.  
01-DEC-1999; 99WO-US28634.  
02-DEC-1999; 99WO-US28551.  
02-DEC-1999; 99WO-US28564.  
02-DEC-1999; 99WO-US28565.  
16-DEC-1999; 99WO-US30095.  
20-DEC-1999; 99WO-US30911.  
20-DEC-1999; 99WO-US30999.  
22-DEC-1999; 99WO-US30720.  
30-DEC-1999; 99WO-US31243.  
30-DEC-1999; 99WO-US31274.  
05-JAN-2000; 2000WO-US00219.  
06-JAN-2000; 2000WO-US00277.  
06-JAN-2000; 2000WO-US00376.  
11-FEB-2000; 2000WO-US03565.  
18-FEB-2000; 2000WO-US04341.  
18-FEB-2000; 2000WO-US04342.  
22-FEB-2000; 2000WO-US04414.  
24-FEB-2000; 2000WO-US04914.  
24-FEB-2000; 2000WO-US05004.  
01-MAR-2000; 2000WO-US05601.  
02-MAR-2000; 2000WO-US05746.  
02-MAR-2000; 2000WO-US05841.  
10-MAR-2000; 2000WO-US06319.  
15-MAR-2000; 2000WO-US06884.

20-MAR-2000; 2000WO-US07377.  
21-MAR-2000; 2000WO-US07532.  
30-MAR-2000; 2000WO-US08439.  
17-MAY-2000; 2000WO-US13705.  
22-MAY-2000; 2000WO-US14042.  
30-MAY-2000; 2000WO-US14941.  
02-JUN-2000; 2000WO-US15264.  
28-JUL-2000; 2000WO-US20710.  
11-AUG-2000; 2000WO-US22031.  
23-AUG-2000; 2000WO-US23522.  
24-AUG-2000; 2000WO-US23328.  
08-NOV-2000; 2000WO-US30952.  
10-NOV-2000; 2000WO-US30873.  
01-DEC-2000; 2000WO-US32678.  
20-DEC-2000; 2000WO-US34956.  
28-FEB-2001; 2001WO-US06520.  
01-MAR-2001; 2001WO-US06666.  
25-MAY-2001; 2001WO-US17092.  
01-JUN-2001; 2001WO-US17800.  
20-JUN-2001; 2001WO-US19692.  
22-JUN-2001; 2001WO-US20116.  
29-JUN-2001; 2001WO-US21066.  
09-JUL-2001; 2001WO-US21735.  
28-FEB-2001; 2001US-0747259.  
28-FEB-2001; 2001US-0796498.  
09-MAR-2001; 2001US-0802706.  
14-MAR-2001; 2001US-0809689.  
22-MAR-2001; 2001US-0818744.  
03-APR-2001; 2001US-0825366.  
10-MAY-2001; 2001US-0854208.  
18-MAY-2001; 2001US-0854280.  
25-MAY-2001; 2001US-0860216.  
25-MAY-2001; 2001US-0866028.  
02-JUN-2001; 2001US-0872035.  
05-JUN-2001; 2001US-0874503.  
14-JUN-2001; 2001US-0882636.  
19-JUN-2001; 2001US-0886342.  
21-JUN-2001; 2001US-0887879.  
18-JUL-2001; 2001US-0908827.  
06-AUG-2001; 2001US-0924419.  
09-AUG-2001; 2001US-0927796.  
16-AUG-2001; 2001US-0931836.  
19-DEC-2001; 2001US-0028072.  
(GETH ) GENENTECH INC.  
Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
WPI; 2003-148238/14.  
N-PSDE; ABX89341.  
Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
are therapeutically useful for enhancing immune response and in cancer  
treatments .  
Claim 12; Fig 402; 659pp; English.  
The invention describes an isolated human PRO polypeptide. The PRO  
polypeptides are useful in detecting PRO polypeptides in a sample, in  
linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
in modulating at least one biological activity of a cell expressing a PRO  
polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
stimulate adrenal cortical capillary endothelial growth, and PRO536,  
PRO943, PRO826, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
PRO1340 and PRO1387 induce c-fos in endothelial cells, and are thus  
useful for treating conditions or disorders where angiogenesis would be  
beneficial, e.g. wound healing and antagonist of this polypeptide are  
useful for treating cancerous tumours. PRO812 inhibits vascular

endothelial growth factor (VEGF) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth in mammals which would be beneficial in inhibiting tumour growth. PRO826, PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of stimulated T-lymphocytes and are therapeutically useful for enhancing immune response. PRO828, PRO829, PRO1068 or PRO1332 enhance survival of retinal neurons cells (PRO1132 is also enhances survival/proliferation of rod photoreceptor cells) and therefore are useful for treating retinal disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813 and PRO1066 induce proliferation of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathies associated with dermatitis, herpeticiformis or Crohn's disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the proliferation and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This is the amino acid sequence of a novel human PRO protein.

Query Match 100.0%; Score 657; DB 24; Length 123;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-65;  
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 1 MACRCLSPFLMGTFTLSVSGTQLAQLDALLVPPGVAQLSCTLSQHVITRDYGVSWYQQR 60  
 QY 61 AGSAPRYLLYRSEEDHRRPADIPRFAANDEAHNACVLTISVPQEDDADYCVGVG 120  
 Db 61 AGSAPRYLLYRSEEDHRRPADIPRFAANDEAHNACVLTISVPQEDDADYCVGVG 120  
 QY 121 FSP 123  
 Db 121 FSP 123

RESULT 9  
 ABUS9071  
 ID ABUS9071 standard; Protein; 123 AA.  
 AC ABUS9071;  
 DT 28-APR-2003 (first entry)  
 XX Novel human secreted or transmembrane protein PRO619.  
 XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
 KW cardiac insufficiency disorder; cancer; tumour; immune response;  
 KW adrenal cortical capillary endothelial growth; c-fos induction;  
 KW vascular endothelial growth factor inhibition; VEGF inhibition;  
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
 KW retinal neurons cell survival; rod photoreceptor cell survival;  
 KW retinal disorder; retinitis pigmentosa; kidney disease;  
 KW mammalian kidney mesangial cell proliferation; Berger disease;  
 KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
 KW chondrocyte redifferentiation; sports injury; arthritis.  
 OS Homo sapiens.  
 XX  
 XX US2002132252-A1.  
 XX  
 XX 19-SEP-2002.  
 XX  
 XX 14-NOV-2001; 2001US-0990442.  
 XX  
 XX 05-NOV-1997; 97WO-US20069.  
 PR 16-SEP-1998; 98WO-US19330.  
 PR 17-SEP-1998; 98WO-US19437.  
 PR 07-OCT-1998; 98WO-US21141.  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 05-JAN-1999; 99WO-US00106.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR

PR 02-JUN-1999; 99WO-US12252.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 06-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 10-MAR-2000; 2000WO-US06319.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 15-MAY-2000; 2000WO-US13358.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 11-AUG-2000; 2000WO-US22031.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 01-DEC-2000; 2000WO-US32878.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 29-JUN-2001; 2001WO-US21066.  
 PR 09-JUL-2001; 2001WO-US21735.  
 PR 16-JUN-1997; 97US-045787P.  
 PR 17-OCT-1997; 97US-062250P.  
 PR 12-NOV-1997; 97US-065186P.  
 PR 13-NOV-1997; 97US-065311P.  
 PR 24-NOV-1997; 97US-066770P.  
 PR 25-FEB-1998; 98US-075945P.  
 PR 20-MAR-1998; 98US-078910P.  
 PR 28-APR-1998; 98US-083322P.  
 PR 07-MAY-1998; 98US-084600P.  
 PR 28-MAY-1998; 98US-087108P.  
 PR 02-JUN-1998; 98US-087607P.  
 PR 02-JUN-1998; 98US-087609P.  
 PR 02-JUN-1998; 98US-087599P.  
 PR 04-JUN-1998; 98US-087827P.  
 PR 04-JUN-1998; 98US-088021P.  
 PR 04-JUN-1998; 98US-088025P.  
 PR 04-JUN-1998; 98US-088028P.  
 PR 04-JUN-1998; 98US-088028P.  
 PR 04-JUN-1998; 98US-088029P.  
 PR 04-JUN-1998; 98US-088030P.  
 PR 04-JUN-1998; 98US-088033P.  
 PR 04-JUN-1998; 98US-088326P.  
 PR 05-JUN-1998; 98US-088167P.  
 PR 05-JUN-1998; 98US-088202P.  
 PR 05-JUN-1998; 98US-088212P.  
 PR 05-JUN-1998; 98US-088217P.  
 PR 09-JUN-1998; 98US-088655P.  
 PR 10-JUN-1998; 98US-088734P.  
 PR 10-JUN-1998; 98US-088738P.  
 PR 10-JUN-1998; 98US-088742P.  
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 PR 11-JUN-1998; 98US-088876P.  
 PR 12-JUN-1998; 98US-089105P.

16-JUN-1998; 98US-089440P.  
16-JUN-1998; 98US-089512P.  
16-JUN-1998; 98US-089514P.  
17-JUN-1998; 98US-089532P.  
17-JUN-1998; 98US-089538P.  
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17-JUN-1998; 98US-089599P.  
17-JUN-1998; 98US-089600P.  
17-JUN-1998; 98US-089653P.  
18-JUN-1998; 98US-089801P.  
18-JUN-1998; 98US-089907P.  
18-JUN-1998; 98US-089908P.  
28-AUG-2001; 2001US-0941992.  
(GETH ) GENENTECH INC.  
Ashkenazi AJ, Baker KP, Botstein D, Deanovoyers L, Eaton DL;  
Ferrara N, Fong S, Gerber H, Gertsen ME, Goddard A, Godowski PJ;  
Grimaldi JC, Gurney AL, Kijavini JJ, Napier MA, Pan J, Paoni NF;  
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
Zhang Z;  
WPI; 2003-247083/24.  
N-PSDB; ABX80195.  
Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
are therapeutically useful for enhancing immune response and in cancer  
treatments -  
Claim 12; Fig 68; 648pp; English.  
The invention describes an isolated human PRO polypeptide. The PRO  
polypeptides are useful in detecting PRO polypeptides in a sample, in  
linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
in modulating at least one biological activity of a cell expressing a PRO  
polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
stimulate adrenal cortical capillary endothelial growth, and PRO536,  
PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
useful for treating conditions or disorders where angiogenesis would be  
beneficial, e.g. wound healing and antagonist of this polypeptide are  
useful for treating cancerous tumours. PRO812 inhibits vascular  
endothelial growth factor (VEGF) stimulated proliferation of endothelial  
cells and is thus useful for inhibiting endothelial cell growth in  
mammals which would be beneficial in inhibiting tumour growth. PRO826,  
PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
stimulated T-lymphocytes and are therapeutically useful for enhancing  
immune response. PRO828, PRO826, PRO1068 or PRO132 enhance survival of  
retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
rod photoreceptor cells) and therefore are useful for treating retinal  
disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813  
and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
and therefore are useful for treating kidney disorders associated with  
decreased mesangial cell function such as Berger disease or Crohn's  
nephropathies associated with dermatitis, herpeticiformis or Crohn's  
disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
proliferation and/or redifferentiation of chondrocytes in culture and  
are thus useful for treating sports injuries, and arthritis. This  
is the amino acid sequence of a novel human PRO protein.

2y 1 MACRCLSLMGTLISVQTVAQLDALLVPPGVAQLSCTLSPOHVTIRDYGVSWYQQR 60  
db 1 MACRCLSLMGTLISVQTVAQLDALLVPPGVAQLSCTLSPOHVTIRDYGVSWYQQR 60  
2y 61 AGSAPRYLLYYRSEEDHRRPADIPDRFSAAKDEAHNACVLITISPVQPEDDADYICSVGYG 120

Db 61 AGSAPRYLLYYRSEEDHRRPADIPDRFSAAKDEAHNACVLITISPVQPEDDADYICSVGYG 120  
Qy 121 FSP 123  
Db 121 FSP 123  
RESULT 10  
ABUS9218  
ID ABUS9218 standard; Protein; 123 AA.  
XX AC ABUS9218;  
XX DT 22-APR-2003 (first entry)  
XX DE Human secreted/transmembrane protein, #43.  
XX KW Human; PRO; secreted; transmembrane; pharmaceutical;  
KW diagnostic; biosensor; bioreactor; tumour; therapeutic;  
KW gene therapy; tumour-associated antigenic target; TAT; ADEPT;  
KW antibody-dependent enzyme mediated prodrug therapy; cytostatic.  
XX OS Homo sapiens.  
XX PN US2003027162-A1.  
XX PD 06-FEB-2003.  
XX PF 15-NOV-2001; 2001US-0997428.  
XX PR 05-NOV-1997; 97WO-US20069.  
PR 15-SEP-1998; 98WO-US19330.  
PR 07-OCT-1998; 98WO-US19437.  
PR 01-DEC-1998; 98WO-US21141.  
PR 05-JAN-1999; 99WO-US25108.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12552.  
PR 15-SEP-1999; 99WO-US21090.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28634.  
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PR 05-JAN-2000; 2000WO-US00219.  
PR 08-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
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PR 20-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
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PR 11-AUG-2000; 2000WO-US22031.  
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PR 29-JUN-2001; 2001WO-US21066.

PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-049787P.  
PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.  
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PR 25-FEB-1998; 98US-075945P.  
PR 28-MAR-1998; 98US-078910P.  
PR 28-APR-1998; 98US-083322P.  
PR 07-MAY-1998; 98US-084600P.  
PR 28-MAY-1998; 98US-087106P.  
PR 02-JUN-1998; 98US-087607P.  
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PR 03-JUN-1998; 98US-087759P.  
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PR 04-JUN-1998; 98US-088029P.  
PR 04-JUN-1998; 98US-088030P.  
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PR 05-JUN-1998; 98US-088367P.  
PR 05-JUN-1998; 98US-088402P.  
PR 05-JUN-1998; 98US-088412P.  
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PR 09-JUN-1998; 98US-088655P.  
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PR 10-JUN-1998; 98US-088826P.  
PR 11-JUN-1998; 98US-088858P.  
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PR 12-JUN-1998; 98US-088910P.  
PR 16-JUN-1998; 98US-089440P.  
PR 16-JUN-1998; 98US-089512P.  
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PR 17-JUN-1998; 98US-089532P.  
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PR 17-JUN-1998; 98US-089653P.  
PR 18-JUN-1998; 98US-089801P.  
PR 18-JUN-1998; 98US-089907P.  
PR 18-JUN-1998; 98US-089908P.  
PR 19-JUN-1998; 98US-089947P.  
PR 19-JUN-1998; 98US-089948P.  
PR 19-JUN-1998; 98US-089952P.  
PR 22-JUN-1998; 98US-090246P.  
PR 22-JUN-1998; 98US-090252P.  
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PR 23-JUN-1998; 98US-090349P.  
PR 23-JUN-1998; 98US-090355P.  
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PR 25-JUN-1998; 98US-090676P.  
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PR 26-JUN-1998; 98US-090863P.  
PR 01-JUL-1998; 98US-091360P.  
PR 01-JUL-1998; 98US-091544P.  
PR 02-JUL-1998; 98US-091478P.  
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PR 02-JUL-1998; 98US-091626P.  
PR 02-JUL-1998; 98US-091628P.  
PR 02-JUL-1998; 98US-091633P.  
PR 02-JUL-1998; 98US-091646P.  
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PR 20-JUL-1998; 98US-093339P.  
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PR 04-AUG-1998; 98US-095282P.  
PR 04-AUG-1998; 98US-095285P.  
PR 04-AUG-1998; 98US-095301P.  
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PR 04-AUG-1998; 98US-095318P.  
PR 04-AUG-1998; 98US-095321P.  
PR 04-AUG-1998; 98US-095325P.  
PR 10-AUG-1998; 98US-095916P.  
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PR 10-AUG-1998; 98US-096012P.  
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PR 17-AUG-1998; 98US-096757P.  
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PR 19-AUG-1998; 98US-097141P.  
PR 20-AUG-1998; 98US-097218P.  
PR 24-AUG-1998; 98US-097661P.  
PR 26-AUG-1998; 98US-097952P.  
PR 26-AUG-1998; 98US-097954P.  
PR 26-AUG-1998; 98US-097955P.  
PR 26-AUG-1998; 98US-097971P.  
PR 26-AUG-1998; 98US-097974P.  
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PR 26-AUG-1998; 98US-097979P.  
PR 26-AUG-1998; 98US-097986P.  
PR 26-AUG-1998; 98US-098014P.  
PR 31-AUG-1998; 98US-098525P.  
PR 16-SEP-1998; 98US-100634P.  
PR 17-SEP-1998; 98US-100858P.  
PR 22-DEC-1998; 98US-113296P.  
PR 12-MAR-1999; 99US-123957P.  
PR 23-JUN-1999; 99US-141037P.

Query Match 100.0%; Score 657; DB 24; Length 123;

Best Local Similarity 100.0%; Pred. No. 5,9e-65;

Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MACRCLSPFLMGTLFSLVSQTVLAQDALLVFPQVLAQSLCTLSPOHVTIRDYGVSWYQQR 60

DB 1 MACRCLSPFLMGTLFSLVSQTVLAQDALLVFPQVLAQSLCTLSPOHVTIRDYGVSWYQQR 60

Y 61 AGSAPRYLLYRSEEDHHRPADIPORFSAKDEAHNACVLITSPVQPEDDADYYCSVGYG 120  
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b 61 AGSAPRYLLYRSEEDHHRPADIPORFSAKDEAHNACVLITSPVQPEDDADYYCSVGYG 120  
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Y 121 FSP 123  
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b 121 FSP 123  
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RESULT 11  
BUE59367  
D AEU59367 standard; Protein; 123 AA.  
X C AEU59367;  
X T 22-APR-2003 (first entry)  
X X Novel human secreted or transmembrane protein PRO943.  
X X Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
W cardiac insufficiency disorder; cancer; tumour; immune response;  
W adrenal cortical capillary endothelial growth; c-fos induction;  
W vascular endothelial growth factor inhibition; VEGF inhibition;  
W endothelial cell growth inhibitor; T-lymphocytes stimulation;  
W retinal neurons cell survival; rod photoreceptor cell survival;  
W retinal disorder; retinitis pigmentosa; kidney disorder;  
W mammalian kidney mesangial cell proliferation; Berger disease;  
W dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
W chondrocyte redifferentiation; sports injury; arthritis.  
X X Homo sapiens.  
X X US2003027985-A1.  
X X 06-FEB-2003.  
X X 14-NOV-2001; 2001US-0990562.  
X X 05-NOV-1997; 97WO-US200069.  
X X 16-SEP-1998; 98WO-US19330.  
X X 17-SEP-1998; 98WO-US19437.  
X X 07-OCT-1998; 98WO-US21141.  
X X 01-DEC-1998; 98WO-US25108.  
X X 05-JAN-1999; 99WO-US30106.  
X X 08-MAR-1999; 99WO-US305028.  
X X 02-JUN-1999; 99WO-US12252.  
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X X 01-DEC-1999; 99WO-US28634.  
X X 16-DEC-1999; 99WO-US30095.  
X X 20-DEC-1999; 99WO-US30911.  
X X 05-JAN-2000; 2000WO-US00219.  
X X 06-JAN-2000; 2000WO-US00376.  
X X 11-FEB-2000; 2000WO-US03565.  
X X 18-FEB-2000; 2000WO-US04341.  
X X 22-FEB-2000; 2000WO-US0414.  
X X 24-FEB-2000; 2000WO-US04914.  
X X 24-FEB-2000; 2000WO-US05004.  
X X 02-MAR-2000; 2000WO-US05841.  
X X 10-MAR-2000; 2000WO-US06319.  
X X 15-MAR-2000; 2000WO-US06884.  
X X 20-MAR-2000; 2000WO-US07377.  
X X 30-MAR-2000; 2000WO-US08439.  
X X 15-MAY-2000; 2000WO-US13358.  
X X 17-MAY-2000; 2000WO-US13705.  
X X 20-MAY-2000; 2000WO-US14042.  
X X 30-MAY-2000; 2000WO-US14941.  
X X 02-JUN-2000; 2000WO-US15264.  
X X 28-JUL-2000; 2000WO-US20710.  
X X 11-AUG-2000; 2000WO-US22031.  
X X 23-AUG-2000; 2000WO-US23522.

PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
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PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-049787P.  
PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-066770P.  
PR 25-FEB-1998; 98US-075945P.  
PR 20-MAR-1998; 98US-078910P.  
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PR 04-JUN-1998; 98US-088025P.  
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PR 05-JUN-1998; 98US-088167P.  
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PR 10-JUN-1998; 98US-088734P.  
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PR 11-JUN-1998; 98US-088861P.  
PR 11-JUN-1998; 98US-088876P.  
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PR 11-AUG-1998; 98US-096143P.  
PR 11-AUG-1998; 98US-096146P.  
PR 12-AUG-1998; 98US-096329P.  
PR 17-AUG-1998; 98US-096757P.  
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PR 17-AUG-1998; 98US-096768P.  
PR 17-AUG-1998; 98US-096773P.  
PR 17-AUG-1998; 98US-096791P.  
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PR 17-AUG-1998; 98US-096891P.  
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PR 18-AUG-1998; 98US-096959P.  
PR 18-AUG-1998; 98US-096960P.  
PR 18-AUG-1998; 98US-097022P.  
PR 19-AUG-1998; 98US-097141P.  
PR 20-AUG-1998; 98US-097218P.  
PR 24-AUG-1998; 98US-097661P.  
PR 26-AUG-1998; 98US-097952P.  
PR 26-AUG-1998; 98US-097954P.  
PR 26-AUG-1998; 98US-097955P.  
PR 26-AUG-1998; 98US-097971P.  
PR 26-AUG-1998; 98US-097974P.  
PR 26-AUG-1998; 98US-097978P.  
PR 26-AUG-1998; 98US-097979P.  
PR 26-AUG-1998; 98US-097986P.  
PR 26-AUG-1998; 98US-098014P.

Query Match 100.0%; Score 657; DB 24; Length 123;

Best Local Similarity 100.0%; Pred. No. 5.9e-65; Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MACRCISFLIMGTFLSVSQTVLIAQLDALIVFFGQVAQLSCTLSPOHVTIRDYGVSWYQQR 60  
DB 1 MACRCISFLIMGTFLSVSQTVLIAQLDALIVFFGQVAQLSCTLSPOHVTIRDYGVSWYQQR 60

QY 61 AGSAPRYLLYRSEEDHHPADIPDRFSAKDEAHNACVLITISVPQEDDADYYCSGVG 120  
DB 61 AGSAPRYLLYRSEEDHHPADIPDRFSAKDEAHNACVLITISVPQEDDADYYCSGVG 120  
QY 121 FSP 123  
DB 121 FSP 123  
RESULT 12  
ABU60502  
ID ABU60502 standard; Protein; 123 AA.  
XX  
AC ABU60502;  
XX  
XX 01-MAY-2003 (first entry)  
XX Human secreted/transmembrane protein, #43.  
DE Human; PRO; secreted; transmembrane; signal peptide;  
XX pharmaceutical; diagnostic; therapeutic; gene therapy.  
KW Homo sapiens.  
OS  
XX US2002160384-A1.  
PN  
XX 31-OCT-2002.  
XX  
XX 14-NOV-2001; 2001US-0992598.  
PR 05-NOV-1997; 97WO-US200069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 16-DEC-1999; 99WO-US28634.  
PR 20-DEC-1999; 99WO-US30095.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
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PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.

PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-049787P.  
PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-066770P.  
PR 25-FEB-1998; 98US-075945P.  
PR 20-MAR-1998; 98US-078910P.  
PR 28-APR-1998; 98US-083322P.  
PR 07-MAY-1998; 98US-084600P.  
PR 28-MAY-1998; 98US-087106P.  
PR 02-JUN-1998; 98US-087607P.  
PR 02-JUN-1998; 98US-087609P.  
PR 02-JUN-1998; 98US-087759P.  
PR 03-JUN-1998; 98US-087827P.  
PR 04-JUN-1998; 98US-088021P.  
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PR 04-JUN-1998; 98US-088028P.  
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PR 04-JUN-1998; 98US-088326P.  
PR 05-JUN-1998; 98US-088167P.  
PR 05-JUN-1998; 98US-088202P.  
PR 05-JUN-1998; 98US-088212P.  
PR 05-JUN-1998; 98US-088217P.  
PR 09-JUN-1998; 98US-088655P.  
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PR 10-JUN-1998; 98US-088738P.  
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PR 10-JUN-1998; 98US-088810P.  
PR 10-JUN-1998; 98US-088824P.  
PR 10-JUN-1998; 98US-088826P.  
PR 11-JUN-1998; 98US-088858P.  
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PR 11-JUN-1998; 98US-088876P.  
PR 12-JUN-1998; 98US-089105P.  
PR 16-JUN-1998; 98US-089440P.  
PR 16-JUN-1998; 98US-089512P.  
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PR 18-JUN-1998; 98US-089908P.  
PR 28-AUG-2001; 2001US-0941992.  
XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
XX Ferrara N, Fong S, Garber H, Gerritsen ME, Goddard A, Godowski PJ,  
XX Grimaldi JC, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF,  
XX Roy MA, Stewart TA, Tamas D, Watanabe CK, Williams PM, Wood WI,  
XX Zhang Z;  
XX WPI; 2003-288106/28.  
XX N-PSDB; ABX90174.

XX New transmembrane polypeptides and nucleic acids encoding the  
XX polypeptides, useful in gene therapy, in chromosome identification, as  
XX chromosome markers, or in generating probes -

XX Claim 12; Fig 68; 650pp; English.

XX The invention discloses isolated PRO secreted/transmembrane polypeptides  
XX comprising a sequence without signal peptide and the nucleic acid  
XX encoding them. The polypeptides can be used to raise antibodies that  
XX specifically bind to the PRO polypeptide, for linking a bioactive

CC molecule to a cell expressing a PRO protein and for modulating at least  
CC one biological activity of a cell. The PRO polypeptides or  
CC polynucleotides are also useful in gene therapy, in chromosome  
CC identification, as chromosome markers, or in generating probes. The PRO  
CC polypeptides are useful as molecular markers for protein  
CC electrophoresis, and the isolated nucleic acids may be used for  
CC recombinantly expressing those markers. The PRO polypeptides and nucleic  
CC acids may also be used in tissue typing. Anti-PRO antibodies are useful  
CC in diagnostic assays for PRO, and in affinity purification of PRO from  
CC recombinant cell culture or natural sources. The sequences presented in  
CC ABU60478-ABU60624 are the PRO polynucleotides of the invention.  
CC Note: The sequence data for this patent is also available in electronic  
CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).

XX Sequence 123 AA;

Query Match 100.0%; Score 657; DB 24; Length 123;  
Best Local Similarity 100.0%; Pred. No. 5.9e-65;  
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MACRCLSFLIMGTFLSVSQTIVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQQR 60  
DB 1 MACRCLSFLIMGTFLSVSQTIVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQQR 60  
QY 61 AGSAPRYLLYRSEEDHHRPADIPDRFSAKDEAHNACVLTITSPVQPEDDADYICSVGYG 120  
DB 61 AGSAPRYLLYRSEEDHHRPADIPDRFSAKDEAHNACVLTITSPVQPEDDADYICSVGYG 120  
QY 121 FSP 123  
DB 121 FSP 123

RESULT 13

ABU57993  
ID ABU57993 standard; Protein; 123 AA.

XX AC ABU57993;

XX DT 14-APR-2003 (first entry)

XX DE Human PRO polypeptide #25.

XX KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;  
XX KW horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;  
XX KW antibody-dependent enzyme mediated prodrug therapy.

XX OS Homo sapiens.

XX FN US2003027163-A1.

XX PD 06-FEB-2003.

XX PF 15-NOV-2001; 2001US-0997666.

XX PR 05-NOV-1997; 97WO-US20069.

XX PR 16-SEP-1998; 98WO-US19330.

XX PR 17-SEP-1998; 98WO-US19437.

XX PR 07-OCT-1998; 98WO-US21141.

XX PR 01-DEC-1998; 98WO-US25108.

XX PR 05-JAN-1999; 99WO-US00106.

XX PR 08-MAR-1999; 99WO-US05028.

XX PR 02-JUN-1999; 99WO-US12252.

XX PR 15-SEP-1999; 99WO-US21090.

XX PR 30-NOV-1999; 99WO-US21547.

XX PR 01-DEC-1999; 99WO-US28301.

XX PR 01-DEC-1999; 99WO-US28634.

XX PR 16-DEC-1999; 99WO-US30095.

XX PR 20-DEC-1999; 99WO-US30911.

XX PR 05-JAN-2000; 2000WO-US00219.

XX PR 06-JAN-2000; 2000WO-US00376.

XX PR 11-FEB-2000; 2000WO-US03565.





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R 26-AUG-1998; 98US-097952P.
R 26-AUG-1998; 98US-097954P.
R 26-AUG-1998; 98US-097955P.
R 26-AUG-1998; 98US-097971P.
R 26-AUG-1998; 98US-097974P.
R 26-AUG-1998; 98US-097978P.
R 26-AUG-1998; 98US-097979P.
R 26-AUG-1998; 98US-097986P.
R 26-AUG-1998; 98US-098014P.
R 31-AUG-1998; 98US-098525P.
R 16-SEP-1998; 98US-100634P.
R 17-SEP-1998; 98US-100858P.
R 22-DEC-1998; 98US-113296P.
R 12-MAR-1999; 98US-123957P.
R 23-JUN-1999; 98US-141037P.
R 07-JUL-1999; 98US-143048P.

Query Match 100.0%; Score 657; DB 24; Length 123;
Best Local Similarity 100.0%; Pred. No. 5.9e-65;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ib 1 MACRCLFLLMGTFLSVQTSLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQOR 60

iy 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDAAHNAACVLTITSPVQPEDDADYYCSVGYG 120
ib 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDAAHNAACVLTITSPVQPEDDADYYCSVGYG 120

iy 121 FSP 123
ib 121 FSP 123

RESULT 14
ABUS6924
.D ABUS6924 standard; Protein; 123 AA.
CX AC ABUS6924;
CX XT 16-APR-2003 (first entry)
CX ZE Human secreted/transmembrane protein, #43.
CX TW Human; PRO; secreted; transmembrane; signal peptide;
CX CW pharmaceutical; diagnostic; biosensor; tumour; therapeutic;
CX CW colon cancer; lung cancer; breast cancer; cancer; gene therapy.
CX XS Homo sapiens.
CX PN US2002142961-A1.
CX PD 03-OCT-2002.
CX PF 19-NOV-2001; 2001US-0989721.
CX PR 05-NOV-1997; 97WO-US20069.
CX PR 17-SEP-1998; 98WO-US19437.
CX PR 07-OCT-1998; 98WO-US21141.
CX PR 01-DEC-1998; 98WO-US25108.
CX PR 05-JAN-1999; 99WO-US00106.
CX PR 08-MAR-1999; 99WO-US05028.
CX PR 02-JUN-1999; 99WO-US12252.
CX PR 15-SEP-1999; 99WO-US21547.
CX PR 30-NOV-1999; 99WO-US28313.
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CX PR 01-DEC-1999; 99WO-US28634.
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CX PR 05-JAN-2000; 2000WO-US00219.
CX PR 06-JAN-2000; 2000WO-US00376.
CX PR 11-FEB-2000; 2000WO-US03565.
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PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
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PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 15-MAY-2000; 2000WO-US13358.
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PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
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PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
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PR 29-JUN-2001; 2001WO-US21066.
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PR 16-JUN-1997; 97US-049787P.
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PR 13-NOV-1997; 97US-065311P.
PR 24-NOV-1997; 97US-066770P.
PR 25-FEB-1998; 98US-075945P.
PR 20-MAR-1998; 98US-078910P.
PR 28-APR-1998; 98US-083322P.
PR 07-MAY-1998; 98US-084600P.
PR 28-MAY-1998; 98US-087106P.
PR 02-JUN-1998; 98US-087607P.
PR 02-JUN-1998; 98US-087509P.
PR 02-JUN-1998; 98US-087759P.
PR 03-JUN-1998; 98US-087827P.
PR 04-JUN-1998; 98US-088021P.
PR 04-JUN-1998; 98US-088025P.
PR 04-JUN-1998; 98US-088026P.
PR 04-JUN-1998; 98US-088028P.
PR 04-JUN-1998; 98US-088029P.
PR 04-JUN-1998; 98US-088030P.
PR 04-JUN-1998; 98US-088033P.
PR 04-JUN-1998; 98US-088326P.
PR 05-JUN-1998; 98US-088167P.
PR 05-JUN-1998; 98US-088202P.
PR 05-JUN-1998; 98US-088212P.
PR 05-JUN-1998; 98US-088217P.
PR 05-JUN-1998; 98US-088555P.
PR 09-JUN-1998; 98US-088734P.
PR 10-JUN-1998; 98US-088738P.
PR 10-JUN-1998; 98US-088742P.
PR 10-JUN-1998; 98US-088810P.
PR 10-JUN-1998; 98US-088824P.
PR 10-JUN-1998; 98US-088826P.
PR 11-JUN-1998; 98US-088858P.
PR 11-JUN-1998; 98US-088861P.
PR 11-JUN-1998; 98US-088876P.
PR 12-JUN-1998; 98US-089105P.
PR 16-JUN-1998; 98US-089440P.
PR 16-JUN-1998; 98US-089512P.
PR 16-JUN-1998; 98US-089514P.
PR 16-JUN-1998; 98US-089532P.
PR 17-JUN-1998; 98US-089538P.
PR 17-JUN-1998; 98US-089598P.
PR 17-JUN-1998; 98US-089599P.
PR 17-JUN-1998; 98US-089600P.
PR 17-JUN-1998; 98US-089653P.
PR 18-JUN-1998; 98US-089801P.
PR 18-JUN-1998; 98US-089907P.

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PR 18-JUN-1998; 98US-089908P.  
 PR 28-AUG-2001; 2001US-0941992.  
 XX (GETH ) GENENTECH INC.  
 PA  
 PI Askenazi AJ, Baker KP, Botstein D, Deanovers L, Eaton DL;  
 PI Ferrarini N, Fong S, Garber H, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Kljavin IV, Napier MA, Pan J, Paoni NF;  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams FM, Wood WI;  
 PI Zhang Z;  
 XX WPI; 2003-155950/15.  
 DR  
 PT New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184,  
 PT PRO361 or PRO846) useful as targets for therapeutic intervention in  
 PT cancers (e.g. lung or breast cancers), or for diagnosing these cancers  
 PT  
 XX Claim 12; Fig 68; 647pp; English.  
 PS  
 XX The invention discloses isolated PRO secreted/transmembrane polypeptides  
 CC comprising a sequence without signal peptide and the nucleic acid  
 CC encoding them. The polypeptides can be used to raise antibodies that  
 CC specifically bind to the PRO polypeptide, for linking a bioactive  
 CC molecule to a cell expressing a PRO protein and for modulating at least  
 CC one biological activity of a cell. The PRO polypeptides or  
 CC polynucleotides are also useful as pharmaceuticals, diagnostics,  
 CC biosensors or bioreactors, for detecting or treating e.g. tumours in  
 CC mammals, e.g. humans, dogs, cats, cattle, horses, sheep, goats or  
 CC rabbits as targets for therapeutic intervention in certain cancers (e.g.  
 CC colon, lung or breast cancers) and diagnostic determination of the  
 CC presence of these cancers. The PRO polypeptides are also useful as  
 CC molecular weight markers or for chromosome identification. The PRO genes  
 CC are useful as hybridisation probes or for screening libraries of human  
 CC cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene  
 CC therapy, particularly for replacing a defective gene. The sequences  
 CC presented in ABUS8900-ABUS9046 are the PRO polypeptides of the invention.  
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 DT 26-FEB-2003 (first entry)  
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 XX PF 20-NOV-2001; 2001US-0989731.  
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 XX 05-NOV-1997; 97WO-US20069.  
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 PR 10-MAR-2000; 2000WO-US06319.  
 PR 15-MAR-2000; 2000WO-US06884.  
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 PR 22-MAY-2000; 2000WO-US14042.  
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 PR 28-JUL-2000; 2000WO-US20710.  
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 PR 20-JUN-2001; 2001WO-US19692.  
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 PR 09-JUL-2001; 2001WO-US21735.  
 PR 16-JUN-1997; 97US-045787P.  
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 PR 05-JUN-1998; 98US-088202P.  
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Run on: February 9, 2004, 12:47:07 ; Search time 36.0135 Seconds  
(without alignments)  
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Title: US-09-981-876-200

Perfect score: 657

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Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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#### ALIGNMENTS

#### RESULT 1

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; Sequence 117, Application US/09989722  
; Patent No. US20020072067A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Borstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tamas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secured and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C63  
; CURRENT APPLICATION NUMBER: US/09/989, 722  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17

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; Sequence 117, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Forg, Sherman
; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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; APPLICANT: Gurney, Austin L.
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; APPLICANT: Pan, James
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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;; PRIOR FILING DATE: 1998-07-09  
  
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QY 121 FSP 123  
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; Sequence 117, Application US/09989279  
; Patent No. US20020072496A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Geritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C56  
; CURRENT APPLICATION NUMBER: US/09/989,279  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16



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 19 PRIOR APPLICATION NUMBER: 60/092182  
 20 PRIOR FILING DATE: 1998-07-09

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Db	61	AGSAPRYLLYYTSEEDHRRPADIPDRFSAAKDAHNACVLTISPVPQEDDADYYCSGVYG	120
QY	121	FSP	123
Db	121	FSP	123

RESULT 4  
US-09-989-727-117  
Sequence 117, Application US/09989727  
Patent No. US20020072497A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Psconi, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCES: P2730PIC65  
CURRENT APPLICATION NUMBER: US/09/989,727  
CURRENT FILING DATE: 2001-11-19  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

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DB 61 AGSAPRYLLYTRSEEDHRRPADIPRFSAAKDEAHNACVLTISPQVEDDADYYCSVGYG 120  
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US-09-989-731-117  
; Sequence 117, Application US/09989731  
; Patent No. US20020103125A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C70  
; CURRENT APPLICATION NUMBER: US/09/989,731  
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PRIOR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-07-09

Query March          100.0%; Score 657; DB 10; Length 123;
Best Local Similarity 100.0%; Pred No. 2,1e-63;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 1 MACRCLFLLMGTFSLVSQTVLAQLDALLVFPQVQAQLSCTLSPOHVTIRDYGVSWYQOR 60
2b 1 MACRCLFLLMGTFSLVSQTVLAQLDALLVFPQVQAQLSCTLSPOHVTIRDYGVSWYQOR 60

2Y 61 AGSAPRYLLYRSSEDRHRPADIPDRFSAKDEAHNACVLTISPVQPEDADYGVSVGVG 120
2b 61 AGSAPRYLLYRSSEDRHRPADIPDRFSAKDEAHNACVLTISPVQPEDADYGVSVGVG 120

2Y 121 FSP 123
2b 121 FSP 123

RESULT 6
JS-09-989-732-117
Sequence 117, Application US/09989732
Patent No. US20020123463A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730F1C57
CURRENT APPLICATION NUMBER: US/09/989,732
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
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CURRENT APPLICATION NUMBER: US/09/991,073
CURRENT FILING DATE: 2001-11-14
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PRIOR FILING DATE: 1997-06-16
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PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876

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;; PRIOR FILING DATE: 1998-06-25  
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;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 657; DB 10; Length 123;  
Best Local Similarity 100.0%; Pred. No. 2,1e-63;  
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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QY 61 AGSAPRYLLYRSEEDHRRPADIDRFSAAKDEAHNAACVLITISPVQPEDDADYICSVGYG 120  
DB |||||  
QY 121 FSP 123  
DB |||||  
121 FSP 123

RESULT 8  
US-09-990-442-117  
; Sequence 117, Application US/09990442  
; Patent No. US20020132252A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same

;; FILE REFERENCE: P2730PIC8  
;; CURRENT APPLICATION NUMBER: US/09/990,442  
;; PRIOR FILING DATE: 2001-11-14  
;; PRIOR APPLICATION NUMBER: 60/049787  
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 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 657; DB 10; Length 123;

Best Local Similarity 100.0%; Pred. No. 2.le-63; Mismatches 0; Indels 0; Gaps 0;  
 Matches 123; Conservative 0;

QY 1 MACRCLSFLMGTFLSVSTVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQOR 60  
 DB 1 MACRCLSFLMGTFLSVSTVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQOR 60  
 QY 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISPVPQEDDADYICSVGYG 120  
 DB 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISPVPQEDDADYICSVGYG 120  
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RESULT 9

US-09-991-163-117  
 Sequence 117, Application US/09991163

Patent No. US20020132253A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
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 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
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 APPLICANT: Napier, Mary A.  
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 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic



PRIOR APPLICATION NUMBER: 60/090695  
 PRIOR FILING DATE: 1998-06-25  
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 PRIOR FILING DATE: 1998-06-25  
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 PRIOR FILING DATE: 1998-07-07  
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 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 657; DB 10; Length 123;  
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 b 1 MACRLSFLMGTLTSVQVLAQLDALLVFPQVAQLSCTLSPOHVTIRYGVSWYQOR 60

Y 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISPQPEDDADYICSVGYG 120  
 b 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISPQPEDDADYICSVGYG 120

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 b 121 PSP 123

RESULT 10  
 IS-09-993-604-117  
 Sequence 117, Application US/09993604  
 Patent No. US20020137075A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
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 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
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 APPLICANT: Gurney, Austin L.  
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 APPLICANT: Napier, Mary A.  
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 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2730P1C25  
 CURRENT APPLICATION NUMBER: US/09/993,604  
 CURRENT FILING DATE: 2001-11-14  
 PRIOR FILING DATE: 1997-06-16  
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 PRIOR FILING DATE: 1997-10-17  
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PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 657; DB 10; Length 123;  
Best Local Similarity 100.0%; Pred. No. 2.1e-63; Indels 0; Gaps 0;  
Matches 123; Conservative 0; Mismatches 0

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DB 1 MACRCLSFILMGTFILSVQTVLAQLDALLVFPQVQAQSCITLSPQHVITRDYGVSWYQQR 60  
QY 61 AGSAPRYLLVYRSEEDHHPADIPIRFSAAKDEAHNACVLTISPQPEDDADYICSVGYG 120  
DB 61 AGSAPRYLLVYRSEEDHHPADIPIRFSAAKDEAHNACVLTISPQPEDDADYICSVGYG 120  
QY 121 FSP 123  
DB 121 FSP 123

RESULT 11  
US-09-990-456-117  
Sequence 117, Application US/09990456  
Patent No. US20020137890A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C22  
CURRENT APPLICATION NUMBER: US/09/990,456  
CURRENT FILING DATE: 2001-11-14

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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

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b 1 MACRCLSLFLMGTFLSVTSQVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQOR 60  
Y 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISPPQEDDADYICSVGYG 120  
b 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISPPQEDDADYICSVGYG 120  
Y 121 FSP 123  
b 121 FSP 123

RESULT 12  
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Patent No. US20020142961A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
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APPLICANT: Gurney, Austin L.  
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APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C55  
CURRENT APPLICATION NUMBER: US/09/989,721  
CURRENT FILING DATE: 2001-11-19  
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Query Match 100.0%; Score 657; DB 10; Length 123;  
Best Local Similarity 100.0%; Pred. No. 2.le-63; Indels 0; Gaps 0;  
Matches 123; Conservative 0; Mismatches 0;

Qy 1 MACRCLSFLMGTFLLSVSQTVLQAQLDALLVFPFGVAQLSCTLSFQHVITRDYGVSWYQOR 60  
Db 1 MACRCLSFLMGTFLLSVSQTVLQAQLDALLVFPFGVAQLSCTLSFQHVITRDYGVSWYQOR 60

Qy 61 AGSAPRYLLYRSEEDHHRPADIPRFSAAKDEAHNACVLTISPQPEDDADYCVSYG 120  
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Db 121 FSP 123

RESULT 13  
US-09-992-598-117  
Sequence 117, Application US/09992598  
Patent No. US20020160384A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2730P1C20  
 CURRENT APPLICATION NUMBER: US/09/992,598  
 PRIOR FILING DATE: 2001-11-14  
 PRIOR APPLICATION NUMBER: 60/049787  
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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 657; DB 10; Length 123;  
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b 1 MACRCLSFLIMGTFLSVSTVLAQLDALVFPQVAQLSCTLSPQHVTRIDYGVSWYQOR 60

Y 61 AGSAPRYLLYRSEEDHRRPADIPRFSAAKDEAHNACVLTISPQVEDDADYCSVGYG 120  
b 61 AGSAPRYLLYRSEEDHRRPADIPRFSAAKDEAHNACVLTISPQVEDDADYCSVGYG 120

Y 121 FSP 123  
b 121 FSP 123

RESULT 14  
US-09-981-876-200  
Sequence 200, Application US/09981876  
Patent No. US20020164669A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 70 Human Secreted Proteins  
FILE REFERENCE: P2001P1  
CURRENT APPLICATION NUMBER: US/09/981,876  
CURRENT FILING DATE: 2001-10-19  
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PRIOR FILING DATE: 1997-04-11  
PRIOR APPLICATION NUMBER: 60/048,974  
PRIOR FILING DATE: 1997-06-06

PRIOR APPLICATION NUMBER: 60/056,886  
PRIOR FILING DATE: 1997-08-22  
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PRIOR FILING DATE: 1997-05-23  
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PRIOR APPLICATION NUMBER: 60/047,588  
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PRIOR APPLICATION NUMBER: 60/043,578  
PRIOR FILING DATE: 1997-04-11  
PRIOR APPLICATION NUMBER: 60/043,576  
PRIOR FILING DATE: 1997-04-11  
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PRIOR FILING DATE: 1997-05-23  
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PRIOR FILING DATE: 1997-09-05  
PRIOR APPLICATION NUMBER: 60/056,884  
PRIOR FILING DATE: 1997-08-22  
NUMBER OF SEQ ID NOS: 280  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 200  
LENGTH: 123

Query Match 100.0%; Score 657; DB 10; Length 123;  
Best Local Similarity 100.0%; Pred. No. 2.1e-63;  
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MACRCLSFLLMGTFLSVSQTVLAAQDALLVPPGQVAQLSCTLSPOHVTIRDYGVSWYQOR 60  
Db 1 MACRCLSFLLMGTFLSVSQTVLAAQDALLVPPGQVAQLSCTLSPOHVTIRDYGVSWYQOR 60  
Qy 61 AGSAPRYLLYRSEEDHHRPADIPDRFSAKDEAHNACVLTISPVPQEDDADYCVSVYG 120  
Db 61 AGSAPRYLLYRSEEDHHRPADIPDRFSAKDEAHNACVLTISPVPQEDDADYCVSVYG 120  
Qy 121 FSP 123  
Db 121 FSP 123

RESULT 15  
US-09-989-293A-117  
Sequence 117, Application US/09989293A  
Patent No. US20020177164A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deanoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
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APPLICANT: Stewart, Timothy A.

APPLICANT: Tamas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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FILE REFERENCE: P2730PIC66  
CURRENT APPLICATION NUMBER: US/09/989,293A  
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PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089907  
PRIOR FILING DATE: 1998-06-18  
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PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089947  
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PRIOR FILING DATE: 1998-06-24  
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PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090540  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090542  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090676  
PRIOR FILING DATE: 1998-06-25

PRIOR APPLICATION NUMBER: 60/090678  
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PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090694  
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PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 657; DB 10; Length 123;  
Best Local Similarity 100.0%; Pred. No. 2.1e-63;  
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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db 1 MACRCLSPFLMGTFSLVSQTVLAQLDALLVFPQVAGLSCTLSFQHVHTIRDYGVSWYQOR 60

Qy 61 AGSAPRYLLYRSEBHHRPADIPDRFSAKDEAHNACVLTISPQVOPEDDADYCVSVYG 120  
Db 61 AGSAPRYLLYRSEBHHRPADIPDRFSAKDEAHNACVLTISPQVOPEDDADYCVSVYG 120

Qy 121 FSP 123  
Db 121 FSP 123

Search completed: February 9, 2004, 12:56:22  
Job time : 37.0135 secs

GenCore version 5.1.6  
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4 protein - protein search, using sw model

in on: February 9, 2004, 12:44:37 ; Search time 15.5135 Seconds  
(without alignments)  
335.465 Million cell updates/sec

itle: US-09-981-876-200  
affect score: 657  
sequence: 1 MACRCLFLLMGLTSLVSQT.....PVQPEDDADYCSVGXGFSF 123

oring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

sarched: 328717 seqs, 42310858 residues

oral number of hits satisfying chosen parameters: 328717

inimum DB seq length: 0  
aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
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6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	657	100.0	123	4	US-09-996-243-117 Sequence 117, Appl
2	201.5	30.7	249	4	US-08-918-148-79 Sequence 74, Appl
3	193	29.4	109	3	US-09-157-370-5 Sequence 5, Appl
4	193	29.4	245	4	US-10-039-785-42 Sequence 42, Appl
5	191	29.1	110	1	US-07-988-923-16 Sequence 16, Appl
6	191	29.1	110	2	US-08-362-780-16 Sequence 16, Appl
7	187	28.5	235	3	US-09-049-672A-10 Sequence 10, Appl
8	187	28.5	245	4	US-10-039-785-49 Sequence 49, Appl
9	186.5	28.4	238	4	US-08-793-450-6 Sequence 6, Appl
10	186	28.3	107	4	US-09-025-769B-34 Sequence 34, Appl
11	186	28.3	107	4	US-09-025-769B-55 Sequence 55, Appl
12	186	28.3	112	2	US-08-665-202-39 Sequence 39, Appl
13	186	28.3	112	4	US-09-315-574-39 Sequence 39, Appl
14	184.5	28.1	131	1	US-08-305-683A-4 Sequence 4, Appl
15	183	27.9	109	4	US-09-025-769B-32 Sequence 32, Appl
16	183	27.9	109	4	US-09-025-769B-51 Sequence 51, Appl
17	183	27.9	111	2	US-08-652-816A-15 Sequence 48, Appl
18	183	27.9	245	4	US-10-039-785-48 Sequence 5, Appl
19	183	27.9	258	2	US-08-665-202-5 Sequence 5, Appl
20	183	27.9	258	4	US-09-315-574-5 Sequence 51, Appl
21	182	27.7	245	4	US-10-039-785-51 Sequence 52, Appl
22	182	27.7	245	4	US-10-039-785-52 Sequence 63, Appl
23	181.5	27.6	110	3	US-09-240-274-63 Sequence 14, Appl
24	181.5	27.6	111	2	US-08-958-201-14 Sequence 7, Appl
25	181.5	27.6	236	3	US-09-049-672A-7 Sequence 40, Appl
26	181	27.5	111	2	US-08-665-202-40 Sequence 40, Appl
27	181	27.5	111	4	US-09-315-574-40 Sequence 40, Appl

## ALIGNMENTS

### RESULT 1

US-09-996-243-117  
; Sequence 117, Application US/09996243  
; Patent No. 6478825  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fogt, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C13  
; CURRENT APPLICATION NUMBER: US/09/996,243  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28

Sequence 12, Appl  
Sequence 79, Appl  
Sequence 20, Appl  
Sequence 47, Appl  
Sequence 11, Appl  
Sequence 36, Appl  
Sequence 36, Appl  
Sequence 18, Appl  
Sequence 7, Appl  
Sequence 4, Appl  
Sequence 53, Appl  
Sequence 19, Appl  
Sequence 112, Appl

28 180.5 27.5 111 2 US-08-958-201-12  
29 180.5 27.5 244 4 US-08-318-148-79  
30 180 27.4 108 4 US-09-025-769B-20  
31 180 27.4 245 4 US-10-039-785-47  
32 179.5 27.3 310 4 US-09-079-029-11  
33 179 27.2 111 2 US-08-665-202-36  
34 179 27.2 111 4 US-09-315-574-36  
35 179 27.2 112 4 US-09-025-769B-18  
36 179 27.2 262 4 US-09-069-821-4  
37 179 27.2 282 4 US-09-420-592A-7  
38 178.5 27.2 249 4 US-10-039-785-53  
39 178.5 27.2 278 3 US-09-260-527-1  
40 178.5 27.2 280 3 US-09-372-425A-4  
41 178 27.0 234 4 US-09-025-769B-33  
42 177.5 27.0 110 4 US-09-025-769B-53  
43 177.5 27.0 110 4 US-09-025-769B-19  
44 177.5 27.0 112 4 US-09-025-769B-19  
45 177 26.9 113 1 US-08-211-202-112

1	PRIOR FILING DATE: 1998-06-17	
2	PRIOR APPLICATION NUMBER: 60/089653	
3	PRIOR FILING DATE: 1998-06-17	
4	PRIOR APPLICATION NUMBER: 60/089801	
5	PRIOR FILING DATE: 1998-06-18	
6	PRIOR APPLICATION NUMBER: 60/089907	
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58	PRIOR APPLICATION NUMBER: 60/090862	
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62	PRIOR APPLICATION NUMBER: 60/091360	
63	PRIOR FILING DATE: 1998-07-01	
64	PRIOR APPLICATION NUMBER: 60/091478	
65	PRIOR FILING DATE: 1998-07-02	
66	PRIOR APPLICATION NUMBER: 60/091544	
67	PRIOR FILING DATE: 1998-07-01	
68	PRIOR APPLICATION NUMBER: 60/091519	
69	PRIOR FILING DATE: 1998-07-02	
70	PRIOR APPLICATION NUMBER: 60/091626	
71	PRIOR FILING DATE: 1998-07-02	
72	PRIOR APPLICATION NUMBER: 60/091633	
73	PRIOR FILING DATE: 1998-07-02	

PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 657; DB 4; Length 123;  
Best Local Similarity 100.0%; Pred. No. 1.6e-62;  
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MACRCLFLLMGTFLLSVQTLAQLDALLVPPGVAQLSCTLSPOHVTIRDYGVSVYQOR 60  
1 MACRCLFLLMGTFLLSVQTLAQLDALLVPPGVAQLSCTLSPOHVTIRDYGVSVYQOR 60  
61 AGSAPRYLLYRSEEDHRRPADIPDRFSAAKDEAHNACVLTISPVPQEDDADYYCSVG 120  
61 AGSAPRYLLYRSEEDHRRPADIPDRFSAAKDEAHNACVLTISPVPQEDDADYYCSVG 120  
121 FSP 123  
121 FSP 123

RESULT 2  
S-08-918-148-74  
Sequence 74, Application US/08918148A  
Patent No. 6342220  
GENERAL INFORMATION:  
APPLICANT: Adams, Camellia  
APPLICANT: W.  
APPLICANT: Carter, Paul J.  
APPLICANT: Fendly, Brian M.  
APPLICANT: Gurney, Austin L.  
TITLE OF INVENTION: Agonist Antibodies  
FILE REFERENCE: P0979  
CURRENT APPLICATION NUMBER: US/08/918,148A  
CURRENT FILING DATE: 1997-08-25  
NUMBER OF SEQ ID NOS: 79  
SEQ ID NO 74  
LENGTH: 249  
TYPE: PRT  
ORGANISM: artificial  
S-08-918-148-74

Query Match 30.7%; Score 201.5; DB 4; Length 249;  
Best Local Similarity 47.5%; Pred. No. 8.3e-14;  
Matches 47; Conservative 16; Mismatches 29; Indels 7; Gaps 3;

18 SQTVAQLDALLVPPGVAQLSCTLSPOHVTIRDYGVSVYQORAGSAPRYLLYRSEEDH 77  
136 SQSVLTQPSVSGSPQSITISCTGTSSGVGGYNY-VSWYQQHPKAPKLLIYGN- 190  
78 HRPADIPDRFSAAKDEAHNACVLTISPVPQEDDADYYCS 116  
191 NRPSGVDRFSAK--SGNTASLTISGLQAEDEADYFCS 227

RESULT 3  
S-09-157-370-5  
Sequence 5, Application US/09157370A  
Patent No. 626238  
GENERAL INFORMATION:  
APPLICANT: STEIPE, Boris  
APPLICANT: STEINBACHER, Stefan  
TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES  
FILE REFERENCE: P8341-8072  
CURRENT APPLICATION NUMBER: US/09/157,370A  
CURRENT FILING DATE: 1998-09-21  
EARLIER APPLICATION NUMBER: 08/765,179  
EARLIER FILING DATE: 1997-01-14  
EARLIER APPLICATION NUMBER: PCT/EP95/02626  
EARLIER FILING DATE: 1995-07-06

EARLIER APPLICATION NUMBER: DE/P44 25 115.7  
EARLIER FILING DATE: 1994-07-15  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 109  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-157-370-5

Query Match 29.4%; Score 193; DB 3; Length 109;  
Best Local Similarity 41.7%; Pred. No. 2.4e-13;  
Matches 45; Conservative 18; Mismatches 29; Indels 16; Gaps 4;

QY 19 QTVLAQLDALLVPPGVAQLSCTLSPOHVTIRDYGVSVYQORAGSAPRYLLYRSEEDH 78  
DB 1 QSELTQPPSVSPGQVTITSCGSDSLGIGY----VSWYQQHPKAPKLLIY----DDNK 52  
QY 79 RPADIPDRFSAAKDEAHNACVLTISPVPQEDDADYYC-----SVGYG 120  
DB 53 RPSGIPDRFSGSK--SGNTASLTISGLQAEDEADYYCQSWDSSSVVFG 98

RESULT 4  
US-10-039-785-42  
Sequence 42, Application US/10039785  
Patent No. 6538938  
GENERAL INFORMATION:  
APPLICANT: Salcedo et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL  
FILE REFERENCE: PF550  
CURRENT APPLICATION NUMBER: US/10/039,785  
CURRENT FILING DATE: 2002-05-07  
PRIOR APPLICATION NUMBER: 60/369,860  
PRIOR FILING DATE: 2002-04-05  
PRIOR APPLICATION NUMBER: 60/341,237  
PRIOR FILING DATE: 2001-12-20  
PRIOR APPLICATION NUMBER: 60/331,310  
PRIOR FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/331,044  
PRIOR FILING DATE: 2001-11-07  
PRIOR APPLICATION NUMBER: 60/327,364  
PRIOR FILING DATE: 2001-10-09  
PRIOR APPLICATION NUMBER: 60/323,807  
PRIOR FILING DATE: 2001-09-21  
PRIOR APPLICATION NUMBER: 60/309,176  
PRIOR FILING DATE: 2001-08-02  
PRIOR APPLICATION NUMBER: 60/294,981  
PRIOR FILING DATE: 2001-06-04  
PRIOR APPLICATION NUMBER: 60/293,473  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 42  
LENGTH: 245  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: T1014A04 scFv  
US-10-039-785-42

Query Match 29.4%; Score 193; DB 4; Length 245;  
Best Local Similarity 38.5%; Pred. No. 6.5e-13;  
Matches 47; Conservative 19; Mismatches 32; Indels 24; Gaps 4;

QY 12 GTFLSVS-----QTVLAQLDALLVPPGVAQLSCTLSPOHVTIRDYGV 54  
DB 111 GTWVTVSSGGGGGGGGGSAQSVLTQPPSAGSGPQSVTISCTGTSDVGGYNY-V 169  
QY 55 SWYQORAGSAPRYLLYRSEEDHRRPADIPDRFSAAKDEAHNACVLTISPVPQEDDADYY 114  
DB 170 SWYQQHPKAPKLLIYGNQ-----RPSGVDRFSGSK--SGNTASLTISGLQAEDEADYY 223

$$\begin{array}{c} \text{y} \\ 115 \text{ CS} \quad 116 \\ \quad \quad \quad \parallel \\ 224 \text{ CS} \quad 225 \\ \text{p} \end{array}$$

ESULT 5  
S-07-988-925-16  
Sequence 16, Application US/07988925  
Patent No. 5585097

APPLICANT: Bolt, Sarah L  
APPLICANT: Clark, Michael R  
APPLICANT: Gorman, Scott D  
APPLICANT: Routledge, Edward G  
APPLICANT: Waldmann, Herman  
TITLE OF INVENTION: antibody preparation  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:

ADDRESS: Nixon and Vanderhye pc  
STREET: 11th Floor, 1100 No. 5585097th Glebe Road  
CITY: Arlington  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22201

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/988,925  
FILING DATE:

CLASSIFICATION: 424  
PRIOR APPLICATION NUMBER: GB 9206422.9  
APPLICATION NUMBER: GB 9206422.9  
FILING DATE: 24-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/GB92/01933  
FILING DATE: 21-OCT-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Michard, Leonard C  
REGISTRATION NUMBER: 29009  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 7038164000  
TELEFAX: 7038164100  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 110 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
988-925-16

Query Match 29.1%; Score 191; DB 1; Length 110;  
Best Local Similarity 43.2%; Pred. No. 4e-13;  
Matches 41; Conservative 17; Mismatches 31; Indels 6; Gaps 2;

QY 21 VLAQLDALLVPPGQVAQLSCTLS PQHVTIRDYGVSWYQQAGSAPRYLLYYRSEDHHP 80  
:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
Db 3 MLTPHVSVPSPGKTVIIISCTLSSGN--IENNYHWYQOGRGATVTVF---DDDKRP 56

Qy 81 ADIPDRFSAAKDEAHNACVLITISVPQEDDADYIC 115  
:||||:|:|:||||:|:|:|  
Db 57 DGVPDRFGSIRSSNSASLTISGLOTEADADYIC 91

RESULT 6  
US-08-362-780-16  
; Sequence 16, Application US/08362780  
; Patent No. S968509  
; GENERAL INFORMATION:

APPLICANT: Gorman, Scott D  
 APPLICANT: Routledge, Edward G  
 APPLICANT: Walckmann, Herman  
 TITLE OF INVENTION: Antibody Preparation  
 NUMBER OF SEQUENCES: 26  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Nixon and Vanderhye pc  
 STREET: 8th Floor, 1100 No. 5968509th Glee Road  
 CITY: Arlington  
 STATE: Virginia  
 COUNTRY: USA  
 ZIP: 22201  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/362,780

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/362,780

APPLICATION NUMBER: US/08/362,780

FILING DATE: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/862,543  
 FILING DATE: 23-JUNE-1992  
 APPLICATION NUMBER: GB 9021679.7  
 FILING DATE: 05-OCT-1990  
 PRIOR APPLICATION DATA: WO PCT/GB91/01726  
 FILING DATE: 04-OCT-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mitchard, Leonard C  
 REGISTRATION NUMBER: 29009  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 7038164000

TELEFAX: 7038164100  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 110 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 362-780-15

Query Match 29.1%; Score 191; DB 2; Length 110;  
Best Local Similarity 43.2%; Pred. No. 4e-13;  
Matches 41; Conservative 17; Mismatches 31; Indels 6; Gaps 2;

[illegible]

QY 81 ADIPDRFSAAKDEAHNACVLTIISPQPEDDADYYC 115  
: : : : :  
pb 57 DGVDPFRSGSIDRSSNSALTSIGLQTEDEADYYC 91

RESULT 7  
US-09-049-672A-10  
; Sequence 10, Application US/09049672A  
; Patent No. 6135941  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.

APPLICANT: Hillman, Jennifer L.  
APPLICANT: Lal, Preeti  
APPLICANT: Tang, Y. Tom  
APPLICANT: Yue, Henry  
APPLICANT: Au-Young, Janice  
APPLICANT: Corley, Neil C.  
APPLICANT: Guegler, Karl J.  
APPLICANT: Baughn, Mariah R.  
TITLE OF INVENTION: HUMAN IMMUN  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:



ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Forter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/049,672A  
FILING DATE: HEREWITH  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Carrione, Michael C  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PF-0497 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-853-0555  
TELEFAX: 650-845-4166  
TELEX:

INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: THYRN0T10  
CLONE: 2872705

S-09-049-672A-10  
Query Match 28.5%; Score 187; DB 3; Length 235;  
Best Local Similarity 42.3%; Pred. No. 2.7e-12;  
Matches 47; Conservative 20; Mismatches 36; Indels 8; Gaps 4;

Y 6 LSFLLMGTFLSVQTVLAQLDALLVPPGVAQLSCTLSFQHVITRDYGVSWYQQRAGSAP 65  
b 8 LTLITQGTG-SWAQSALTQPAVSFGSGSITISCTGSSDVGGYNY-VSWYQQRSGTAP 65  
Y 66 RYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISVPQPEDDADYYCS 116  
b 66 KLMTY----EVSNRPSGVNRFSGSK--SGNTASLTISGLQADDEADYYCS 110

RESULT 8  
US-10-039-785-49  
Sequence 49, Application US/10039785  
Patent No. 6538938  
GENERAL INFORMATION:  
APPLICANT: Salcedo et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL  
TITLE OF INVENTION: Receptors  
FILE REFERENCE: PF550  
CURRENT APPLICATION NUMBER: US/10/039,785  
CURRENT FILING DATE: 2002-05-07  
PRIOR APPLICATION NUMBER: 60/369,860  
PRIOR FILING DATE: 2002-04-05  
PRIOR APPLICATION NUMBER: 60/341,237  
PRIOR FILING DATE: 2001-12-20  
PRIOR APPLICATION NUMBER: 60/331,310  
PRIOR FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/331,044  
PRIOR FILING DATE: 2001-11-07  
PRIOR APPLICATION NUMBER: 60/327,364  
PRIOR FILING DATE: 2001-10-09  
PRIOR APPLICATION NUMBER: 60/323,807  
PRIOR FILING DATE: 2001-09-21

PRIOR APPLICATION NUMBER: 60/309,176  
PRIOR FILING DATE: 2001-08-02  
PRIOR APPLICATION NUMBER: 60/294,981  
PRIOR FILING DATE: 2001-06-04  
PRIOR APPLICATION NUMBER: 60/293,473  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 49  
LENGTH: 245  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: T1014G04 scFv  
US-10-039-785-49

Query Match 28.5%; Score 187; DB 4; Length 245;  
Best Local Similarity 37.7%; Pred. No. 2.8e-12;  
Matches 46; Conservative 18; Mismatches 34; Indels 24; Gaps 4;

QY 12 GTFLSVS-----QTVAQLDALLVPPGVAQLSCTLSFQHVITRDYGV 54  
DB 111 GTLVTVSSGGGGGGGGGSAQPVLTQPPGASGPGSVTISCTGSSDVGSVEY-V 169  
QY 55 SWYQQRAGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISVPQPEDDADYY 114  
DB 170 SWYQQRHPCAKPRLMI-----SEVNRPSGVNRFSGSK--SGNTASLTISGLQADDEADYY 223  
QY 115 CS 116  
DB 224 CS 225

RESULT 9  
US-08-793-450-6  
Sequence 6, Application US/08793450  
Patent No. 6312690  
GENERAL INFORMATION:  
APPLICANT: EDELMAN, LENA  
APPLICANT: MARGARITTE, CHRISTEL  
APPLICANT: KACZOREK, MICHEL  
APPLICANT: CHABETHI, HASSAN  
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D  
TITLE OF INVENTION:  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESSEE: P.C.  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/793,450  
FILING DATE: 03-MAR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 94/10566  
FILING DATE: 02-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION/DOCKET NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 660-118-0 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 6:



TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to  
TITLE OF INVENTION: Tumor Antigens  
NUMBER OF SEQUENCES: 141  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 13-JUN-1996  
CLASSIFICATION: 424

PRIOR APPLICATION NUMBER: US 60/000,238  
FILING DATE: 14-JUN-1995  
PRIOR APPLICATION DATA:  
FILING DATE: 15-JUN-1995  
APPLICATION NUMBER: US 60/000,250  
FILING DATE: 15-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom

REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 02307E-061410  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 112 amino acids  
TYPE: amino acid

STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-09-665-202-39

Query Match 28.3%; Score 186; DB 2; Length 112;  
Best Local Similarity 41.8%; Pred. No. 1.4e-12;  
Matches 41; Conservative 21; Mismatches 28; Indels 8; Gaps 4;

19 QTVLAQLDALLVFGQVAQLSCTLSPOHVTIRYGVSWYQQRAGSAPRYLLYRSEEDHH 78  
1 QSVLTQPPSVSAAPGQKVTISCGSSNIG-NNY-VSWYQQLPGTAPKLLIY----SDNQ 54

79 RPADIPDRFSAKDEAHNACVLTISPVQPEDDADYYCS 116  
55 RPSGVDPDRFSGSK--SGTSASLAISGLRSEDEADYYCA 90

RESULT 13

US-09-315-574-39  
Sequence 39, Application US/09315574  
Patent No. 6512097

GENERAL INFORMATION:

APPLICANT: Marks, James D.

APPLICANT: Schier, Robert

TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to  
Tumor Antigens

NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:

ADDRESSEE: Majestic, Parsons, Siebert & Heule P.C.

STREET: Four Embarcadero Center, Suite 1100

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-4106

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 20-MAY-99  
CLASSIFICATION: 530

PRIOR APPLICATION NUMBER: US 60/000,238  
FILING DATE: 14-JUN-1995  
PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 60/000,250  
FILING DATE: 15-JUN-1995  
PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 08/665,202  
FILING DATE: 13-JUN-1996  
ATTORNEY/AGENT INFORMATION:

NAME: Hunter, Tom

REGISTRATION NUMBER: 38,498

REFERENCE/DOCKET NUMBER: 02307E-061411

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 112 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-315-574-39

Query Match 28.3%; Score 186; DB 4; Length 112;  
Best Local Similarity 41.8%; Pred. No. 1.4e-12;  
Matches 41; Conservative 21; Mismatches 28; Indels 8; Gaps 4;

19 QTVLAQLDALLVFGQVAQLSCTLSPOHVTIRYGVSWYQQRAGSAPRYLLYRSEEDHH 78  
1 QSVLTQPPSVSAAPGQKVTISCGSSNIG-NNY-VSWYQQLPGTAPKLLIY----SDNQ 54

79 RPADIPDRFSAKDEAHNACVLTISPVQPEDDADYYCS 116  
55 RPSGVDPDRFSGSK--SGTSASLAISGLRSEDEADYYCA 90

RESULT 14

US-08-305-683A-4  
Sequence 4, Application US/08305683A  
Patent No. 5646041

GENERAL INFORMATION:

APPLICANT: HARFELDT, Elisabeth

APPLICANT: LAKE, Philip

APPLICANT: NOTTAGE, Barbara

APPLICANT: OSTBERG, Lars G.

TITLE OF INVENTION: MONOCLONAL ANTIBODY TO HERPES SIMPLEX

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew

STREET: 379 Lytton Avenue

CITY: Palo Alto

STATE: California

COUNTRY: US

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/305,683A

FILING DATE: 13-SEP-1994

CLASSIFICATION: 424

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/759,279

FILING DATE: 13-SEP-1991

ATTORNEY/AGENT INFORMATION:

NAME: Liebeschuetz, Joe

REGISTRATION NUMBER: 37,505

REFERENCE/DOCKET NUMBER: 11823-005230

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 131 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

JS-08-305-683A-4

Query Match 28.1%; Score 184.5; DB 1; Length 131;

Best Local Similarity 42.0%; Pred. No. 2.4e-12;

Matches 42; Conservative 19; Mismatches 32; Indels 7; Gaps 3;

2Y 16 SVSQTVLAQLDALLVPPGQVQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYRSEE 75

2b 17 SWAQSVLTQPPSVSGAPGQGVLTSGTSRSGNIG-AGYDVHWYQHLPGTAPKLLIY----G 71

2Y 76 DHRPADIPDRSAAXDEAHNACVLTISPVQPEDDADYVC 115

Db 72 DNRPSGVPDRFSGSK--SGTSASLAITGLQAEDEADYIC 109

## RESULT 15

US-09-025-769B-32

; Sequence 32, Application US/09025769B

; Patent No. 6300064

; GENERAL INFORMATION:

; APPLICANT: Krappik, Achim

; APPLICANT: Pack, Peter

; APPLICANT: Ilag, Vic

; APPLICANT: Ge, Liming

; APPLICANT: Moroney, Simon

; APPLICANT: Flueckthun, Andreas

; TITLE OF INVENTION: Protein/(Poly)peptide libraries

; NUMBER OF SEQUENCES: 373

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish &amp; Neave

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10021

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/025,769B

; FILING DATE: 18-FEB-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 95 11 3021.0

; FILING DATE: 18-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: James F. Haley, Jr., Esq.

; REGISTRATION NUMBER: 27,794

; REFERENCE/DOCKET NUMBER: MORPHO/5

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 596-9000

; TELEFAX: (212) 596-9090

; INFORMATION FOR SEQ ID NO: 32:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 109 amino acids

; TYPE: amino acid

; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-025-769B-32

Query Match 27.9%; Score 183; DB 4; Length 109;

Best Local Similarity 40.0%; Pred. No. 2.8e-12;

Matches 42; Conservative 22; Mismatches 33; Indels 8; Gaps 4;

QY 19 QTVLAQLDALLVPPGQVQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYRSEDDHH 78

Db 1 QSVLTQPPSVSGAPGQGVLTSGTSRSGNIG-SNI-VSWYQQLPGTAPKLLIY----DNNQ 54

QY 79 RPADIPDRSAAXDEAHNACVLTISPVQPEDDADYVC 123

Db 55 RPSGVPDRFSGSK--SGTSASLAITGLQAEDEADYVCQHYTTP 97

Search completed: February 9, 2004, 12:49:04

Job time : 15.5135 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

M protein - protein search, using sw model

un on: February 9, 2004, 09:56:08 ; Search time 14.7162 Seconds  
(without alignments)  
646.953 Million cell updates/sec

file: US-09-981-876-200\_COPY\_25\_123

effect score: 538  
sequence: 1 LDALLVFPQVQLSCTLSLSP.....PVQPEDDADYCVSGVGFSP 99

coring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

searched: 283308 seqs, 96168682 residues

total number of hits satisfying chosen parameters: 283308

inimum DB seq length: 0  
aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

atabase : PIR 76: \*  
1: P1:1: \*  
2: P1:2: \*  
3: P1:3: \*  
4: P1:4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	372.5	69.2	123	2 S35302	B-cell protein 8HS-20 precursor - mouse
2	233.5	43.4	142	2 B28344	VpreB protein precursor - mouse
3	229.5	42.7	142	2 A28344	VpreB protein precursor - mouse
4	207.5	38.6	139	2 S00258	VpreB protein - hu
5	207.5	38.6	145	2 I57832	Vpre-B protein - h
6	200	37.2	111	1 L6HUST	Ig lambda chain V-
7	197	36.6	112	1 L6HUAR	Ig lambda chain V-
8	192.5	35.8	232	2 S17399	Ig lambda chain pr
9	191.5	35.6	243	2 S25755	Ig lambda chain -
10	189.5	35.2	120	2 PS0055	Ig lambda chain pr
11	185.5	34.5	99	2 S36058	Ig lambda chain -
12	185.5	34.5	111	1 L2HDMC	Ig lambda chain V-
13	185	34.4	111	1 L6HULT	Ig lambda chain V-
14	184.5	34.3	120	2 PS0056	Ig lambda chain pr
15	184.5	34.3	136	2 S16848	Ig lambda chain V-
16	183.5	34.1	118	2 A32529	Ig lambda chain pr
17	183	34.0	131	1 L6HUEB	Ig lambda chain pr
18	182.5	33.9	133	2 A28565	Ig lambda chain (D
19	182.5	33.9	216	2 S69120	Ig lambda chain -
20	181.5	33.7	99	2 S36057	Ig lambda chain -
21	180.5	33.6	98	2 S36068	Ig lambda chain pr
22	180.5	33.6	111	1 L2HUBO	Ig lambda chain V-
23	180.5	33.6	117	2 S04525	Ig lambda chain V
24	180	33.5	107	2 B46516	Ig lambda chain -
25	178.5	33.2	235	2 S25758	Ig lambda chain V
26	176.5	32.8	94	2 C32529	Ig lambda chain V
27	176.5	32.8	111	2 S46397	Ig lambda chain V
28	176.5	32.8	112	2 S31515	Ig lambda chain V
29	176	32.7	108	2 S38498	Ig lambda chain -

30 175.5 32.6 99 2 S36051  
31 175.5 32.6 106 2 S40091  
32 175.5 32.6 112 1 L2HUNG  
33 175.5 32.6 234 2 A39956  
34 175 32.5 111 1 L2HUNW  
35 174.5 32.4 99 2 S36056  
36 173.5 32.2 111 2 S19673  
37 173.5 32.2 132 2 A55410  
38 173 32.2 112 2 D44151  
39 173 32.2 113 2 A29700  
40 172.5 32.1 99 2 S36052  
41 172.5 32.1 99 2 S36053  
42 172.5 32.1 109 1 L2HUBR  
43 172.5 32.1 112 2 S51148  
44 172.5 32.1 118 2 S12627  
45 171.5 31.9 110 2 S57412

ALIGNMENTS

RESULT 1

S35302  
B-cell protein 8HS-20 precursor - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 31-Dec-1993 #sequence\_revision 02-Jun-1994 #text\_change 20-Jun-2000  
C:Accession: S35302  
R:Shirasawa, T.; Ohnishi, K.; Hagiwara, S.; Shigemoto, K.; Takebe, Y.; Rajewsky, K.; Tal  
EMBO J. 12, 1827-1834, 1993  
A>Title: A novel gene product associated with mu chains in immature B cells.  
A:Reference number: S35302; MUID:93259124; PMID:8491176  
A:Accession: S35302  
A:Molecule type: DNA  
A:Residues: 1-123 <SHI>  
A:Cross-references: EMBL:D13208; NID:9286064; PIDN:BAA02495.1; PID:9286065  
C:Genetics:  
A:Gene: 8HS-20  
A:Introns: 18/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: B-cell  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-123/Product: B-cell protein 8HS-20 #status predicted <MAT>

Query Match 69.2%; Score 372.5; DB 2; Length 123;  
Best Local Similarity 69.4%; Pred. No. 2.4e-31;  
Matches 68; Conservative 11; Mismatches 18; Indels 1; Gaps 1;

QY 2 DALLVFPQVQLSCTLSLSPQHVITRDYGVSVYQVQAGSAPRYLLYRSEEDHHRPADIPD 61

Db 27 DAFSVFPQGDHLSCITNSQATAGDIGSVYQVQVQGSAP-HLLYYAAEEHYPADIPD 85

QY 62 RPSAAKDEAHNACVLTISPQVEDDADYCVSGVGFSP 99

Db 86 RFSATVDAAHNAACILITSPVLPEDDADYCVSGVGFSP 123

RESULT 2

B28344  
VpreB protein precursor - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 05-Nov-1999  
C:Accession: B28344  
R:Kudo, A.; Melchers, F.  
EMBO J. 6, 2267-2272, 1987  
A>Title: A second gene, VpreB in the lambda-5 locus of the mouse, which appears to be se  
A:Reference number: A91077; MUID:88029315; PMID:3117530  
A:Accession: B28344  
A:Molecule type: DNA  
A:Residues: 1-142 <KUD>  
A:Cross-references: GB:X05563; GB:Y00079; NID:955415; PIDN:CAA29077.1; PID:955416  
A>Note: the authors translated the codon GAG for residue 110 as Gln  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F;20-142/Product: VpreB protein #status predicted <MAT>

Query Match 43.4%; Score 233.5; DB 2; Length 142;  
Best Local Similarity 54.7%; Pred. No. 5.8e-17;  
Matches 47; Conservative 9; Mismatches 29; Indels 1; Gaps 1;  
1y 9 GQVAQLSCTLSPOHVTIRDYGVSWYQQRAGSAPRYLLYRSEEDHHRPADIPDRFSAAKD 68  
1b 34 GATIRLSCTLSNDH-NIGIYSYVWYQQRGHPHPRLLRYFSHSDKHQGPDIIPRFSGSKD 92  
1y 69 EAHNACVLITSPVQPEDDADYYCSVG 94  
1b 93 TARNGLYLSISELQPEDEAVYICAVG 118  
RESULT 3  
128344  
VpreB protein precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 21-Jul-2000  
C:Accession: A28344  
C:Kudo, A.; Melchers, F.  
EMBO J. 6, 2267-2272, 1987  
A:Title: A second gene, VpreB in the lambda-5 locus of the mouse, which appears to be se  
A:Reference number: A91077; MUID:88029315; PMID:3117530  
A:Accession: A28344  
A:Molecule type: DNA  
A:Residues: 1-142 <KUD>  
A:Cross-references: GB:X05556; GB:Y00079; NID:G55409; PIDN:CAA29071.1; PID:G55410  
A:Note: the authors translated the codon GAG for residue 110 as Gln  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:20-142/Product: VpreB protein #status predicted <MAT>  
Query Match 42.7%; Score 229.5; DB 2; Length 142;  
Best Local Similarity 53.5%; Pred. No. 1.5e-16;  
Matches 46; Conservative 9; Mismatches 30; Indels 1; Gaps 1;  
1y 9 GQVAQLSCTLSPOHVTIRDYGVSWYQQRAGSAPRYLLYRSEEDHHRPADIPDRFSAAKD 68  
1b 34 GATIRLSCTLSNDH-NIGIYSYVWYQQRGHPHPRLLRYFSHSDKHQGPDIIPRFSGSKD 92  
1y 69 EAHNACVLITSPVQPEDDADYYCSVG 94  
1b 93 TARNGLYLSISELQPEDEAVYICAVG 118  
RESULT 4  
S00258  
VpreB protein - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 05-Nov-1999  
C:Accession: S00258  
R:Bauer, S.R.; Kudo, A.; Melchers, F.  
EMBO J. 7, 111-116, 1988  
A:Title: Structure and pre-B lymphocyte restricted expression of the VpreB gene in human  
A:Reference number: S00258; MUID:88196069; PMID:3258819  
A:Accession: S00258  
A:Molecule type: DNA  
A:Residues: 1-139 <BAU>  
A:Cross-references: EMBL:M34927; NID:G340304; PIDN:AAA61292.1; PID:G340305  
C:Genetics:  
A:Gene: GDB:VPREB1  
A:Cross-references: GDB:120493; OMIM:146770  
A:Map position: 22q11.2-22q11.2  
A:Superfamily: immunoglobulin V region; immunoglobulin homology  
Query Match 38.6%; Score 207.5; DB 2; Length 139;  
Best Local Similarity 48.8%; Pred. No. 2.7e-14;  
Matches 42; Conservative 12; Mismatches 31; Indels 1; Gaps 1;  
1y 9 GQVAQLSCTLSPOHVTIRDYGVSWYQQRAGSAPRYLLYRSEEDHHRPADIPDRFSAAKD 68  
1b 34 GATIRLSCTLSNDH-NIGIYSYVWYQQRGHPHPRLLRYFSHSDKHQGPDIIPRFSGSKD 92

1y 69 EAHNACVLITSPVQPEDDADYYCSVG 94  
1b 93 TARNGLYLSISELQPEDEAVYICAVG 118  
RESULT 5  
157832  
Vpre-B protein - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
C:Accession: I57832  
R:Guelpa-Fonlupt, V.; Bossy, D.; Alzari, P.; Fumoux, F.; Fougereau, M.; Schiff, C.  
Mol. Immunol. 31, 1099-1108, 1994  
A:Title: The human pre-B cell receptor: structural constraints for a tentative model of  
A:Reference number: I57832; MUID:95021318; PMID:7935499  
A:Accession: I57832  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-145 <RES>  
A:Cross-references: GB:S74019; NID:G693810; PIDN:AA832118.1; PID:G693811  
C:Genetics:  
A:Gene: Vpre-B  
A:Introns: 16/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
Query Match 38.6%; Score 207.5; DB 2; Length 145;  
Best Local Similarity 48.8%; Pred. No. 2.8e-14;  
Matches 42; Conservative 12; Mismatches 31; Indels 1; Gaps 1;  
1y 9 GQVAQLSCTLSPOHVTIRDYGVSWYQQRAGSAPRYLLYRSEEDHHRPADIPDRFSAAKD 68  
1b 34 GATIRLSCTLSNDH-NIGIYSYVWYQQRGHPHPRLLRYFSHSDKHQGPDIIPRFSGSKD 92  
1y 69 EAHNACVLITSPVQPEDDADYYCSVG 94  
1b 93 TARNGLYLSISELQPEDEAVYICAVG 118  
RESULT 6  
16H08T  
Ig lambda chain V-VI region (SUT) - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 02-Sep-1997  
C:Accession: A01988  
R:Solomon, A.; Kyle, R.A.; Frangione, B.  
in Amyloidosis, Glenner, G.G., Casserman, E.F., Benditt, E.P., Calkins, E., Cohn, A.S., <  
A:Title: Light chain variable region subgroups of monoclonal immunoglobulins in amyloid  
A:Reference number: A01988  
A:Accession: A01988  
A:Molecule type: protein  
A:Residues: 1-111 <SOL>  
C:Genetics:  
A:Gene: GDB:IGLV6  
A:Cross-references: GDB:119342; OMIM:147240  
A:Map position: 22q11.2-22q11.2  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into li  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-22/Region: framework 1  
F:15-93/Domain: immunoglobulin homology <IMM>  
F:23-35/Region: complementarity-determining 1  
F:36-50/Region: framework 2  
F:51-57/Region: complementarity-determining 2  
F:58-91/Region: framework 3  
F:92-100/Region: complementarity-determining 3  
F:101-111/Region: framework 4  
F:22-91/Disulfide bonds: #status predicted  
Query Match 37.2%; Score 200; DB 1; Length 111;  
Best Local Similarity 48.8%; Pred. No. 1.2e-13;  
Matches 41; Conservative 12; Mismatches 25; Indels 6; Gaps 2;

```
8 PQVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
14 PGKTVIISCTSDG--TIAGYVQWYQORPGRAPTTVIF---EDTQPSGVDPDRFSGSI 67
68 DEAHNACVLTISPVPQEDDADYYC 91
68 DRSSNSASLTISGLQTEDEADYYC 91

RESULT 7
SHUAR
; lambda chain V-VI region (AR) - human (tentative sequence)
; Species: Homo sapiens (man)
; Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 31-Mar-2000
; Accession: A01987
; Sletten, K.; Natvig, J.B.; Hueby, G.; Juul, J.
; Ischem. J. 195, 561-572, 1991
; Title: The complete amino acid sequence of a prototype immunoglobulin-lambda light-chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lambda dimeric forms. In other cases, such as IgG and IgE, the subunits associate into lambda monomeric forms. In some cases, such as IgA and IgM, the subunits associate into lambda dimeric forms. In other cases, such as IgG and IgE, the subunits associate into lambda monomeric forms.
; Superfamily: immunoglobulin V region; immunoglobulin homology
; Keywords: amyloid; heterotetramer; immunoglobulin
; 15-93/Domain: immunoglobulin homology <IMM>
; 22-91/Disulfide bonds: #status predicted

Query Match 36.6%; Score 197; DB 1; Length 112;
Best Local Similarity 47.6%; Pred. No. 2.6e-13;
Matches 40; Conservative 15; Mismatches 23; Indels 6; Gaps 2;

8 PQVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
14 PGKTVIISCTSDG--SIADSFVQWYQORPGSAPTIVY----DDNQPSGVDPDRFSGSI 67
68 DEAHNACVLTISPVPQEDDADYYC 91
68 DDSGASASLTISGLKTEDEADYYC 91

Query Match 36.6%; Score 197; DB 1; Length 112;
Best Local Similarity 47.6%; Pred. No. 2.6e-13;
Matches 40; Conservative 15; Mismatches 23; Indels 6; Gaps 2;

8 PQVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
14 PGKTVIISCTSDG--SIADSFVQWYQORPGSAPTIVY----DDNQPSGVDPDRFSGSI 67
68 DEAHNACVLTISPVPQEDDADYYC 91
68 DDSGASASLTISGLKTEDEADYYC 91

Query Match 36.6%; Score 197; DB 1; Length 112;
Best Local Similarity 47.6%; Pred. No. 2.6e-13;
Matches 40; Conservative 15; Mismatches 23; Indels 6; Gaps 2;
```

```
9 GOVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKD 68
30 GASARLTCTLSAHKT---YTDWYQOQGEAPRYLMHIKSDGSYTKGTGVDRFSGSSS 86
69 EAHNACVLTISPVPQEDDADYYCVGY 95
87 GADR--YLIIPVQADDEADYYCGADY 111

RESULT 9
S25755
; lambda chain - human
; Species: Homo sapiens (man)
; Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
; Accession: S25755
; Rombaut, G.; Klobbeck, H.G.
; Eur. J. Immunol. 21, 1513-1522, 1991
; Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda chain.
; Reference number: S16439; MUID:91257162; PMID:1904362
; Accession: S25755
; A>Status: preliminary; translation not shown
; A:Molecule type: mRNA
; A:Residues: 1-243 <COM>
; A:Cross-references: EMBL:X57820; NID:g33739; PIDN:CAA40957.1; PID:g33740
; C:Superfamily: immunoglobulin V region; immunoglobulin homology
; C:Keywords: heterotetramer; immunoglobulin
; F:158-226/Domain: immunoglobulin homology <IMM>

Query Match 35.6%; Score 191.5; DB 2; Length 243;
Best Local Similarity 41.1%; Pred. No. 2.2e-12;
Matches 37; Conservative 19; Mismatches 33; Indels 1; Gaps 1;

9 GOVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKD 68
34 GASVRLTCMLS--SGFSVGFWRWYQKPGNPPRYLLYHSDNKGQSGVGPDRFSGSND 92
69 EAHNACVLTISPVPQEDDADYYCVSGYGS 98
93 ASANAGILRLISGLQLEADYYCGTWHSNS 122

RESULT 10
PS0055
; lambda chain precursor V-II region - rabbit
; Species: Oryctolagus cuniculus (domestic rabbit)
; Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 23-Jul-1999
; Accession: PS0055
; R.Hayzer, D.J.; Jaton, J.C.
; Gene 80, 185-191, 1989
; Title: Cloning and sequencing of two functional rabbit germ-line immunoglobulin V lambda
; Reference number: A91614; MUID:90006781; PMID:2507399
; Accession: PS0055
; A:Molecule type: DNA
; A:Residues: 1-120 <HAY>
; A:Cross-references: GB:M27840; NID:g341760; PIDN:AAA31363.1; PID:G552407
; A>Note: the authors translated the codon TTG for residue 97 as Trp
; C:Genetics:
; A:Introns: 17/1
; C:Superfamily: immunoglobulin V region; immunoglobulin homology
; C:Keywords: heterotetramer; immunoglobulin
; F:1-20/Domain: signal sequence #status predicted <SIG>
; F:21-120/Product: Ig lambda chain V-II region #status predicted <MAT>

Query Match 35.2%; Score 189.5; DB 2; Length 120;
Best Local Similarity 43.7%; Pred. No. 1.6e-12;
Matches 38; Conservative 13; Mismatches 31; Indels 5; Gaps 2;

9 GOVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKD 68
35 GASAKLTCTLSAHKT---YTDWYQOQGEAPRYLMOLKSDGSYTKGTGVDRFSGSSS 91
69 EAHNACVLTISPVPQEDDADYYCVGY 95
```





Superfamily: immunoglobulin V region; immunoglobulin homology  
Keywords: heterotetramer; immunoglobulin  
1-20/Domain: signal sequence #status predicted <SIG>  
21-120/Product: Ig lambda chain V-II region #status predicted <MAT>  
Query Match 34.3%; Score 184.5; DB 2; Length 120;  
Best Local Similarity 44.7%; Pred. No. 5.4e-12;  
Matches 39; Conservative 13; Mismatches 29; Indels 5; Gaps 2;  
9 GOVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYRSEEDHRRPADIPDRPSAAK 68  
35 GSSAKLTCTLSAHT---YIIWYQQQGEAPRYLMQLKSDGYTKGTGVPDRFSGSS 91  
69 EAHNACVLTISPQPEDDADYYCSV 93  
92 GADR--YLIISVQADDEADYICGV 114  
RESULT 15  
16848  
g lambda chain V-II region precursor - human  
Species: Homo sapiens (man)  
Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000  
Accession: S60297; S16848  
Kueppers, R.; Fischer, U.; Rajewsky, K.; Gause, A.  
Muncl. Lett. 34, 57-62, 1992  
Title: Immunoglobulin heavy and light chain gene sequences of a human CD5 positive imm  
Reference number: S60295; MUID:93122853; PMID:1282498  
Accession: S60297  
Status: preliminary  
Molecule type: DNA  
Residues: 1-136 <KU2>  
Cross-references: EMBL:X62125; NID:g38334; PIDN:CAA44056.1; PID:g38335  
Superfamily: immunoglobulin V region; immunoglobulin homology  
Keywords: heterotetramer; immunoglobulin  
34-111/Domain: immunoglobulin homology <IMM>  
Query Match 34.3%; Score 184.5; DB 2; Length 136;  
Best Local Similarity 45.9%; Pred. No. 6.2e-12;  
Matches 39; Conservative 14; Mismatches 25; Indels 7; Gaps 3;  
Y 8 PGQVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYRSEEDHRRPADIPDRPSAAK 67  
b 33 PGQSVTISCTGTSSDVGAANY-VSWYQHHPGKAPKLMYEVSE----RPSGVDRFRSGSK 87  
Y 68 DEAHNACVLTISPQPEDDADYYCS 92  
b 88 --SGNTASLTVSGLOAEADYYCT 110  
earch completed: February 9, 2004, 12:46:33  
ob time : 14.7162 secs

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M protein - protein search, using sw model

un on: February 9, 2004, 12:31:07, Search time 9.36487 Seconds  
(without alignments)  
497.139 Million cell updates/sec

title: US-09-981-876-200\_copy\_25\_123

effect score: 538  
sequence: 1 LDALLVFGQVQLSCTLSP.....PVQPEDDADYCVGVGFSP 99

coring table: BLOSUM62

Gapop 10.0, Gapext 0.5

searched: 127863 seqs, 47026705 residues

total number of hits satisfying chosen parameters: 127863

minimum DB seq length: 0  
maximum DB seq length: 200000000

post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

database: SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

result	No.	Score	Query Match	Length	DB ID	Description
1	538	100.0	123	1	VPR3_HUMAN	Q9UK13 homo sapien
2	233.5	43.4	142	1	VPR2_MOUSE	P13373 mus musculus
3	229.5	42.7	142	1	VPR1_MOUSE	P13372 mus musculus
4	207.5	38.6	145	1	VPRE_HUMAN	P12018 homo sapien
5	200	37.2	111	1	LV6C_HUMAN	P06317 homo sapien
6	197	36.6	112	1	LV6A_HUMAN	P01721 homo sapien
7	185.5	34.5	111	1	LV2F_HUMAN	P01709 homo sapien
8	185	34.4	111	1	LV6D_HUMAN	P06318 homo sapien
9	183	34.0	131	1	LV6E_HUMAN	P06319 homo sapien
10	182.5	33.9	111	1	LV2L_HUMAN	P80422 homo sapien
11	180.5	33.6	111	1	LV2K_HUMAN	P04209 homo sapien
12	175.5	32.6	112	1	LV2I_HUMAN	P01712 homo sapien
13	175	32.5	111	1	LV2E_HUMAN	P01708 homo sapien
14	172.5	32.1	109	1	LV2E_HUMAN	P01714 homo sapien
15	171	31.8	108	1	LV3A_HUMAN	P01713 homo sapien
16	167.5	31.1	110	1	LV2J_HUMAN	P01702 homo sapien
17	167.5	31.1	111	1	LV1D_HUMAN	P06316 homo sapien
18	167	31.0	130	1	LV1G_HUMAN	P01719 homo sapien
19	165	30.7	108	1	LV5A_HUMAN	P04208 homo sapien
20	165	30.7	109	1	LV1F_HUMAN	P80748 homo sapien
21	164	30.5	111	1	LV3B_HUMAN	P01705 homo sapien
22	163.5	30.4	111	1	LV2B_HUMAN	P01711 homo sapien
23	163.5	30.4	111	1	LV2H_HUMAN	P01718 homo sapien
24	162	29.9	106	1	LV4D_HUMAN	P01716 homo sapien
25	161	29.9	106	1	LV4B_HUMAN	P01822 homo sapien
26	161	29.9	109	1	KV3D_HUMAN	P01717 homo sapien
27	160	29.7	107	1	LV4C_HUMAN	P01619 homo sapien
28	160	29.7	108	1	KV3A_HUMAN	P04211 homo sapien
29	159.5	29.6	117	1	LV0A_HUMAN	P01715 homo sapien
30	158	29.4	106	1	LV4A_HUMAN	P18135 homo sapien
31	158	29.4	129	1	KV3L_HUMAN	P01620 homo sapien
32	156	29.0	109	1	KV3G_HUMAN	P04306 homo sapien
33	156	29.0	109	1	KV3G_HUMAN	P04306 homo sapien

34	155.5	28.9	112	1	LV1H_HUMAN	P06887 homo sapien
35	154.5	28.7	111	1	LV2A_HUMAN	P01704 homo sapien
36	154.5	28.7	111	1	LV2C_HUMAN	P01706 homo sapien
37	154.5	28.7	112	1	LV1B_HUMAN	P01700 homo sapien
38	153.5	28.5	111	1	LV2D_HUMAN	P01707 homo sapien
39	153	28.4	111	1	LV1C_HUMAN	P01701 homo sapien
40	152	28.3	112	1	LV6B_HUMAN	P01722 homo sapien
41	152	28.3	129	1	KV3M_HUMAN	P18136 homo sapien
42	148	27.5	100	1	KV3C_HUMAN	P01621 homo sapien
43	147.5	27.4	109	1	KV3E_HUMAN	P01623 homo sapien
44	147	27.3	109	1	LV1I_HUMAN	P06888 homo sapien
45	146	27.1	106	1	LV4E_HUMAN	P06889 homo sapien

ALIGNMENTS

RESULT 1  
VPR3\_HUMAN  
ID VPR3\_HUMAN STANDARD; PRT; 123 AA.  
AC Q9UK13;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Pre-B lymphocyte protein 3 precursor (VpreB3 protein) (N27C7-2).  
GN VPREB3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20169186; PubMed=10702669;  
RA Rosnet O., Mattei M.-G., Delattre O., Schiff C.;  
RT "VPREB3: cDNA characterization and expression in human and chromosome  
mapping in human and mouse."  
RL Cytogenet. Cell Genet. 87:205-208(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Shimizu N., Minosima S., Kawasaki K., Sasaki T., Hosono K.;  
RT "Molecular cloning of N27C7-2 gene."  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Vallalou D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,  
Schnerch A., Schein J.E., Jones S.J.M., Marra W.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences."  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR  
COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS.  
CC -!- TISSUE SPECIFICITY: EXPRESSED IN B CELL PRECURSORS. EXPRESSED IN  
FETAL LIVER, BONE MARROW, SPLEEN, AND LYMPH NODE.  
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

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C -----  
R EMBL; AF163825; AAF09451.1; -  
R EMBL; AB050772; BAB83034.1; -  
R EMBL; BC020666; AAH20666.1; -  
R HSSP; P01709; 2MCG; VPREB3.  
R GENE; HGNC:12710; VPREB3.  
R MIM; 605017; -  
R InterPro; IPR007110; IG-like.  
R InterPro; IPR003006; IG\_MHC.  
R InterPro; IPR003596; IG\_V.  
R Pfam; PF00047; IG\_1.  
R SMART; SM00406; IGV; 1.  
R PROSITE; PS00835; IG\_LIKE; 1.  
R Immunoglobulin domain; B-cell; Signal.  
T SIGNAL 1 20 POTENTIAL.  
T CHAIN 21 123 PRE-B LYMPHOCYTE PROTEIN 3.  
T DOMAIN 21 123 IG-LIKE.  
T DISULFID 40 115 BY SIMILARITY.  
SQ SEQUENCE 123 AA; 13710 MW; BF09AC5196059E85 CRC64;

Query Match 100.0%; Score 538; DB 1; Length 123;  
Best Local Similarity 100.0%; Pred. No. 2.5e-51;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 1 LDALLVFPQVQAQLSCTLSQVHTIRYGVSWYQVQAGSAPRYLLYRSEEDHRRPADIP 60  
2b 25 LDALLVFPQVQAQLSCTLSQVHTIRYGVSWYQVQAGSAPRYLLYRSEEDHRRPADIP 84  
2y 61 DRFSAAKDEAHNACVLTISPQVEDDADYCVSGYGFSP 99  
2b 85 DRFSAAKDEAHNACVLTISPQVEDDADYCVSGYGFSP 123

RESULT 2  
VPR1 MOUSE STANDARD; PRT; 142 AA.  
ID VPR1 MOUSE STANDARD; PRT; 142 AA.  
AC P13373;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Immunoglobulin omega chain precursor (VpreB1 protein).  
GN VPREB1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
CX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6 X DBA/2J;  
RX MEDLINE=88029315; PubMed=3117530;  
RA Kudo A., Melchers F.;  
RT "A second gene, VpreB in the lambda 5 locus of the mouse, which  
RT appears to be selectively expressed in pre-B lymphocytes.";  
RL ENBO J. 6:2267-2272(1987).  
CC -1- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR  
CC COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS. THIS  
CC COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE EARLY  
CC STEPS OF B-CELL DIFFERENTIATION.  
CC -1- TISSUE SPECIFICITY: ONLY EXPRESSED BY PRE-B-CELLS.  
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
DR EMBL; X05563; CAA29077.1; -  
DR PIR; B28344; B28344.  
DR HSSP; P01607; IREI.  
DR MGD; MGI:98937; VpreB2.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
DR Immunoglobulin domain; B-cell; Signal.  
T SIGNAL 1 19 POTENTIAL.  
T CHAIN 20 142 IMMUNOGLOBULIN OMEGA CHAIN.  
T DOMAIN 20 41 FRAMEWORK-1.  
T DOMAIN 42 56 COMPLEMENTARITY-DETERMINING-1.  
T DOMAIN 57 70 FRAMEWORK-2.  
T DOMAIN 71 81 COMPLEMENTARITY-DETERMINING-2.  
T DOMAIN 82 115 FRAMEWORK-3.  
T DISULFID 41 115 BY SIMILARITY.  
SQ SEQUENCE 142 AA; 16052 MW; 7EA7128A4E63D920 CRC64;

Query Match 43.4%; Score 233.5; DB 1; Length 142;  
Best Local Similarity 54.7%; Pred. No. 2.4e-18;  
Matches 47; Conservative 9; Mismatches 29; Indels 1; Gaps 1;

Qy 9 GQVAQLSCTLSQVHTIRYGVSWYQVQAGSAPRYLLYRSEEDHRRPADIPDRFSAKD 68  
Db 34 GATIRLSCTLSNDH-NIGIYIYVQVQPGHPPFLRYFSHSDKHQGPDPFRFSGSKD 92  
Qy 69 EAHNACVLTISPQVEDDADYCVSGV 94  
Db 93 TRNLGYLSISELQFEDAVYCAVG 118

RESULT 3  
VPR1 MOUSE STANDARD; PRT; 142 AA.  
ID VPR1 MOUSE STANDARD; PRT; 142 AA.  
AC P13372;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Immunoglobulin iota chain precursor (VpreB1 protein).  
GN VPREB1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
CX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6 X DBA/2J;  
RX MEDLINE=88029315; PubMed=3117530;  
RA Kudo A., Melchers F.;  
RT "A second gene, VpreB in the lambda 5 locus of the mouse, which  
RT appears to be selectively expressed in pre-B lymphocytes.";  
RL ENBO J. 6:2267-2272(1987).  
CC -1- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR  
CC COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS. THIS  
CC COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE EARLY  
CC STEPS OF B-CELL DIFFERENTIATION.  
CC -1- TISSUE SPECIFICITY: ONLY EXPRESSED BY PRE-B-CELLS.  
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

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EMBL; X05556; CAA29071.1; -.  
EMBL; X05557; CAA29072.1; -.  
PIR; A28344; A28344.  
HSP; P01607; IRE1.  
MGD; MGI:98936; Vpreb1.  
GO; GO:0005886; C:plasma membrane; IPI.  
GO; GO:0004872; P:receptor activity; IPI.  
GO; GO:0030097; P:hemoipoiesis; IMP.  
GO; GO:0006955; P:immune response; IPI.  
InterPro; IPR007110; IG-like.  
InterPro; IPR003006; IG\_MHC.  
InterPro; IPR003596; IG\_v.  
SMART; SM00406; IGV; 1.  
PROSITE; PS00835; IG\_LIKE; 1.  
Immunoglobulin domain; B-cell; Signal.  
SIGNAL 1 19 POTENTIAL.  
CHAIN 20 142 IMMUNOGLOBULIN IOTA CHAIN.  
DOMAIN 20 41 FRAMEWORK-1.  
DOMAIN 42 56 COMPLEMENTARITY-DETERMINING-1.  
DOMAIN 57 70 FRAMEWORK-2.  
DOMAIN 71 81 COMPLEMENTARITY-DETERMINING-2.  
DOMAIN 82 115 FRAMEWORK-3.  
DISULFID 41 115 BY SIMILARITY.  
SEQUENCE 142 AA; 16:25 MW; 2E18BF963A0F448C CRC64;  
Query Match 42.7%; Score 229.5; DB 1; Length 142;  
Best Local Similarity 53.5%; Pred. No. 6.4e-18;  
Matches 46; Conservative 9; Mismatches 30; Indels 1; Gaps 1;  
Y 9 GQVALSTLSQVHTIRDYGVSVYQQRAGSAPRYLLYRSSEEDHHRPADIPDRSAKD 68  
b 34 GATIRLSTLSDNR-NIGTIVSYWYQQRPHPRFLIRFSDHDKHGPDIPDRFSGKD 92  
Y 69 EAHNACVLITISVPQEDDADYCSVG 94  
b 93 TTRNLGYLSISELQPEDEAVYCAVG 118  
RESULT 4  
PRE HUMAN STANDARD; PRT; 145 AA.  
D VPRE HUMAN STANDARD; PRT; 145 AA.  
C P12018;  
T 01-OCT-1999 (Rel. 12, Created)  
T 16-OCT-2001 (Rel. 40, Last sequence update)  
T 15-SEP-2003 (Rel. 42, Last annotation update)  
E Immunoglobulin Iota chain precursor (V(pre)B protein) (VpreB protein)  
E (CD179a antigen).  
N VPREB1 OR VPRESB.  
X Homo sapiens (Human).  
X Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
X Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
X NCBI\_TaxID=9606;  
UN [1]  
UN SEQUENCE FROM N.A.  
UN MEDLINE=95021318; PubMed=7935499;  
UN Quelipa-Fonlupt V., Bossy D., Alkari P., Fumoux F., Fougereau M.,  
UN Schaff C.;  
UN "The human pre-B cell receptor: structural constraints for a tentative  
UN model of the pseudo-light (psi L) chain.";  
UN Mol. Immunol. 31:1099-1108(1994).  
UN [2]  
UN SEQUENCE FROM N.A.  
UN MEDLINE=97228902; PubMed=9074928;  
UN Kawasaki K., Minoshima S., Mine S., Shibuya K., Shintani A.,  
UN Schmeltz J.L., Wang J., Shimizu N.;  
UN "One-megabase sequence analysis of the human immunoglobulin lambda  
UN gene locus.";  
UN Genome Res. 7:250-261(1997).  
UN [3]  
UN SEQUENCE OF 1-139 FROM N.A.  
UN MEDLINE=88196069; PubMed=3258819;  
UN Bauer S.R., Kudo A., Melchers F.;

RT EMBL; X05556; CAA29071.1; -.  
RT EMBL; X05557; CAA29072.1; -.  
RT PIR; A28344; A28344.  
RL HSP; P01607; IRE1.  
CC MGD; MGI:98936; Vpreb1.  
CC GO; GO:0005886; C:plasma membrane; IPI.  
CC GO; GO:0004872; P:receptor activity; IPI.  
CC GO; GO:0030097; P:hemoipoiesis; IMP.  
CC GO; GO:0006955; P:immune response; IPI.  
CC InterPro; IPR007110; IG-like.  
CC InterPro; IPR003006; IG\_MHC.  
CC InterPro; IPR003596; IG\_v.  
CC SMART; SM00406; IGV; 1.  
CC PROSITE; PS00835; IG\_LIKE; 1.  
CC Immunoglobulin domain; B-cell; Signal.  
CC SIGNAL 1 19 POTENTIAL.  
CC CHAIN 20 142 IMMUNOGLOBULIN IOTA CHAIN.  
CC DOMAIN 20 41 FRAMEWORK-1.  
CC DOMAIN 42 56 COMPLEMENTARITY-DETERMINING-1.  
CC DOMAIN 57 70 FRAMEWORK-2.  
CC DOMAIN 71 81 COMPLEMENTARITY-DETERMINING-2.  
CC DOMAIN 82 115 FRAMEWORK-3.  
CC DISULFID 41 115 BY SIMILARITY.  
CC SEQUENCE 142 AA; 16:25 MW; 2E18BF963A0F448C CRC64;  
Query Match 42.7%; Score 229.5; DB 1; Length 142;  
Best Local Similarity 53.5%; Pred. No. 6.4e-18;  
Matches 46; Conservative 9; Mismatches 30; Indels 1; Gaps 1;  
Y 9 GQVALSTLSQVHTIRDYGVSVYQQRAGSAPRYLLYRSSEEDHHRPADIPDRSAKD 68  
b 34 GATIRLSTLSDNR-NIGTIVSYWYQQRPHPRFLIRFSDHDKHGPDIPDRFSGKD 92  
Y 69 EAHNACVLITISVPQEDDADYCSVG 94  
b 93 TTRNLGYLSISELQPEDEAVYCAVG 118  
RESULT 4  
PRE HUMAN STANDARD; PRT; 145 AA.  
D VPRE HUMAN STANDARD; PRT; 145 AA.  
C P12018;  
T 01-OCT-1999 (Rel. 12, Created)  
T 16-OCT-2001 (Rel. 40, Last sequence update)  
T 15-SEP-2003 (Rel. 42, Last annotation update)  
E Immunoglobulin Iota chain precursor (V(pre)B protein) (VpreB protein)  
E (CD179a antigen).  
N VPREB1 OR VPRESB.  
X Homo sapiens (Human).  
X Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
X Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
X NCBI\_TaxID=9606;  
UN [1]  
UN SEQUENCE FROM N.A.  
UN MEDLINE=95021318; PubMed=7935499;  
UN Quelipa-Fonlupt V., Bossy D., Alkari P., Fumoux F., Fougereau M.,  
UN Schaff C.;  
UN "The human pre-B cell receptor: structural constraints for a tentative  
UN model of the pseudo-light (psi L) chain.";  
UN Mol. Immunol. 31:1099-1108(1994).  
UN [2]  
UN SEQUENCE FROM N.A.  
UN MEDLINE=97228902; PubMed=9074928;  
UN Kawasaki K., Minoshima S., Mine S., Shibuya K., Shintani A.,  
UN Schmeltz J.L., Wang J., Shimizu N.;  
UN "One-megabase sequence analysis of the human immunoglobulin lambda  
UN gene locus.";  
UN Genome Res. 7:250-261(1997).  
UN [3]  
UN SEQUENCE OF 1-139 FROM N.A.  
UN MEDLINE=88196069; PubMed=3258819;  
UN Bauer S.R., Kudo A., Melchers F.;

"Structure and pre-B lymphocyte restricted expression of the VpreB in  
humans and conservation of its structure in other mammalian  
species.";  
EMBO J. 7;111-116(1988).  
-1- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR  
COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS. THIS  
COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE EARLY  
STEPS OF B-CELL DIFFERENTIATION.  
-1- SUBUNIT: Associates non-covalently with IGLL1.  
-1- TISSUE SPECIFICITY: ONLY EXPRESSED BY PRE-B-CELLS.  
-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
-1- DATABASE: NAME=PROV; NOTE=PROV 1:59-63(2000);  
WWW="http://www.ncbi.nlm.nih.gov/prov/guide/574153212.g.htm".  
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EMBL; D86992; BAA19897.1; -.  
EMBL; D88270; BAA20030.1; -.  
EMBL; S74019; AAB32118.1; -.  
EMBL; M34927; AAB61292.1; -.  
PIR; I57832; I57832.  
PIR; S00258; S00258.  
HSP; P80748; 2LOI.  
Genew; HGNC:12709; VPREB1.  
MIM; 605141; -.  
GO; GO:0005576; C:extracellular; NAS.  
GO; GO:0003823; F:antigen binding activity; NAS.  
GO; GO:0006955; P:immune response; NAS.  
InterPro; IPR007110; IG-like.  
InterPro; IPR003006; IG\_MHC.  
InterPro; IPR003596; IG\_v.  
PIfam; PF00047; IG\_1.  
SMART; SM00406; IGV; 1.  
PROSITE; PS00835; IG\_LIKE; 1.  
Immunoglobulin domain; B-cell; Signal; Antigen.  
FT SIGNAL 1 19 POTENTIAL.  
FT CHAIN 20 145 IMMUNOGLOBULIN IOTA CHAIN.  
FT DOMAIN 20 41 FRAMEWORK-1.  
FT DOMAIN 42 56 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 57 70 FRAMEWORK-2.  
FT DOMAIN 71 81 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 82 115 FRAMEWORK-3.  
FT DISULFID 41 115 BY SIMILARITY.  
FT CONFLICT 10 10 L -> H (IN REF. 3).  
SQ SEQUENCE 145 AA; 16605 MW; 197665B13AF6D46 CRC64;  
Query Match 38.6%; Score 207.5; DB 1; Length 145;  
Best Local Similarity 48.8%; Pred. No. 1.6e-15;  
Matches 42; Conservative 12; Mismatches 31; Indels 1; Gaps 1;  
QY 9 GQVALSTLSQVHTIRDYGVSVYQQRAGSAPRYLLYRSSEEDHHRPADIPDRSAKD 68  
Db 34 GATIRLSTLSDNR-DIGVSVYWYQQRPHPRFLIRFSDHDKHGPDIPDRFSGKD 92  
QY 69 EAHNACVLITISVPQEDDADYCSVG 94  
Db 93 VARNEGYLSISELQPEDEAVYCAVG 118  
RESULT 5  
LV6C HUMAN STANDARD; PRT; 111 AA.  
ID LV6C HUMAN STANDARD; PRT; 111 AA.  
AC P06317;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE 19 lambda chain V-VI region SUI.

S Homo sapiens (Human).  
 C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 X NCBI\_TaxID=9606;  
 P SEQUENCE.  
 A Solomon A., Kyle R.A., Frangione B.;  
 I "Light chain variable region subgroups of monoclonal immunoglobulins  
 I in amyloidosis AL";  
 L (in) Glenner G.G., Osserman E.F., Benditt E.P., Calkins E.,  
 L Cohen A.S., Zucker-Franklin D. (eds.);  
 L Amyloidosis, pp.449-462, Plenum Press, New York (1986).  
 R PIR; A01988; LGHUST.  
 R PDB; 1CD0; 06-YAR-00.  
 R InterPro; IPR007110; IG-LIKE.  
 R InterPro; IPR003006; IG-MHC.  
 R InterPro; IPR003596; IG\_V.  
 R Pfam; PF00047; IG; 1.  
 R SMART; SM00406; IGV; 1.  
 R PROSITE; PS00835; IG-LIKE; 1.  
 W Immunoglobulin V region; 3D-structure.  
 T DOMAIN 1 22  
 T FRAMEWORK-1.  
 T DOMAIN 23 35  
 T COMPLEMENTARITY-DETERMINING-1.  
 T DOMAIN 36 50  
 T FRAMEWORK-2.  
 T DOMAIN 51 57  
 T COMPLEMENTARITY-DETERMINING-2.  
 T DOMAIN 58 91  
 T FRAMEWORK-3.  
 T DOMAIN 92 100  
 T COMPLEMENTARITY-DETERMINING-3.  
 T DOMAIN 101 111  
 T FRAMEWORK-4.  
 T DISULFID 22 91  
 T BY SIMILARITY.  
 T NON\_TER 111 111  
 T SEQUENCE 111 AA; 12247 MW; 0941DD547D983598 CRC64;

Query Match 37.2%; Score 200; DB 1; Length 111;

Best Local Similarity 48.8%; Pred. No. 7.5e-15;

Matches 41; Conservative 12; Mismatches 25; Indels 6; Gaps 2;

2y 8 PGQVQLSCTLSFQHVIRDYGVSVYQQRAGSAPRYLLYRSSEDEHRRPADIPDRPSAAK 67

3b 14 PKTVITSTRDGG--TIAGVYVQYQQRPGAPTTVIY----EDQRPSPGVDPDRPSGI 67

2y 68 DEAHNACVLTISPQVEDDADYYC 91

3b 68 DRSSNSASLTISGLTDEADYYC 91

# RESULT 6

ID LV6A\_HUMAN STANDARD; PRT; 112 AA.  
 AC P01721;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig lambda chain V-VI region AR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE (AMYLLOID PROTEIN AR).  
 RX MEDLINE=82091000; PubMed=6797401;  
 RA Sletten K., Natvig J.B., Husby G., Juul J.;  
 RT "The complete amino acid sequence of a prototype  
 RT immunoglobulin-lambda light-chain-type amyloid-fibril protein AR.";  
 RL Biochem J 195;561-572(1981).  
 CC -1- MISCELLANEOUS: ABOUT HALF OF THE LAMBDA CHAIN C REGION IS MISSING  
 CC FROM THIS PROTEIN.  
 CC -1- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE SPLEEN OF A  
 CC PATIENT WITH AMYLOIDOSIS.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A01987; LGHUAR.  
 DR HSP; P01709; 2MCG.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; IG-LIKE.

DR InterPro; IPR003006; IG-MHC.

DR InterPro; IPR003596; IG\_V.

DR Pfam; PF00047; IG; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG-LIKE; 1.

KW Immunoglobulin V region; Amyloid.

FT DOMAIN 1 107 IG-LIKE.

FT NON\_TER 112 112

SQ SEQUENCE 112 AA; 11918 MW; 570BCD9A368BF1FE CRC64;

Query Match 36.6%; Score 197; DB 1; Length 112;

Best Local Similarity 47.6%; Pred. No. 1.6e-14;

Matches 40; Conservative 15; Mismatches 23; Indels 6; Gaps 2;

Qy 8 PGQVQLSCTLSFQHVIRDYGVSVYQQRAGSAPRYLLYRSSEDEHRRPADIPDRPSAAK 67

Db 14 PKTVITSTRDGG--SIADSFVQYQQRPGAPTTVIY----DDQRPSPGVDPDRPSGI 67

Qy 68 DEAHNACVLTISPQVEDDADYYC 91

Db 68 DRSSNSASLTISGLTDEADYYC 91

# RESULT 7

ID LV2F\_HUMAN STANDARD; PRT; 111 AA.  
 AC P01709;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig lambda chain V-II region MGC.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=75013804; PubMed=4415202;  
 RA Fetz J.W., Deutsch H.F.;  
 RT "Primary structure of the Mgc lambda chain.";  
 RL Biochemistry 13:4102-4114(1974).  
 RN [2]  
 RP LAMBDA CHAIN GENES.  
 RX MEDLINE=76093781; PubMed=812801;  
 RA Fetz J.W., Deutsch H.F.;  
 RT "A new lambda-chain gene.";  
 RL Immunochimistry 12:643-652(1975).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
 RX Edmundson A.B., Ely K.R., Abola E.E., Schiffer M.,  
 RA Panagiotopoulos N.;  
 RT "Rotational allomerism and divergent evolution of domains in  
 RT immunoglobulin light chains.";  
 RL Biochemistry 14:3953-3961(1975).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY.  
 RX MEDLINE=90133913; PubMed=2515285;  
 RA Ely K.R., Herron J.N., Harter M., Edmundson A.B.;  
 RT "Three-dimensional structure of a light chain dimer crystallized in  
 RT water. Conformational flexibility of a molecule in two crystal  
 RT forms.";  
 RL J. Mol. Biol. 210:601-615(1989).  
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 CC -1- MISCELLANEOUS: THE MCG-TYPE C REGION APPEARS TO BE CORRELATED WITH  
 CC A VERY UNUSUAL V-REGION SUBSTITUTION, 103-THR ABOVE FOR GLY,  
 CC SUGGESTING THAT THE V-C JOINING MECHANISM IS NOT ALWAYS RANDOM.  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+  
 CC MARKERS.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A90381; LGHJMC.  
 DR PDB; 2MCG; 15-JUL-92.

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PDB: 1A8J; 17-JUN-98.
PDB: 1DCL; 15-MAY-97.
GO: GO:0005576; C:extracellular; NAS.
GO: GO:0003823; F:antigen binding activity; NAS.
GO: GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
PROSITE; PS0835; IG_LIKE; 1.
Immunoglobulin V region; 3D-structure;
Pyroglutamate carboxylic acid.
IG-LIKE.
DOMAIN 1 108
MOD RES 1 1
DISULFID 22 90
STRAND 5 5
STRAND 10 12
STRAND 18 23
TURN 26 32
TURN 36 40
TURN 42 43
STRAND 50 51
TURN 52 54
STRAND 55 55
TURN 62 63
STRAND 66 68
TURN 72 77
TURN 82 84
STRAND 86 93
STRAND 99 101
STRAND 105 109
STRAND 111 111
NON TER 111 111
SEQUENCE 111 AA; 11558 MW; 7CCID6E2FA3377BA CRC64;

Query Match 34.5%; Score 185.5; DB 1; Length 111;
Best Local Similarity 47.6%; Pred.No. 2.8e-13;
Matches 40; Conservative 14; Mismatches 23; Indels 7; Gaps 3;

Y 9 GQVAQLSCTLSPOHVTIRDYGVSWYQQRAGSAPRYLLYRSEEDHHRPADIPDRFSAAK 68
b 15 GQSVTISCTGSSDVGYNV-VSWYQQRAGKPKVIY---EVNKRPSGVDRFSGSK- 68
Y 69 EAHNACVLTISPQPEDDADYCS 92
b 69 -SGNTASLTISGLQAEDEADYCS 91

RESULT 8
LV6E HUMAN STANDARD; PRT; 111 AA.
AC P06318,
01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG lambda chain V-VI region WLT.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
SEQUENCE FROM N.A.
MEDLINE=86122667; PubMed=4089539;
Dwulet F.E., Strako K., Benson M.D.;
"Amino acid sequence of a lambda VI primary (AL) amyloid protein
(WLT).";
Scand. J. Immunol. 22:653-660 (1985).
PIR; A01989; L6HULT.
HSSP; P01709; 2MCG.
GO: GO:0005576; C:extracellular; NAS.
GO: GO:0003823; F:antigen binding activity; NAS.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
PROSITE; PS0835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
FT CHAIN 1 19
FT DOMAIN 20 41
FT DOMAIN 42 54
FT DOMAIN 55 69
FT DOMAIN 70 76
FT DOMAIN 77 110
FT DOMAIN 111 118
FT DISULFID 41 110
FT NON TER 131 131
SEQUENCE 131 AA; 14147 MW; 02A9179C8C05C2CD CRC64;

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DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 22
FT DOMAIN 23 35
FT DOMAIN 36 50
FT DOMAIN 51 57
FT DOMAIN 58 91
FT DOMAIN 92 101
FT DOMAIN 102 111
FT DISULFID 22 91
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11966 MW; 0C88B2FE37BCE24F CRC64;

Query Match 34.4%; Score 185; DB 1; Length 111;
Best Local Similarity 45.2%; Pred.No. 3.1e-13;
Matches 38; Conservative 16; Mismatches 24; Indels 6; Gaps 2;

QY 8 PQQVAQLSCTLSPOHVTIRDYGVSWYQQRAGSAPRYLLYRSEEDHHRPADIPDRFSAAK 67
DB 14 PEKVTISCTGSSG--SIGSNYVQWYQQRPGSAPTNIY---ENNQRPEVDFRSGSI 67
QY 68 DEAKNACVLTISPQPEDDADYCS 91
DB 68 DSSNSASLTISGLKTEDEADYCS 91

RESULT 9
LV6E HUMAN STANDARD; PRT; 131 AA.
AC P06319,
01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG lambda chain V-VI region EB4 precursor.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
SEQUENCE FROM N.A.
MEDLINE=85215660; PubMed=3923440;
Anderson M.L.M., Brown L., McKenzie E., Kellow J.E., Young B.D.;
"Cloning and sequence analysis of an Ig lambda light chain mRNA
expressed in the Burkitt's lymphoma cell line EB4.";
Nucleic Acids Res. 13:2931-2941 (1985).
PIR; A01990; L6HUEB.
HSSP; P01709; 2MCG.
GO: GO:0005576; C:extracellular; NAS.
GO: GO:0003823; F:antigen binding activity; NAS.
GO: GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS0835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
FT CHAIN 1 19
FT DOMAIN 20 41
FT DOMAIN 42 54
FT DOMAIN 55 69
FT DOMAIN 70 76
FT DOMAIN 77 110
FT DOMAIN 111 118
FT DISULFID 41 110
FT NON TER 131 131
SEQUENCE 131 AA; 14147 MW; 02A9179C8C05C2CD CRC64;

```

Query Match 34.0%; Score 183; DB 1; Length 131;  
Best Local Similarity 45.2%; Pred. No. 6.2e-13;  
Matches 38; Conservative 13; Mismatches 27; Indels 6; Gaps 2;  
Y 8 PGQVQLSCTLSFQHVITRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIDPFRSAK 67  
b 33 PGKVTITSTCT--GNSGSIASNTVQWQRRVSAPTIVY----EDNQRLGVDPDFSGSI 86  
Y 69 DEAHNACVLITSPVQPEDDADYYC 91  
b 87 DSSNSASLTISGLKTEDEADYYC 110  
RESULT 10  
V2L HUMAN  
ID LV2L HUMAN STANDARD; PRT; 111 AA.  
AC P80422;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE IG gamma lambda chain V-II region DOT.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
XN NCBI\_TaxID=9606;  
XN [1]  
XP SEQUENCE.  
Y MEDLINE=95255298; PubMed=7737190;  
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;  
RT "Characterization of the two unique human anti-flavin monooxylal  
RT immunoglobulins."  
RL Eur. J. Biochem. 228:886-893(1995).  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR HSP; P01709; 2MCG.  
DR GO: 0005576; C:extracellular; NAS.  
DR GO: 0003823; F:antigen binding activity; NAS.  
DR GO: 0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-LIKE.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein;  
KW Pyridolone carboxylic acid.  
FT MOD\_RES 1 106 IG-LIKE.  
FT DISULFID 22 90 BY SIMILARITY.  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 11787 MW; F358B1EA2CD7109A CRC64;  
Query Match 33.9%; Score 182.5; DB 1; Length 111;  
Best Local Similarity 47.6%; Pred. No. 5.9e-13;  
Matches 40; Conservative 12; Mismatches 25; Indels 7; Gaps 3;  
Y 8 PGQVQLSCTLSFQHVITRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIDPFRSAK 67  
b 14 PGQAVITSTGLS-VVDDNFVSWYQTPGAPPELLIY----DSDLRPGVFNRFSGSK 68  
Y 68 DEAHNACVLITSPVQPEDDADYYC 91  
b 69 SDTKAA--LTISGLQPDDEATVFC 90  
RESULT 11  
LV2G HUMAN  
ID LV2G HUMAN STANDARD; PRT; 111 AA.  
AC P01710;  
DT 21-JUN-1986 (Rel. 01, Created)  
DT 21-JUN-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE IG lambda chain V-II region BO.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
XN NCBI\_TaxID=9606;  
XN [1]  
XP SEQUENCE.  
Y MEDLINE=71103825; PubMed=5532228;  
RA Wikler M., Putnam F.W.;  
RT "Amino acid sequence of human lambda chains. 3. Tryptic peptides,  
RT chymotryptic peptides, and sequence of protein Bo."  
RL J. Biol. Chem. 245:4488-4507(1970).  
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR HSP; A01976; L2HUBO.  
DR HSP; P01709; 2MCG.  
DR GO: 0005576; C:extracellular; NAS.  
DR GO: 0003823; F:antigen binding activity; NAS.  
DR GO: 0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-LIKE.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein;  
KW Pyridolone carboxylic acid.  
FT MOD\_RES 1 106 IG-LIKE.  
FT DISULFID 22 90 BY SIMILARITY.  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 11785 MW; 92F5A1BF72421BAC CRC64;  
Query Match 33.6%; Score 180.5; DB 1; Length 111;  
Best Local Similarity 44.7%; Pred. No. 9.6e-13;  
Matches 39; Conservative 14; Mismatches 26; Indels 7; Gaps 3;  
Y 8 PGQVQLSCTLSFQHVITRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIDPFRSAK 67  
b 14 PGQSVTISTCTGSSDVGDKY-VSWYQHPGAPKLVI---EVSQRPVGVDPDFSGSK 68  
Y 68 DEAHNACVLITSPVQPEDDADYYCS 92  
b 69 SD--NTASITVSLRAEDADYYCS 91  
RESULT 12  
LV2K HUMAN  
ID LV2K HUMAN STANDARD; PRT; 112 AA.  
AC P04209;  
DT 20-MAR-1987 (Rel. 04, Created)  
DT 20-MAR-1987 (Rel. 04, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE IG lambda chain V-II region NIG-84.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
XN NCBI\_TaxID=9606;  
XN [1]  
XP SEQUENCE.  
Y MEDLINE=85204333; PubMed=3922791;  
RA Tuncike H., Kametani F., Hoshi A., Shinoda T., Isobe T.;  
RT "Amino acid sequence of an amyloidogenic Bence Jones protein in  
RT myeloma-associated systemic amyloidosis."  
RL FEBS Lett. 185:139-141(1985).  
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN ISOLATED FROM AN  
CC INDIVIDUAL WITH MYELOMA-ASSOCIATED SYSTEMIC AMYLOIDOSIS.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR HSP; A01971; L2HUNG.  
DR HSP; P01709; 2MCG.  
DR GO: 0005576; C:extracellular; NAS.  
DR GO: 0003823; F:antigen binding activity; NAS.  
DR GO: 0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-LIKE.  
DR InterPro; IPR003596; IG\_V.  
DR InterPro; IPR003596; IG\_V.

```
R Pfam: PF00047; IG: 1.
R SMART: SM00406; IGV: 1.
R PROSITE: PS50835; IG LIKE: 1.
W Immunoglobulin V region, Antyloid; Bence-Jones protein.
I DOMAIN 1 102 IG-LIKE.
I DISULFID 22 90 BY SIMILARITY.
I NON TER 112 112
Q SEQUENCE 112 AA; 11581 MW; 989FEF363AE1E4F3 CRC64;
Query Match 32.6%; Score 175.5; DB 1; Length 112;
Best Local Similarity 47.1%; Pred. No. 3.4e-12;
Matches 40; Conservative 13; Mismatches 25; Indels 7; Gaps 3;
Y 8 PGQVAQLSCTLSPOHVTIRDYGVSWYQQRAGSAPRYLLYRSEEDHHRPADIPDRFSAK 67
b 14 PGQSVTISCTGTSYGVYDF-VSWYQHPGKAPKLIY----DVNGRPSGINSRFGSK 68
Y 68 DEAHNACVLITSPVQPEDDADYCS 92
b 69 --SGNTASLTISGLQAEDEADYCS 91
RESULT 13
V21 HUMAN
D LV21 HUMAN STANDARD; PRT; 111 AA.
C P01712;
T 21-JUL-1986 (Rel. 01, Created)
T 21-JUL-1986 (Rel. 01, Last sequence update)
T 15-SEP-2003 (Rel. 42, Last annotation update)
E Ig lambda chain V-II region WIN.
S Homo sapiens (Human).
C Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
X NCBI_TaxID=9606;
N [1]
P SEQUENCE.
MEDLINE=79062503; PubMed=102365;
A Chen B.L., Chiu Y.-Y.H., Humphrey R.L., Poljak R.J.;
T "Amino acid sequence of the human myeloma lambda chain Win.";
L Biochim. Biophys. Acta 537:9-21(1978).
C -|- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
C -|- SIMILARITY: Contains 1 immunoglobulin-like domain.
R PIR; A01978; L2HJWN.
R HSSP; P01709; 2MCG.
R GO; GO:0005576; C:extracellular; NAS.
R GO; GO:0003823; F:antigen binding activity; NAS.
R GO; GO:0006955; P:immune response; NAS.
R InterPro; IPR007110; IG-like.
R InterPro; IPR003006; IG_MHC.
R Pfam; PF00047; IG_V.
R SMART; SM00406; IGV: 1.
R PROSITE; PS50835; IG LIKE: 1.
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 106
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 90 BY SIMILARITY.
FT SITE 91 91
FT NON TER 111 111
FT SEQUENCE 111 AA; 11694 MW; 8C3CE95FE721B87C CRC64;
Query Match 32.5%; Score 175; DB 1; Length 111;
Best Local Similarity 44.9%; Pred. No. 3.8e-12;
Matches 40; Conservative 15; Mismatches 26; Indels 8; Gaps 4;
Y 8 PGQVAQLSCTLSPOHVTIRDYGVSWYQQRAGSAPRYLLYRSEEDHHRPADIPDRFSAK 67
b 14 PGQSVTISCTGTSYGVYDF-VSWYQHPGKAPKLIY----DVNGRPSGINSRFGSK 68
Y 68 DEAHNACVLITSPVQPEDDADYCSVGY 96
b 69 --SANTASLTISGLQANNEADYCS-SYG 94
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RESULT 14
LV2E HUMAN
ID LV2E HUMAN STANDARD; PRT; 109 AA.
AC P01708;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-II region BUR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=80006606; PubMed=113407;
RA Infante A.J., Putnam F.W.;
RT "Primary structure of a human IgA1 immunoglobulin. V. Amino acid
sequence of a human IgA lambda light chain (Bur).";
RL J. Biol. Chem. 254:9006-9016(1979).
CC -|- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+
MARKERS.
CC -|- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
CC -|- SIMILARITY: Contains 1 immunoglobulin-like domain.
R PIR; A01974; L2HUBR.
R HSSP; P01709; 2MCG.
R GO; GO:0005576; C:extracellular; NAS.
R GO; GO:0003823; F:antigen binding activity; NAS.
R GO; GO:0006955; P:immune response; NAS.
R InterPro; IPR007110; IG-like.
R InterPro; IPR003006; IG_MHC.
R Pfam; PF00047; IG_V.
R SMART; SM00406; IGV: 1.
R PROSITE; PS50835; IG LIKE: 1.
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 106
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 90 BY SIMILARITY.
FT SITE 91 91
FT NON TER 109 109
FT SEQUENCE 109 AA; 11506 MW; BFD8AE1C5D267FAB CRC64;
Query Match 32.1%; Score 172.5; DB 1; Length 109;
Best Local Similarity 45.2%; Pred. No. 6.9e-12;
Matches 38; Conservative 12; Mismatches 27; Indels 7; Gaps 3;
QY 8 PGQVAQLSCTLSPOHVTIRDYGVSWYQQRAGSAPRYLLYRSEEDHHRPADIPDRFSAK 67
Db 14 PGHVTISCTGTSYGVYDF-VSWYQHPGKAPKLIY----EVSRRPSGVDRFGSK 68
QY 68 DEAHNACVLITSPVQPEDDADYCY 91
Db 69 --SGNTASLTISGLQAEDEADYCY 90
RESULT 15
LV3A HUMAN
ID LV3A HUMAN STANDARD; PRT; 108 AA.
AC P01714;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-III region SH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70166723; PubMed=4909564;
RA Titani K., Wikier M., Shinoda T., Putnam F.W.;
```



"The amino acid sequence of a lambda type Bence-Jones protein. 3. The complete amino acid sequence and the location of the disulfide bridges."

J. Biol. Chem. 245:2171-2176 (1970).

-1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.

-1- SIMILARITY: Contains 1 immunoglobulin-like domain.

PIR; A01980; LSHUSH.

HSPP; P80748; 2L01.

GO; GO:0005576; C:extracellular; NAS.

GO; GO:0003823; F:antigen binding activity; NAS.

GO; GO:0006955; P:immune response; NAS.

InterPro; IPR007110; Ig-like.

InterPro; IPR003006; Ig\_MHC.

InterPro; IPR003596; Ig\_v.

Pfam; PF00047; Ig; 1.

SMART; SM00406; IGV; 1.

PROSITE; PS00835; IG\_LIKE; 1.

Immunoglobulin V region; Bence-Jones protein.

DOMAIN 1 97 IG-LIKE.

DISULFID 21 86

NON TER 108 108

SEQUENCE 108 AA; 11392 MW; E7EL229586411A56 CRC64;

Query Match 31.8%; Score 171; DB 1; Length 108;

Best Local Similarity 42.2%; Pred. No. 9.9e-12;

Matches 38; Conservative 17; Mismatches 25; Indels 10; Gaps 4;

3 ALLVPPGVQVQLSCTLSQHVITRDYGVSWYQORAGSAPRYLLYYRSEEDHHRPADIPDR 62

8 AVSVLGGTVVITC-----QGDLSLEGYDAWYQKPGQAPLLVIYGR----NNRPSGIPDR 59

63 FSAAKDEAHNACVLTISVPQEDDADYICS 92

60 FSGS--SSGHTAS-LTITGAQAEADYICN 87

Search completed: February 9, 2004, 12:47:05

Job time : 10.3649 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

M protein - protein search, using sw model

run on: February 9, 2004, 12:38:06 / Search time 31.2162 Seconds  
(without alignments)  
818.395 Million cell updates/sec

file: us-09-981-876-200\_COPY\_25\_123

effect score: 538

sequence: 1 LDALLVFQVQLSCTLSP.....PVQPEDDADYCVGVGFSP 93

coiling table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 830525 seqs, 258052604 residues

total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Maximum Match 100%

Listing first 45 summaries

database :

SPTREMBL 23:

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_proteob:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	372.5	69.2	123	11 Q61243	Q61243 mus musculus
2	199	37.0	135	4 Q9H524	Q9H524 homo sapien
3	197	36.6	112	4 Q96JD1	Q96JD1 homo sapien
4	193	35.9	112	4 Q96JD2	Q96JD2 homo sapien
5	189.5	35.2	116	4 Q96JD0	Q96JD0 homo sapien
6	175	32.5	237	4 Q8WTU6	Q8WTU6 homo sapien
7	174.5	32.4	236	4 Q96E61	Q96E61 homo sapien
8	172.5	32.1	237	4 Q8WUK4	Q8WUK4 homo sapien
9	172.5	32.1	240	4 Q9NSD6	Q9NSD6 homo sapien
10	169	31.4	107	4 Q9UL86	Q9UL86 homo sapien
11	166	30.9	109	4 Q8TBC9	Q8TBC9 homo sapien
12	165	30.7	233	4 Q9N355	Q9N355 homo sapien
13	161	29.9	234	4 Q9N355	Q9N355 homo sapien
14	161	29.7	235	11 Q99M11	Q99M11 mus musculus
15	160	29.7	108	4 Q96S80	Q96S80 homo sapien
16	158	29.4	109	4 Q9UL78	Q9UL78 homo sapien

17	158	29.4	235	4 Q8NEJ1	Q8NEJ1 homo sapien
18	157	29.2	110	4 Q8TB63	Q8TB63 homo sapien
19	155	28.8	233	4 Q96169	Q96169 homo sapien
20	151.5	28.2	100	6 O77624	O77624 bos taurus
21	151	28.1	101	4 Q81ZD8	Q81ZD8 homo sapien
22	151	28.1	233	4 Q8NSF4	Q8NSF4 homo sapien
23	150.5	28.0	105	4 Q8WVJ6	Q8WVJ6 homo sapien
24	148	27.5	107	4 Q9UL82	Q9UL82 homo sapien
25	138	25.7	132	4 Q8TSD0	Q8TSD0 homo sapien
26	137	25.5	108	4 Q9UL83	Q9UL83 homo sapien
27	135	25.1	234	4 Q8NEK1	Q8NEK1 homo sapien
28	134	24.9	97	4 Q43234	Q43234 homo sapien
29	134	24.9	107	11 Q9ERZ9	Q9ERZ9 mus musculus
30	133.5	24.8	484	11 Q8VEA0	Q8VEA0 mus musculus
31	132	24.5	109	4 Q9UL85	Q9UL85 homo sapien
32	130.5	24.3	99	11 Q9UL74	Q9UL74 mus musculus
33	128	23.8	107	4 Q96SA9	Q96SA9 homo sapien
34	128	23.8	108	4 Q9UL77	Q9UL77 homo sapien
35	127.5	23.7	239	4 Q8NEK0	Q8NEK0 homo sapien
36	127	23.6	108	4 Q9UL79	Q9UL79 homo sapien
37	124.5	23.1	114	4 Q9UL80	Q9UL80 homo sapien
38	124	23.0	494	4 Q96K68	Q96K68 homo sapien
39	123.5	23.0	113	11 Q8CGS1	Q8CGS1 mus musculus
40	123.5	23.0	234	11 Q8R062	Q8R062 mus musculus
41	123.5	23.0	469	11 Q8R3V9	Q8R3V9 mus musculus
42	123	22.9	111	11 Q920E9	Q920E9 mus musculus
43	120.5	22.4	93	4 Q9UL76	Q9UL76 homo sapien
44	120.5	22.4	121	4 Q9UL96	Q9UL96 homo sapien
45	120.5	22.4	239	4 Q8TCD0	Q8TCD0 homo sapien

#### ALIGNMENTS

#### RESULT 1

Q61243 Q61243 PRELIMINARY; PRT; 123 AA.  
AC Q61243 Q61243  
DT 01-NOV-1996 (TREMELrel. 01, Created)  
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)  
DE 8HS20 protein precursor (Pre-B lymphocyte gene 3).  
GN VP8B3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C;  
RX MEDLINE=93259124; PubMed=8491176;  
RA Shirasawa T., Ohnishi K., Hagiwara S., Shigemoto K., Takebe Y.,  
RA Rajewsky K., Takemori T.,  
RT "A novel gene product associated with mu chains in immature B cells.";  
RL EMBO J. 12:1827-1834(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Stomach;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinesawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldi M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

A Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,  
 A Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 A Wyshaw-Solis A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,  
 A Hayashizaki Y.,  
 T "Functional annotation of a full-length mouse cDNA collection."  
 L Nature 409:685-690(2001).  
 R EMBL; AK008794; BAB28899.1; -.  
 R HSP; P01709; 2MCG.  
 R MGD; MGI:98938; Vpreb3.  
 R InterPro; IPR007110; IG-like.  
 R InterPro; IPR003596; IG\_MHC.  
 R InterPro; IPR003596; IG\_v.  
 R Pfam; PF00047; IG; 1.  
 R SMART; SM00406; IGV; 1.  
 R PROSITE; PS50835; IG\_LIKE; 1.  
 T CHAIN 20 123  
 T SEQUENCE 123 AA; 13400 MW; 2A1AD371D1CE98F CRC64;  
 IQ  
 Query Match 69.2%; Score 372.5; DB 11; Length 123;  
 Best Local Similarity 69.4%; Pred. No. 6.2e-35;  
 Matches 68; Conservative 11; Mismatches 18; Indels 1; Gaps 1;  
 Y 2 DALLVPPGVAQLSCTLSPPQVTRDYGVSYYQORAGSAPRYLLYRSEEDHRRPADIPD 61  
 b 27 DAFSVFPGQDAHLSTINSQATAGDIGVSYYQQPGSAP-HLLYYVAEEHVRPADIPD 85  
 Y 62 RESAAKDEAHNAVLITISPVQEDADYYCISGVGFSFP 99  
 b 86 RFSATVDAAHNAVLITISPVLPEDADYYCISGVGFSFP 123  
 RESULT 2  
 ID Q9H524 PRELIMINARY; PRT; 135 AA.  
 AC Q9H524;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Hypothetical protein FLJ22755.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP TISSUE=ileal mucosa;  
 RC  
 RA Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,  
 RA Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,  
 RA Yamada K., Fujii Y., Ozaki K., Hirao M., Omori Y., Ota T., Suzuki Y.,  
 RA Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,  
 RA Iscagi T., Sugano S.,  
 RA "NEDO human cDNA sequencing project";  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK026408; BAB15473.1; -.  
 DR HSP; P01607; IREL.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 135 AA; 14780 MW; 652492DE930F401 CRC64;  
 Query Match 37.0%; Score 199; DB 4; Length 135;  
 Best Local Similarity 45.3%; Pred. No. 5.2e-15;  
 Matches 34; Conservative 17; Mismatches 24; Indels 0; Gaps 0;  
 Y 24 TIRYGVSVYQORAGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNAVLITISPVQ 83  
 b 7 SVGDFWIRYQKPGNPRYLLYHSDSNKQGGVSRPSGSDASANAGILRISGLQ 66  
 Y 84 EDDADYICSVGVGFS 98  
 A Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,  
 A Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 A Wyshaw-Solis A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,  
 A Hayashizaki Y.,  
 T "Functional annotation of a full-length mouse cDNA collection."  
 L Nature 409:685-690(2001).  
 R EMBL; AK008794; BAB28899.1; -.  
 R HSP; P01709; 2MCG.  
 R MGD; MGI:98938; Vpreb3.  
 R InterPro; IPR007110; IG-like.  
 R InterPro; IPR003596; IG\_MHC.  
 R InterPro; IPR003596; IG\_v.  
 R Pfam; PF00047; IG; 1.  
 R SMART; SM00406; IGV; 1.  
 R PROSITE; PS50835; IG\_LIKE; 1.  
 T CHAIN 20 123  
 T SEQUENCE 123 AA; 13400 MW; 2A1AD371D1CE98F CRC64;  
 IQ  
 Query Match 69.2%; Score 372.5; DB 11; Length 123;  
 Best Local Similarity 69.4%; Pred. No. 6.2e-35;  
 Matches 68; Conservative 11; Mismatches 18; Indels 1; Gaps 1;  
 Y 2 DALLVPPGVAQLSCTLSPPQVTRDYGVSYYQORAGSAPRYLLYRSEEDHRRPADIPD 61  
 b 27 DAFSVFPGQDAHLSTINSQATAGDIGVSYYQQPGSAP-HLLYYVAEEHVRPADIPD 85  
 Y 62 RESAAKDEAHNAVLITISPVQEDADYYCISGVGFSFP 99  
 b 86 RFSATVDAAHNAVLITISPVLPEDADYYCISGVGFSFP 123  
 RESULT 2  
 ID Q9H524 PRELIMINARY; PRT; 135 AA.  
 AC Q9H524;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Hypothetical protein FLJ22755.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP TISSUE=ileal mucosa;  
 RC  
 RA Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,  
 RA Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,  
 RA Yamada K., Fujii Y., Ozaki K., Hirao M., Omori Y., Ota T., Suzuki Y.,  
 RA Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,  
 RA Iscagi T., Sugano S.,  
 RA "NEDO human cDNA sequencing project";  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK026408; BAB15473.1; -.  
 DR HSP; P01607; IREL.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 135 AA; 14780 MW; 652492DE930F401 CRC64;  
 Query Match 37.0%; Score 199; DB 4; Length 135;  
 Best Local Similarity 45.3%; Pred. No. 5.2e-15;  
 Matches 34; Conservative 17; Mismatches 24; Indels 0; Gaps 0;  
 Y 24 TIRYGVSVYQORAGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNAVLITISPVQ 83  
 b 7 SVGDFWIRYQKPGNPRYLLYHSDSNKQGGVSRPSGSDASANAGILRISGLQ 66  
 Y 84 EDDADYICSVGVGFS 98

Db 67 EDEADYICGTWHSNS 81  
 RESULT 3  
 Q96JD1 PRELIMINARY; PRT; 112 AA.  
 ID Q96JD1;  
 AC Q96JD1;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Anyloid lambda 6 light chain variable region FIP (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Bone marrow;  
 RA Perfetti V., Gasarini S., Colli Vignarelli M., Merlini G.,  
 RL "Anyloid lambda 6 light chain variable region FIP."  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF267874; AAK58585.1; -.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 112 112  
 SQ SEQUENCE 112 AA; 12047 MW; 0D3885AC23567B9F CRC64;  
 Query Match 36.6%; Score 197; DB 4; Length 112;  
 Best Local Similarity 47.6%; Pred. No. 7e-15;  
 Matches 40; Conservative 14; Mismatches 24; Indels 6; Gaps 2;  
 Y 8 PQQVQLSCTLSPPQVTRDYGVSYYQORAGSAPRYLLYRSEEDHRRPADIPDRSAK 67  
 b 14 PKKTIISCTSSG--SIASNYVYQORPGSAPTIVY---EDNQRPSGVDPFSGSI 67  
 Y 68 DEAHNAVLITISPVQEDADYYC 91  
 b 68 DSSNSASITISGLKTEDEADYYC 91  
 RESULT 4  
 Q96JD2 PRELIMINARY; PRT; 112 AA.  
 ID Q96JD2;  
 AC Q96JD2;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Anyloid lambda 6 light chain variable region NEG (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Bone marrow;  
 RA Perfetti V., Gasarini S., Colli Vignarelli M., Merlini G.,  
 RL "Anyloid lambda 6 light chain variable region NEG."  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF267873; AAK58585.1; -.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 112 112  
 SQ SEQUENCE 112 AA; 11908 MW; 080B4B37E2360B06 CRC64;

[illegible]

	DR	EMBL; BC022098; AAH22098.1; -- DR InterPro; IPR007110; IG-like. DR InterPro; IPR003006; IG_MHC. DR InterPro; IPR003596; IG_v. DR Pfam; PF00047; Ig; 2. DR SMART; SM00406; IGV; 1. DR PROSITE; PS50835; IG LIKE; 2. DR PROSITE; PS00290; IG_MHC; 1.	KW Hypothetical protein_1 KW Hypothetical protein_1 QY QV DB
	SQ	SEQUENCE 237 AA; 24884 MW; E6CF371E753968E8 CRC64;  Query Match            32.5%; Score 175; DB 4; Length 237; Best Local Similarity 42.9%; Pred.No.5.6e-12; Matches 39; Conservative 16; Mismatches 28; Indels 8; Gaps 4;	
	QY	8 PQGVAQLSCTLSPOHVITRDYGVSWTQQAGAPRYLLYYRSEEDHHRPADIPDFSAAK 67 :   ::     :~::~   :~:::: ~::~   :~:::: ~::~   : DB 33 PGQRTVISCTGSSTNIG-AGYDVHWVQQLPGTAPKLLIYNSS---NEPSGVDPFRFSGSK 87	
	QY	68 DEAHNAVCVLTIISPVQPDDADDYCYSVGCGFS 98 :   :   :   :   :   :   :   :   :   :   :   :   : DB 88 --SGTSASLAITGLQAEDAEADYYCY-SYDYS 115	
	RESULT 7		
O96E61	ID	PRELIMINARY; PRT; 236 AA.	
AC	Q96E61		
DT	01-DEC-2001	(TrEMBRel. 19, Created)	
DT	01-DEC-2001	(TrEMBRel. 19, Last sequence update)	
DE	01-MAR-2003	(TrEMBRel. 23, Last annotation update)	
DE	Hypothetical protein.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Euheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_Taxid=9606;		
RN	[1]		
RC	SEQUENCE FROM N.A.		
RF	TISSUE=Brain;		
RL	Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.		
RR	Strausberg R.;		
RS	EMBL; BC012876; AAH12876.1; --		
DR	InterPro; IPR007110; IG-like.		
DR	InterPro; IPR003006; IG_MHC.		
DR	InterPro; IPR003596; IG_v.		
DR	Pfam; PF00047; Ig; 2.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PS50835; IG LIKE; 2.		
DR	PROSITE; PS00290; IG_MHC; 1.		
KW	Hypothetical protein_1		
SQ	SEQUENCE 236 AA; 24712 MW; 7EC9FB3622FED957 CRC64;  Query Match            32.4%; Score 174.5; DB 4; Length 236; Best Local Similarity 42.9%; Pred.No.6.4e-12; Matches 36; Conservative 17; Mismatches 24; Indels 7; Gaps 3;		
	QY	8 PQGVAQLSCTLSPOHVITRDYGVSWTQQAGAPRYLLYYRSEEDHHRPADIPDFSAAK 67 :   ::     :~::~   :~:::: ~::~   :~:::: ~::~   : DB 33 PGQRTVISCTGSSTNIG-AGYA VHWVQQLPGAAPKVLIY---GNYPSPGVDPFRFSGSK 87	
	QY	68 DEAHNAVCVLTIISPVQPDDADDYYC 91 :   :   :   :   :   :   :   :   :   :   :   : DB 88 --SGTSASLAITGLQAEDAEADYYC 109	
	RESULT 8		
Q8WUK4	ID	PRELIMINARY; PRT; 237 AA.	
AC	Q8WUK4		
DT	01-MAR-2002	(TrEMBRel. 20, Created)	
DT	01-MAR-2002	(TrEMBRel. 20, Last sequence update)	
DE	01-MAR-2003	(TrEMBRel. 23, Last annotation update)	
DE	Hypothetical protein.		

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IS Homo sapiens (Human).
IC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
X NCBI_TaxID=9606;
N [1]
P SEQUENCE FROM N.A.
C TISSUE=Tonsil;
A Strausberg R.;
L Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
R EMBL; BC020233; AAH20233.1; -.
R InterPro; IPR003006; IG_MHC.
R InterPro; IPR003596; IG_V.
R Pfam; PF00047; IG; 2.
R SMART; SM00406; IGV; 1.
R PROSITE; PS00290; IG_MHC; 1.
W Hypothetical protein.
Q SEQUENCE 237 AA; 24897 MW; 73C7D70B8039D186 CRC64;

Query Match 32.1%; Score 172.5; DB 4; Length 237;
Best Local Similarity 41.0%; Pred. No. 1.1e-11;
Matches 37; Conservative 15; Mismatches 25; Indels 7; Gaps 3;

2y . 8 PQGVAQLSCTLSPOHVTIRDYGVSWYQQRAGSAPRYLLYRSEEDHRRPADIPDRFSAK 67
2b 33 PGQVTVISTGSSNIG-AGVDVHYQQLPTAPKLLIYGN-----NRSGVDRPFGSK 87
2y 68 DEAHNACVLTISPVEDDADYYC 91
2b 88 --SGTSASLAITGQAQDEADYYC 109

RESULT 9
ID OSWKU3 PRELIMINARY; PRT; 240 AA.
AC OSWKU3
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tonsil;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
R EMBL; BC020236; AAH20236.1; -.
R InterPro; IPR007110; IG-like.
R InterPro; IPR003006; IG_MHC.
R InterPro; IPR003596; IG_V.
R Pfam; PF00047; IG; 2.
R SMART; SM00406; IGV; 1.
R PROSITE; PS00835; IG_LIKE; 2.
R PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 240 AA; 25977 MW; 921E47DDCA7259F0 CRC64;

Query Match 32.1%; Score 172.5; DB 4; Length 240;
Best Local Similarity 36.4%; Pred. No. 1.1e-11;
Matches 36; Conservative 20; Mismatches 30; Indels 13; Gaps 3;

Qy 7 FPGQVAQLSCTLSPOHVTIRDYGVSWYQQRAGSAPRYLLYRSEEDHRRPADIPDRFSA 66
Db 32 FLGASIKLCTLSREH---SSVTIEWYQQRPGSPQIMVKVSDGSHNKGDGIPDRFGS 88
Qy 67 KDEAHNACVLTISPVEDDADYYC-----SVGYGF 97
Db 89 SSGADR--YLTUSLQSDDEAEYHCGESHTTDGQVGWVF 125

RESULT 10

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Q9NSD6
ID Q9NSD6 PRELIMINARY; PRT; 107 AA.
AC Q9NSD6
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocytes;
RA Hohmann A.;
RL "Autoimmunity";
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
R EMBL; L43092; AAA69746.2; -.
R HSP; P01709; 2MCG.
R InterPro; IPR007110; IG-like.
R InterPro; IPR003006; IG_MHC.
R InterPro; IPR003596; IG_V.
R Pfam; PF00047; IG; 1.
R SMART; SM00406; IGV; 1.
R PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11306 MW; A2B04B37187A5F00 CRC64;

Query Match 31.4%; Score 169; DB 4; Length 107;
Best Local Similarity 41.7%; Pred. No. 1.1e-11;
Matches 35; Conservative 17; Mismatches 22; Indels 10; Gaps 3;

Qy 9 GQVAQLSCTLSPOHVTIRDYGVSWYQQRAGSAPRYLLYRSEEDHRRPADIPDRFSAKD 68
Db 13 GQVTRTC-----QGSLSRYASWYQKPGQAPVLVIYK-----NNRPSGIPDRFSGS-- 62
Qy 69 EAHNACVLTISPVEDDADYYCS 92
Db 63 SSGNTASLTITGQAQDEADYYCN 86

RESULT 11
Q9UL86
ID Q9UL86 PRELIMINARY; PRT; 109 AA.
AC Q9UL86
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98277139; PubMed=9614934;
RA Xu X, Liu B, Van der Merwe P.L., Kalis N.N., Bernay S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
R EMBL; AF03028; AAD56264.1; -.
R HSP; P80362; 1WTL.
R InterPro; IPR007110; IG-like.
R InterPro; IPR003006; IG_MHC.
R InterPro; IPR003596; IG_V.
R Pfam; PF00047; IG; 1.
R SMART; SM00406; IGV; 1.
R PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 109

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SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;
Query Match 30.9%; Score 166; DB 4; Length 109;
Best Local Similarity 44.2%; Pred. No. 2.4e-11;
Matches 42; Conservative 1; Mismatches 32; Indels 10; Gaps 4;
4 LLVFPQVAQLSCTLSPOHVTIRYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRF 63
11 LSLPFGGERATISCRASQ---SVSSSYLAWYQQRPGQAPRLIYGTSS----RATGIPDRF 63
64 SAAKDEAHNACVLITISVPQEDDADYYCISVGYGFS 98
64 SSGSGETD--FTLIISLEPEDFAVYICQ-QYGSS 95
RESULT 12
#TBC9
Q8TBC9 PRELIMINARY; PRT; 233 AA.
Q8TBC9
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
SEQUENCE FROM N.A.
TISSUE=B-cell;
Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
EMBL; BC022823; AAH2823.1; -.
InterPro; IPR003006; IG_MHC.
InterPro; IPR003596; IG_V.
Pfam; PF00047; IG; 2.
SMART; SM00406; IGV; 1.
PROSITE; PS00290; IG MHC; 1.
Hypothetical protein.
SEQUENCE 233 AA; 24867 MW; 367411BFD6F4DF92 CRC64;
Query Match 30.7%; Score 165; DB 4; Length 233;
Best Local Similarity 41.6%; Pred. No. 7.7e-11;
Matches 37; Conservative 15; Mismatches 21; Indels 16; Gaps 4;
6 VFPQVAQLSCT---LSPQHTIRYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDR 62
31 VSPQHTARITCSGDALPKQY-----AYWQKPSQAPVLVIY----KONRPSGIPER 79
63 FSAKDEAHNACVLITISVPQEDDADYYC 91
80 FSGS---SSGTTVTLTISGVQAEADYYC 106
RESULT 13
BN355 PRELIMINARY; PRT; 234 AA.
Q8N355
Q8N355
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
SEQUENCE FROM N.A.
TISSUE=Brain;
Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
EMBL; BC028090; AAH28090.1; -.
InterPro; IPR003599; IG.
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InterPro; IPR007110; IG-like.
DR InterPro; IPR003557; IG_Cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 24792 MW; CC848CAEBA4A9D63 CRC64;
Query Match 29.9%; Score 161; DB 4; Length 234;
Best Local Similarity 40.9%; Pred. No. 2.2e-10;
Matches 36; Conservative 14; Mismatches 28; Indels 10; Gaps 3;
6 VFPQVAQLSCTLSPOHVTIRYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSA 65
31 VAPQHTARITCGGN---NIGSKSVHYQKPSQAPVLVIY----DDSRPSGIPERFSG 82
66 AKDEAHNACVLITISVPQEDDADYYCISV 93
83 S--NSGNTATLITISRVVDAGDEADYYCQL 108
RESULT 14
Q99M11 PRELIMINARY; PRT; 235 AA.
AC Q99M11
Q99M11
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 25.4 kDa protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
SEQUENCE FROM N.A.
Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
EMBL; BC002129; AAH02129.1; -.
HSSP; P01703; 7FAB.
InterPro; IPR003006; IG_MHC.
InterPro; IPR003596; IG_V.
Pfam; PF00047; IG; 2.
SMART; SM00406; IGV; 1.
PROSITE; PS00290; IG MHC; 1.
Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25403 MW; 39807BF56782A3FB CRC64;
Query Match 29.9%; Score 161; DB 11; Length 235;
Best Local Similarity 42.2%; Pred. No. 2.2e-10;
Matches 35; Conservative 13; Mismatches 29; Indels 6; Gaps 2;
9 GQVAQLSCTLSPOHVTIRYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAKD 68
34 GSTAKLPCKASTGN--IGDSYVNWYQYWGKSPPTMIY----GDLRPSGVSDRFSGSID 87
69 EAHNACVLITISVPQEDDADYYC 91
88 SSSNSGAFLITQNVQADDEADYYC 110
RESULT 15
Q96SB0 PRELIMINARY; PRT; 108 AA.
AC Q96SB0
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin lambda light chain
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variable region (Fragment).  
Homo sapiens (Human).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
[1]

SEQUENCE FROM N.A.  
MEDLINE=98375893; PubMed=9712075;  
A Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;  
I "Molecular analysis of polyclonal antibodies from  
T rheumatic arthritis: human anti-N-acetylglucosamine/anti-myosin  
L antibody V region genes."  
J. Immunol. 161:2020-2031(1998).  
R ENBL; U96394; AA868783.1.  
R InterPro; IPR007110; IG-like.  
R InterPro; IPR003006; IG\_MHC.  
R R InterPro; IPR003596; IG\_V.  
R Pfam; PF00047; IG; 1.  
R SMART; SM00406; IGV; 1.  
R PROSITE; PS00835; IG\_LIKE; 1.  
T NON\_TER 1  
Q SEQUENCE 108 AA; 11594 MW; F4B5DC478A043F48 CRC64;

Query Match 29.7%; Score 160; DR 4; Length 108;  
Best Local Similarity 41.2%; Pred. No. 1.2e-10;  
Matches 35; Conservative 19; Mismatches 23; Indels 8; Gaps 4;  
14 PGQVAVLSCTLSPOHVTIRDXGVSWYQORAGSAPRYLLYRSEEDHRRPADIPDRFSAK 67  
14 PGQVAVLSCTLSPOHVTIRDXGVSWYQORAGSAPRYLLYRSEEDHRRPADIPDRFSAK 67  
68 DEAHNACVLTISPVEDDADYCS 92  
68 --SGTSASLAIISGLRSEDEADYCA 90

Search completed: February 9, 2004, 12:48:28  
Job time : 31.2162 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

M protein - protein search, using sw model

run on: February 9, 2004, 08:36:32 ; Search time 30.7703 Seconds  
(without alignments)  
510.685 Million cell updates/sec

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effect score: 538  
sequence: 1 LDALLVFGQVQAQLSCTLSP.....PVQPEDDADYVCYGVGFSP 99

coring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 1107863 seqs, 158726573 residues

total number of hits satisfying chosen parameters: 1107863

minimum DB seq length: 0  
maximum DB seq length: 2000000000

post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

database : A\_Geneseq\_19Jun03.\*

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- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*
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- 6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*
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- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	538	100.0	113	22	AAW41476 Human polypeptide
2	538	100.0	123	19	AAW5123 Human secreted pro
3	538	100.0	123	21	AAW24061 Human PRO619 prote
4	538	100.0	123	21	AAW56655 Membrane-bound pro
5	538	100.0	123	22	AAU12372 Human PRO619 polyp
6	538	100.0	123	22	AAW65178 Human PRO619 (UNQ3
7	538	100.0	123	24	ABU65770 Human PRO polypept
8	538	100.0	123	24	ABU67046 Human secreted/tra
9	538	100.0	123	24	ABU59851 Novel secreted and

10	538	100.0	123	24	ABU59071 Novel human secret
11	538	100.0	123	24	ABU59218 Human secreted/tra
12	538	100.0	123	24	ABU59367 Novel human secret
13	538	100.0	123	24	ABU60502 Human secreted/tra
14	538	100.0	123	24	ABU57993 Human PRO polypept
15	538	100.0	123	24	ABU58924 Human secreted/tra
16	538	100.0	123	24	ABU58924 Human PRO619 polyp
17	538	100.0	123	24	ABU10839 Human PRO polypept
18	538	100.0	123	24	AAW39690 Human polypeptide
19	234.5	43.6	182	22	ABG19759 Novel human diagno
20	231.5	43.0	142	9	AAW83001 V preB-2 protein.
21	227.5	42.3	142	9	AAW80288 V preB-1 protein.
22	223.5	41.5	185	22	ABG29426 Novel human diagno
23	218.5	40.6	256	23	ABP45219 Human Blys binding
24	216.5	40.2	259	23	ABP45474 Human Blys binding
25	215.5	40.1	277	22	ABG19760 Novel human diagno
26	210.5	39.1	105	22	ABG22849 Novel human diagno
27	209.5	38.9	237	22	ABG19300 Novel human diagno
28	209.5	38.9	250	22	ABG19303 Novel human diagno
29	209.5	38.9	259	23	ABP45541 Human Blys binding
30	207.5	38.6	263	23	ABP45267 Human Blys binding
31	202	37.5	248	24	ABU19832 Human VEGF-2 relat
32	198	36.8	113	22	AAU02522 Anti-adipocyte mon
33	197	36.6	125	9	AAW80289 Human Vpre-B prote
34	195	36.2	98	24	ABP56510 Human anti-Fc-epsi
35	195	36.2	134	13	AAW23771 Recombinant light
36	195	36.2	253	23	ABP44898 Human Blys binding
37	195	36.2	253	23	ABP45114 Human Blys binding
38	195	36.2	253	23	ABP45156 Human Blys binding
39	193	35.9	110	23	AAO18434 Anti-GD2 antibody
40	192.5	35.8	118	19	AAW57582 Chimeric H chain S
41	192.5	35.8	118	20	AAW89645 Human antibody hMB
42	192.5	35.8	118	21	AAW77506 Peptide seq ID No:
43	192.5	35.8	118	22	AAW63386 Amino acid sequenc
44	192.5	35.8	118	22	AAW64768 Humanised anti-PTH
45	192.5	35.8	118	22	AAW76884 Human antibody L C

ALIGNMENTS

- RESULT 1  
AAW41476  
ID AAW41476 standard; Protein; 113 AA.  
XX AAW41476;  
AC AAW41476;  
XX 22-OCT-2001 (first entry)  
DT 22-OCT-2001 (first entry)  
DE Human polypeptide SEQ ID NO 6407.  
XX Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia.  
XX Homo sapiens.  
OS  
XX WO200153312-A1.  
FN 26-JUL-2001.  
XX 26-JUL-2001.  
XX 26-DEC-2000; 2000WO-US34263.  
XX 21-JAN-2000; 2000US-0488725.  
PR 25-APR-2000; 2000US-0552317.  
PR 09-JUL-2000; 2000US-0598042.  
PR 19-JUL-2000; 2000US-0620312.  
PR 03-AUG-2000; 2000US-0653450.  
PR 14-SEP-2000; 2000US-0662191.  
PR 19-OCT-2000; 2000US-0693036.



PR	29-NOV-2000; 2000US-0727344.
CX	(HYSE-) HYSEQ INC.
PA	
CA	
PI	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI	Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI	Zhao QA, Zhou P, Goodrich R, Drmanac RT;
CX	WPI: 2001-4425253/47.
R	N-PSDB; AA160632.
CX	
PT	Novel nucleic acids and polypeptides, useful for treating disorders
PT	such as central nervous system injuries -
PS	Example 2; SEQ ID NO 6407; 10078pp; English.
CC	The invention relates to human nucleic acids (AA157798-AA161369) and
CC	the encoded polypeptides (AAAM5842-AAW42113) with neurotropic,
CC	immunosuppressant and cytostatic activity. The polynucleotides are useful
CC	in gene therapy. A composition containing a polypeptide or polynucleotide
CC	of the invention may be used to treat diseases of the peripheral nervous
CC	system, such as peripheral nervous injuries, peripheral neuropathy and
CC	localised neuropathies and central nervous system diseases, such as
CC	Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC	lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC	utilisation of the activities such as: Immune system suppression,
CC	Activin/inhibin activity, chemoradioxic/chemokinetic activity, haemostatic
CC	and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC	assays for receptor activity, arthritis and inflammation, leukaemias and
CC	C.N.S disorders.
CC	Note: The sequence data for this patent did not form part of the printed
CC	specification.
XX	
SQ	Sequence 113 AA;
Query Match	100.0%; Score 538; DB 22; Length 113;
Best Local Similarity	100.0%; Pred. No. 6.7e-53;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 LDALLVFPGQVAQLSCTLSPQHVTIRDYGVSNTQKAGSAPRYLLYRSEDHRRADIP 60
Db	15 LDALLVFPGQVAQLSCTLSPQHVTIRDYGVSNTQKAGSAPRYLLYRSEDHRRADIP 74
OY	61 DRFSAKDGAHNACVLITSPQVEDDADYYCISGVGFSP 99
Db	75 DRFSAKDGAHNACVLITSPQVEDDADYYCISGVGFSP 113
RESULT 2	
AAW75123	
ID	AAW75123 standard; Protein; 123 AA.
AC	
XC	AAW75123;
DT	
XX	25-MAR-2003 (updated)
DT	28-JAN-1999 (first entry)
DE	Human secreted protein encoded by gene 67 clone HRCDF73.
DE	
KW	Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW	diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW	developmental abnormality; foetal deficiency; blood; allergy; renal;
KW	immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW	inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW	cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW	osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW	endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
OS	Homo sapiens.
FN	WO9839446-A2.
PD	
DD	11-SEP-1998.
DD	



Query Match 100.0%; Score 538; DB 21; Length 123;  
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1 LDALLVPPGQVAGLSCTLSFQHVTTIRDVGVSWYQQRAGSAPRYLLYRSSEDDHRRADIP 60  
25 LDALLVPPGQVAGLSCTLSFQHVTTIRDVGVSWYQQRAGSAPRYLLYRSSEDDHRRADIP 84  
  
61 DRPSAKQDAHNAACVLTISFVQPEDDADYICVGVGFSF 99  
85 DRPSAKDAHNAACVLTISFVQPEDDADYICVGVGFSF 123

## RESULT 4

LAY66655

ID AAY66655 standard; protein; 123 AA.

CX AAY66655;

CX 05-APR-2000 (first entry)

CX Membrane-bound protein PRO619.

CX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
CX pharmaceutical; receptor immunoadhesin; gene mapping.

CX Homo sapiens.

CX WC9963088-A2.

CX 09-DEC-1999.

CX 02-JUN-1999; 99WO-US12252.

CX 02-JUN-1998; 98US-0087607.

CX 02-JUN-1998; 98US-0087609.

CX 02-JUN-1998; 98US-0087759.

CX 03-JUN-1998; 98US-0087827.

CX 04-JUN-1998; 98US-0088021.

CX 04-JUN-1998; 98US-0088025.

CX 04-JUN-1998; 98US-0088028.

CX 04-JUN-1998; 98US-0088029.

CX 04-JUN-1998; 98US-0088030.

CX 04-JUN-1998; 98US-0088033.

CX 04-JUN-1998; 98US-0088036.

CX 05-JUN-1998; 98US-0088167.

CX 05-JUN-1998; 98US-0088202.

CX 05-JUN-1998; 98US-0088212.

CX 05-JUN-1998; 98US-0088217.

CX 05-JUN-1998; 98US-0088255.

CX 10-JUN-1998; 98US-0088722.

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CX 10-JUN-1998; 98US-0088825.

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CX 11-JUN-1998; 98US-0088858.

CX 11-JUN-1998; 98US-0088861.

CX 11-JUN-1998; 98US-0088863.

CX 11-JUN-1998; 98US-0088876.

CX 12-JUN-1998; 98US-0089090.

CX 12-JUN-1998; 98US-0089105.

CX 16-JUN-1998; 98US-0089440.

CX 16-JUN-1998; 98US-0089512.

CX 16-JUN-1998; 98US-0089514.

CX 17-JUN-1998; 98US-0089532.

PR 17-JUN-1998; 98US-0089538.  
PR 17-JUN-1998; 98US-0089598.  
PR 17-JUN-1998; 98US-0089599.  
PR 17-JUN-1998; 98US-0089600.  
PR 17-JUN-1998; 98US-0089653.  
PR 18-JUN-1998; 98US-0089801.  
PR 18-JUN-1998; 98US-0089807.  
PR 18-JUN-1998; 98US-0089808.  
PR 19-JUN-1998; 98US-0089947.  
PR 19-JUN-1998; 98US-0089948.  
PR 19-JUN-1998; 98US-0089952.  
PR 22-JUN-1998; 98US-0090246.  
PR 22-JUN-1998; 98US-0090252.  
PR 22-JUN-1998; 98US-0090254.  
PR 23-JUN-1998; 98US-0090349.  
PR 23-JUN-1998; 98US-0090355.  
PR 24-JUN-1998; 98US-0090429.  
PR 24-JUN-1998; 98US-0090431.  
PR 24-JUN-1998; 98US-0090435.  
PR 24-JUN-1998; 98US-0090444.  
PR 24-JUN-1998; 98US-0090461.  
PR 24-JUN-1998; 98US-0090472.  
PR 24-JUN-1998; 98US-0090535.  
PR 24-JUN-1998; 98US-0090538.  
PR 24-JUN-1998; 98US-0090540.  
PR 24-JUN-1998; 98US-0090557.  
PR 25-JUN-1998; 98US-0090676.  
PR 25-JUN-1998; 98US-0090678.  
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PR 26-JUN-1998; 98US-0090862.  
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PR 01-JUL-1998; 98US-0091358.  
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PR 02-JUL-1998; 98US-0091478.  
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PR 02-JUL-1998; 98US-0091673.  
PR 07-JUL-1998; 98US-0091978.  
PR 07-JUL-1998; 98US-0091982.  
PR 09-JUL-1998; 98US-0092182.  
PR 10-JUL-1998; 98US-0092472.  
PR 20-JUL-1998; 98US-0093339.  
PR 30-JUL-1998; 98US-0094651.  
PR 04-AUG-1998; 98US-0095282.  
PR 04-AUG-1998; 98US-0095285.  
PR 04-AUG-1998; 98US-0095301.  
PR 04-AUG-1998; 98US-0095302.  
PR 04-AUG-1998; 98US-0095316.  
PR 04-AUG-1998; 98US-0095321.  
PR 04-AUG-1998; 98US-0095325.  
PR 10-AUG-1998; 98US-0095916.  
PR 10-AUG-1998; 98US-0095929.  
PR 11-AUG-1998; 98US-0096012.  
PR 11-AUG-1998; 98US-0096143.  
PR 11-AUG-1998; 98US-0096146.  
PR 12-AUG-1998; 98US-0096329.  
PR 17-AUG-1998; 98US-0096757.  
PR 17-AUG-1998; 98US-0096766.  
PR 17-AUG-1998; 98US-0096768.  
PR 17-AUG-1998; 98US-0096773.  
PR 17-AUG-1998; 98US-0096791.  
PR 17-AUG-1998; 98US-0096867.

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17-AUG-1998; 98US-0096894.  
17-AUG-1998; 98US-0096895.  
17-AUG-1998; 98US-0096897.  
18-AUG-1998; 98US-0096949.  
18-AUG-1998; 98US-0096950.  
18-AUG-1998; 98US-0096959.  
18-AUG-1998; 98US-0096960.  
18-AUG-1998; 98US-0097022.  
19-AUG-1998; 98US-0097141.  
20-AUG-1998; 98US-0097218.  
24-AUG-1998; 98US-0097661.  
26-AUG-1998; 98US-0097951.  
26-AUG-1998; 98US-0097952.  
26-AUG-1998; 98US-0097954.  
26-AUG-1998; 98US-0097955.  
26-AUG-1998; 98US-0097971.  
26-AUG-1998; 98US-0097974.  
26-AUG-1998; 98US-0097978.  
26-AUG-1998; 98US-0097979.  
26-AUG-1998; 98US-0097986.  
26-AUG-1998; 98US-0098014.  
31-AUG-1998; 98US-0098525.  
16-SEP-1998; 98US-0100634.  
12-JAN-1999; 99US-0115565.  
(GETH ) GENENTECH INC.  
Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
Wood WI, Yuan J;  
WPI; 2000-072883/06.  
N-PSDB; AAZ64983.  
Membrane-bound proteins and related nucleotide sequences -  
Claim 12; Fig 68; 822pp; English.  
The invention provides membrane-bound PRO polypeptides and  
polynucleotides encoding them. The PRO sequences of the invention were  
identified based on extracellular domain homology screening. The PRO  
sequences have homology with proteins including LDL receptors, TIE  
ligands and various enzymes. The membrane-bound proteins and receptor  
molecules are useful as pharmaceutical and diagnostic agents. Receptor  
immunoadhesins, for instance, can be used as therapeutic agents to block  
receptor-ligand interactions. The membrane-bound proteins can also be  
employed for screening of potential peptide or small molecule inhibitors  
of the relevant receptor/ligand interaction. The PRO encoding sequences  
are useful as hybridization probes, in chromosome and gene mapping and in  
the generation of antisense RNA and DNA. PRO nucleic acid sequences  
will also be useful for the preparation of PRO polypeptides, especially  
by recombinant techniques.  
Query Match 100.0%; Score 538; DB 21; Length 123;  
Best Local Similarity 100.0%; Pred. No. 7.4e-53;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
2Y 1 LDALLVFPQVAQLSCTLSPOHVTIRYGVSWYQQAGSAPRYLLYRSEEDHHPADIP 60  
2b 25 LDALLVFPQVAQLSCTLSPOHVTIRYGVSWYQQAGSAPRYLLYRSEEDHHPADIP 84  
2Y 61 DRFSAKDEAHNACVLTISVPQPEDDADYICSVGYGFSP 99  
2b 85 DRFSAKDEAHNACVLTISVPQPEDDADYICSVGYGFSP 123  
RESULT 5  
AAU12372  
ID AAU12372 standard; Protein; 123 AA.  
XX  
AC AAU12372;

XX 24-OCT-2001 (first entry)  
DT Human PRO619 polypeptide sequence.  
DE  
XX  
XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;  
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;  
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;  
KW adipocyte; A-peptide; factor VIIA; gene therapy.  
XX  
OS Homo sapiens.  
XX  
XX WO200140456-A2.  
PN  
XX  
XX 07-JUN-2001.  
XX  
XX 01-DEC-2000; 2000WO-US32678.  
XX  
XX 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 02-DEC-1999; 99WO-US28551.  
PR 02-DEC-1999; 99WO-US28554.  
PR 02-DEC-1999; 99WO-US28555.  
PR 09-DEC-1999; 99US-0170262.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 20-DEC-1999; 99WO-US30999.  
PR 20-DEC-1999; 99WO-US31243.  
PR 30-DEC-1999; 99WO-US31243.  
PR 06-JAN-2000; 2000WO-US00277.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 01-MAR-2000; 2000WO-US05601.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 10-NOV-2000; 2000WO-US30873.  
(GETH ) GENENTECH INC.  
Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
Gerritsen WB, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
WPI; 2001-408281/43.  
N-PSDB; AAS21444.  
Isolated, secretory and transmembrane PRO polypeptide used to detect  
other PRO polypeptides, link bioactive molecules to cells expressing  
PRO polypeptides, and detect the presence of mammalian tumours e.g.  
lung, breast, prostate, cervical -  
Claim 12; Fig 402; 813pp; English.  
AAU12172-AAU12446 represent novel human secretory and transmembrane  
PRO polypeptides. The PRO polypeptides are useful to detect other  
PRO polypeptides, to link bioactive molecules to cells expressing  
PRO polypeptides, to modulate biological activities of cells expressing  
PRO polypeptides, and to detect the presence of mammalian lung, colon,  
breast, prostate, rectal, cervical or liver tumours by comparing PRO  
polypeptide expression in a cell sample to that in a control sample.  
Some of the 275 sequences are also useful to stimulate the release of  
tumour necrosis factor-alpha (TNF-alpha) from human blood, the  
proliferation or differentiation of chondrocytes, the proliferation or  
gene expression in pericyte cells, the release of proteoglycans from

C cartilage, the proliferation of inner ear utricular supporting cells or  
 C of T-lymphocytes, the release of a cytokine from peripheral blood  
 C monocytes (PBMCs), or the proliferation of endothelial cells. Some of  
 C the PRO polypeptides may modulate glucose or free fatty acid uptake by  
 C skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide  
 C to factor VIIA. The PRO polypeptides can be used in assays to identify  
 C molecules involved in binding interactions. The polynucleotides encoding  
 C PRO polypeptides can be used to generate probes, antisense RNA/DNA,  
 C transgenic or knock out animals and can be used in gene therapy.

X Q Sequence 123 AA;

Query Match 100.0%; Score 538; DB 22; Length 123;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-53;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 LDALLVPPGVAQLSCTLSFQVHTIRDYGVSWYQORAGSAPRYLLYRSEEDHRRPADIP 60  
 |||||  
 25 LDALLVPPGVAQLSCTLSFQVHTIRDYGVSWYQORAGSAPRYLLYRSEEDHRRPADIP 84  
 |||||  
 61 DRFSAKDEAHNACVLTISFPQEDDADYICSVGVGFSP 99  
 |||||  
 85 DRFSAKDEAHNACVLTISFPQEDDADYICSVGVGFSP 123

## RESULT 6

AA065178  
 ID AAB65178 standard; Protein; 123 AA.

AC AAB65178;

DT 02-APR-2001 (first entry)

DE Human PRO619 (UNQ555) protein sequence SEQ ID NO:117.

KW Human; secreted and transmembrane protein; PRO; cytostatic;  
 KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
 KW diagnostic assay.

OS Homo sapiens.

FN WO2000073454-A1.

XX 07-DEC-2000.

PF 30-MAR-2000; 2000WO-US08439.

PR 02-JUN-1999; 99WO-US12252.

PR 23-JUN-1999; 99US-0141037.

PR 07-JUL-1999; 99US-0143048.

PR 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.

PR 28-JUL-1999; 99US-0146222.

PR 17-AUG-1999; 99US-0149396.

PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.

PR 08-OCT-1999; 99US-0158663.

PR 30-NOV-1999; 99WO-US28313.

PR 01-DEC-1999; 99WO-US28301.

PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30911.

PR 05-JAN-2000; 2000WO-US00219.

PR 06-JAN-2000; 2000WO-US00376.

PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04341.

PR 22-FEB-2000; 2000WO-US04414.

PR 24-FEB-2000; 2000WO-US04914.

PR 02-MAR-2000; 2000WO-US05004.

PR 15-MAR-2000; 2000WO-US05841.

PR 20-MAR-2000; 2000WO-US06884.

XX 20-MAR-2000; 2000WO-US07377.

PA (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL;  
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi CJ, Gurney AL, Klijavin IJ, Napier MA, Pan J, Paoni NF;  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams EM, Wood WI;  
 PI Zhang Z;

DR WPI; 2001-032160/04.

DR N-PSDB; AAF44129.

XX PRO polynucleotides used to produce polypeptides used to target  
 PT bioactive molecules such as toxins, radiolabels or antibodies, to  
 PT specific cells, to cause targeted cell death -

PS Claim 12; Fig 68; 935pp; English.

XX The present invention describes human secreted and transmembrane PRO  
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins  
 CC can be used for targeted delivery of bioactive molecules, such as  
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
 CC sequences, and their fragments, can be used as hybridisation probes, in  
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA  
 CC and DNA. They may also be used to produce transgenic animals which are  
 CC used to develop and screen therapeutically useful reagents. The PRO  
 CC nucleotide and protein sequence can be used for tissue typing and in  
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
 CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.

XX Sequence 123 AA;

Query Match 100.0%; Score 538; DB 22; Length 123;

Best Local Similarity 100.0%; Pred. No. 7.4e-53;

Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDALLVPPGVAQLSCTLSFQVHTIRDYGVSWYQORAGSAPRYLLYRSEEDHRRPADIP 60  
 |||||  
 25 LDALLVPPGVAQLSCTLSFQVHTIRDYGVSWYQORAGSAPRYLLYRSEEDHRRPADIP 84  
 |||||

OY 61 DRFSAKDEAHNACVLTISFPQEDDADYICSVGVGFSP 99

DB 85 DRFSAKDEAHNACVLTISFPQEDDADYICSVGVGFSP 123

## RESULT 7

ABU66770

ID ABU66770 standard; Protein; 123 AA.

AC ABU66770;

DT 23-MAY-2003 (first entry)

DE Human PRO polypeptide #201.

KW Human; PRO polypeptide; secreted and transmembrane protein;  
 KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;  
 KW differentiation; chondrocyte; tumour; genetic disorder;  
 KW cytostatic.

OS Homo sapiens.

XX US2003036180-A1.

PN 20-FEB-2003.

PD 09-MAY-2002; 2002US-0143114.

PF 31-MAR-1997; 97WO-US05230.

PR 12-JUN-1998; 98WO-US12456.

PR 14-JUL-1998; 98WO-US14552.

PR 28-AUG-1998; 98WO-US17888.



## RESULT 8

BU67046

D ASU67046 standard; Protein; 123 AA.

X C

X C ABU67046;

X T

X T 27-MAY-2003 (first entry)

X E

X E Human secreted/transmembrane, PRO, protein SEQ ID 402.

X W

X W Human; secreted protein; transmembrane protein; PRO;  
X W inflammatory disease; organ failure; atherosclerosis; cardiac injury;  
X W infertility; birth defects; premature aging; AIDS; biosensor;  
X W acquired immunodeficiency syndrome; cancer; diabetic complication;  
X W bioreactor; tumour.

X NS

X NS Homo sapiens.

X N

X N US2003032155-A1.

X D

X D 13-FEB-2003.

X F

X F 03-MAY-2002; 2002US-0137865.

X C

X C 31-MAR-1997; 97WO-US05230.

X R

X R 12-JUN-1998; 98WO-US12456.

X R

X R 14-JUL-1998; 98WO-US14552.

X R

X R 28-AUG-1998; 98WO-US17888.

X R

X R 10-SEP-1998; 98WO-US18824.

X R

X R 14-SEP-1998; 98WO-US19093.

X R

X R 14-SEP-1998; 98WO-US19094.

X R

X R 14-SEP-1998; 98WO-US19177.

X R

X R 16-SEP-1998; 98WO-US19330.

X R

X R 17-SEP-1998; 98WO-US19437.

X R

X R 07-OCT-1998; 98WO-US21141.

X R

X R 29-OCT-1998; 98WO-US22991.

X R

X R 29-OCT-1998; 98WO-US22992.

X R

X R 20-NOV-1998; 98WO-US24855.

X R

X R 01-DEC-1998; 98WO-US25108.

X R

X R 05-JAN-1999; 99WO-US00106.

X R

X R 08-MAR-1999; 99WO-US05028.

X R

X R 10-MAR-1999; 99WO-US05190.

X R

X R 20-APR-1999; 99WO-US08615.

X R

X R 14-MAY-1999; 99WO-US10733.

X R

X R 02-JUN-1999; 99WO-US12252.

X R

X R 01-SEP-1999; 99WO-US20111.

X R

X R 08-SEP-1999; 99WO-US20594.

X R

X R 13-SEP-1999; 99WO-US20944.

X R

X R 15-SEP-1999; 99WO-US21090.

X R

X R 15-SEP-1999; 99WO-US21547.

X R

X R 05-OCT-1999; 99WO-US23089.

X R

X R 29-NOV-1999; 99WO-US28214.

X R

X R 30-NOV-1999; 99WO-US28313.

X R

X R 30-NOV-1999; 99WO-US28409.

X R 01-DEC-1999; 99WO-US28301.

X R 01-DEC-1999; 99WO-US28634.

X R 02-DEC-1999; 99WO-US28551.

X R 02-DEC-1999; 99WO-US28564.

X R 16-DEC-1999; 99WO-US30095.

X R 20-DEC-1999; 99WO-US30911.

X R 20-DEC-1999; 99WO-US30999.

X R 22-DEC-1999; 99WO-US30720.

X R 30-DEC-1999; 99WO-US31243.

X R 30-DEC-1999; 99WO-US31274.

X R 05-JAN-2000; 2000WO-US00219.

X R 06-JAN-2000; 2000WO-US00277.

X R 11-FEB-2000; 2000WO-US00376.

X R 18-FEB-2000; 2000WO-US04341.

X R 22-FEB-2000; 2000WO-US04342.

X R 22-FEB-2000; 2000WO-US04414.

24-FEB-2000; 2000WO-US04914.  
24-FEB-2000; 2000WO-US05004.  
01-MAR-2000; 2000WO-US05601.  
02-MAR-2000; 2000WO-US05746.  
02-MAR-2000; 2000WO-US05841.  
15-MAR-2000; 2000WO-US06319.  
15-MAR-2000; 2000WO-US06884.  
20-MAR-2000; 2000WO-US07377.  
20-MAR-2000; 2000WO-US07532.  
21-MAR-2000; 2000WO-US08439.  
30-MAR-2000; 2000WO-US13705.  
17-MAY-2000; 2000WO-US13705.  
22-MAY-2000; 2000WO-US14042.  
30-MAY-2000; 2000WO-US14941.  
02-JUN-2000; 2000WO-US15264.  
28-JUL-2000; 2000WO-US20710.  
11-AUG-2000; 2000WO-US22031.  
23-AUG-2000; 2000WO-US23522.  
24-AUG-2000; 2000WO-US23328.  
08-NOV-2000; 2000WO-US30952.  
10-NOV-2000; 2000WO-US30873.  
01-DEC-2000; 2000WO-US32678.  
20-DEC-2000; 2000WO-US34956.  
28-FEB-2001; 2001WO-US06520.  
01-MAR-2001; 2001WO-US06666.  
25-MAY-2001; 2001WO-US17092.  
01-JUN-2001; 2001WO-US17800.  
20-JUN-2001; 2001WO-US19692.  
22-JUN-2001; 2001WO-US20116.  
29-JUN-2001; 2001WO-US21066.  
03-JUL-2001; 2001WO-US21735.  
20-DEC-2000; 2000US-0747259.  
28-FEB-2001; 2001US-0796498.  
03-MAR-2001; 2001US-0802706.  
14-MAR-2001; 2001US-0808689.  
22-MAR-2001; 2001US-0816744.  
05-APR-2001; 2001US-0828366.  
10-MAY-2001; 2001US-0854208.  
18-MAY-2001; 2001US-0854280.  
25-MAY-2001; 2001US-0866028.  
25-MAY-2001; 2001US-0866034.  
01-JUN-2001; 2001US-0872035.  
05-JUN-2001; 2001US-0874503.  
14-JUN-2001; 2001US-0882636.  
19-JUN-2001; 2001US-0886342.  
21-JUN-2001; 2001US-0887879.  
18-JUL-2001; 2001US-0908827.  
06-AUG-2001; 2001US-0924419.  
09-AUG-2001; 2001US-0927796.  
16-AUG-2001; 2001US-0931836.  
19-DEC-2001; 2001US-0028072.

(GETH ) GENENTECH INC.

Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
Geritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI: 2003-331925/31.

N-PSDB; ACA04224.

New secreted and transmembrane nucleic acids and polypeptides,  
designated as PRO, useful for treating inflammation, organ failure,  
atherosclerosis, cardiac injury, infertility, birth defects, premature  
aging, AIDS, or cancer

Claim 12; Fig 402; 659pp; English.

The invention relates to an isolated nucleic acid comprising, or which is  
at least 80% identical to, or the full-length coding sequence of, any of  
the 275 nucleotide sequences, encoding the corresponding PRO polypeptide  
(one of 275 secreted or transmembrane proteins). The nucleic acid  
further comprises the full-length coding sequence of the DNA deposited

C under American Type Culture Collection (ATCC) accession number in a list  
C given in the specification. Also included are vectors and host  
C cells for producing PRO proteins, PRO fusion proteins, anti-PRO  
C antibodies, PRO extracellular domains and mature sequences, methods  
C of detecting PRO proteins, methods for stimulating the release of  
C TNF-alpha (tumour necrosis factor alpha) from human blood,  
C (and the proliferation of differentiation of chondrocyte cells, the  
C proteoglycans from cartilage, proliferation of inner ear utricular  
C supporting cells, the proliferation of T-lymphocyte cells, the release  
C of a cytokine from peripheral blood mononuclear cells (PBMC), or the  
C proliferation of endothelial cells), a method for modulating the uptake  
C of glucose or free fatty acid (FFA) by skeletal muscle cells,  
C a method for inhibiting the binding of A-peptide to factor VIIa,  
C or the differentiation of adipocyte cells, a method for detecting the  
C presence of a tumour in a mammal and an oligonucleotide probe derived  
C from any of the nucleotide sequences cited above. The nucleic acids and  
C polypeptides are useful for treating inflammatory diseases, organ  
C failure, atherosclerosis, cardiac injury, infertility, birth defects,  
C premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or  
C diabetic complications. The nucleic acids are useful as hybridisation  
C probes, in chromosome and gene mapping, and in generating antisense RNA  
C or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,  
C biosensors or bioreactors. Both are useful in tissue typing.  
C The present sequence represents a PRO protein of the invention.

X C Sequence 123 AA;  
Q

Query Match 100.0%; Score 538; DB 24; Length 123;  
Best Local Similarity 100.0%; Pred. No. 7.4e-53;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 LDALLVPPGVAQLSCTLSQHTVIRDYGVSVYQQRAGSAPRYLLYRSEEDHRRPADIP 60  
b 25 LDALLVPPGVAQLSCTLSQHTVIRDYGVSVYQQRAGSAPRYLLYRSEEDHRRPADIP 84

Y 61 DRFSAKDEAHNAVLITISFVQPEDDADYICSVGVGFSP 99  
b 85 DRFSAKDEAHNAVLITISFVQPEDDADYICSVGVGFSP 123

RESULT 9  
BU59851  
D ABUS9851 standard; Protein; 123 AA.  
X C ABUS9851;  
X X  
X 13-MAY-2003 (first entry)  
X X  
X Novel secreted and transmembrane protein PRO619.  
X X Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
X W cardiac insufficiency disorder; cancer; tumour; immune response;  
X W adrenal cortical capillary endothelial growth; c-fos induction;  
X W vascular endothelial growth factor inhibition; VEGF inhibition;  
X W endothelial cell growth inhibitor; T-lymphocytes stimulation;  
X W retinal neurons cell survival; rod photoreceptor cell survival;  
X W retinal disorder; retinitis pigmentosa; kidney disorder;  
X W mammalian kidney mesangial cell proliferation; Berger disease;  
X W dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
X W chondrocyte redifferentiation; sports injury; arthritis.

X S Homo sapiens.  
X X  
X US2003017563-A1.  
X X  
X 23-JAN-2003.  
X X  
X 07-MAY-2002; 2002US-0140808.  
X X  
X 31-MAR-1997; 97WO-US05230.  
X PR 12-JUN-1998; 98WO-US12456.  
X PR 14-JUL-1998; 98WO-US14552.

28-AUG-1998; 98WO-US17888.  
10-SEP-1998; 98WO-US18824.  
14-SEP-1998; 98WO-US19093.  
14-SEP-1998; 98WO-US19094.  
16-SEP-1998; 98WO-US19177.  
16-SEP-1998; 98WO-US19330.  
17-SEP-1998; 98WO-US19437.  
07-OCT-1998; 98WO-US21141.  
29-OCT-1998; 98WO-US22991.  
29-OCT-1998; 98WO-US22992.  
29-OCT-1998; 98WO-US24855.  
01-DEC-1998; 98WO-US25108.  
01-DEC-1998; 98WO-US25109.  
08-MAR-1999; 98WO-US05028.  
20-APR-1999; 98WO-US05190.  
14-MAY-1999; 98WO-US08615.  
02-JUN-1999; 98WO-US10733.  
02-JUN-1999; 98WO-US12252.  
01-SEP-1999; 98WO-US20111.  
08-SEP-1999; 98WO-US20594.  
13-SEP-1999; 98WO-US20944.  
15-SEP-1999; 98WO-US21090.  
15-SEP-1999; 98WO-US21547.  
05-OCT-1999; 98WO-US23089.  
29-NOV-1999; 98WO-US28214.  
30-NOV-1999; 98WO-US28313.  
30-NOV-1999; 98WO-US28409.  
01-DEC-1999; 98WO-US28301.  
01-DEC-1999; 98WO-US28634.  
02-DEC-1999; 98WO-US28551.  
02-DEC-1999; 98WO-US28564.  
02-DEC-1999; 98WO-US28565.  
16-DEC-1999; 98WO-US30095.  
20-DEC-1999; 98WO-US30911.  
20-DEC-1999; 98WO-US30999.  
22-DEC-1999; 98WO-US30720.  
30-DEC-1999; 98WO-US31243.  
30-DEC-1999; 98WO-US31274.  
05-JAN-2000; 2000WO-US00219.  
06-JAN-2000; 2000WO-US00277.  
06-JAN-2000; 2000WO-US00376.  
11-FEB-2000; 2000WO-US03565.  
18-FEB-2000; 2000WO-US04341.  
18-FEB-2000; 2000WO-US04342.  
22-FEB-2000; 2000WO-US04414.  
24-FEB-2000; 2000WO-US04914.  
24-FEB-2000; 2000WO-US05004.  
01-MAR-2000; 2000WO-US05601.  
02-MAR-2000; 2000WO-US05746.  
02-MAR-2000; 2000WO-US05841.  
10-MAR-2000; 2000WO-US06319.  
15-MAR-2000; 2000WO-US06884.  
20-MAR-2000; 2000WO-US07377.  
21-MAR-2000; 2000WO-US07532.  
30-MAR-2000; 2000WO-US08439.  
17-MAY-2000; 2000WO-US13705.  
22-MAY-2000; 2000WO-US14042.  
30-MAY-2000; 2000WO-US14941.  
02-JUN-2000; 2000WO-US15264.  
28-JUL-2000; 2000WO-US20710.  
11-AUG-2000; 2000WO-US22031.  
23-AUG-2000; 2000WO-US23522.  
24-AUG-2000; 2000WO-US23328.  
08-NOV-2000; 2000WO-US30952.  
10-NOV-2000; 2000WO-US30873.  
01-DEC-2000; 2000WO-US32678.  
20-DEC-2000; 2000WO-US34956.  
28-FEB-2001; 2001WO-US06520.  
01-MAR-2001; 2001WO-US06666.  
25-MAY-2001; 2001WO-US17092.  
01-JUN-2001; 2001WO-US17800.  
20-JUN-2001; 2001WO-US19692.  
22-JUN-2001; 2001WO-US20116.



R 29-JUN-2001; 2001WO-US21066.  
 R 09-JUL-2001; 2001WO-US21735.  
 R 20-DEC-2000; 2000US-0747259.  
 R 28-FEB-2001; 2001US-0796498.  
 R 09-MAR-2001; 2001US-0802706.  
 R 14-MAR-2001; 2001US-0808689.  
 R 22-MAR-2001; 2001US-0816744.  
 R 05-APR-2001; 2001US-0828366.  
 R 10-MAY-2001; 2001US-0854208.  
 R 18-MAY-2001; 2001US-0854280.  
 R 23-MAY-2001; 2001US-0860216.  
 R 25-MAY-2001; 2001US-0866028.  
 R 25-MAY-2001; 2001US-0866034.  
 R 01-JUN-2001; 2001US-0872035.  
 R 05-JUN-2001; 2001US-0874503.  
 R 14-JUN-2001; 2001US-0882636.  
 R 19-JUN-2001; 2001US-0886342.  
 R 21-JUN-2001; 2001US-0887879.  
 R 18-JUL-2001; 2001US-0908827.  
 R 06-AUG-2001; 2001US-0924419.  
 R 09-AUG-2001; 2001US-0927796.  
 R 16-AUG-2001; 2001US-0931836.  
 R 19-DEC-2001; 2001US-0028072.

(GETH ) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W, Gerritsen ME, Goddard A, Godowski RJ, Gurney AL, Sherwood S, Smith V, Stewart JA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-148238/14.  
 N-PSDB; ABX89341.

Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer treatments -

Claim 12; Fig 402; 659pp; English.

The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in linking a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO132 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO114 and PRO186 stimulate adrenal cortical capillary endothelial growth, and PRO336, PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126, PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus useful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and angiogenesis of this polypeptide are useful for treating cancerous tumours. PRO812 inhibits vascular endothelial growth factor (VEGF) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth in mammals which would be beneficial in inhibiting tumour growth. PRO826, PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of stimulated T-lymphocytes and are therapeutically useful for enhancing immune response. PRO826, PRO1068 or PRO1132 enhance survival of retinal neurons cells (PRO1132 is also enhances survival/proliferation of rod photoreceptor cells) and therefore are useful for treating retinal disorders of injuries e.g. retinitis pigmentosa, AMD, PRO819, PRO813 and PRO1066 induce proliferation of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathies associated with dermatitis, herpeticiformis or Crohn's disease. PRO1310, PRO844, PRO1132, and PRO1387 induce the proliferation and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This is the amino acid sequence of a novel human PRO protein.

SQ Sequence 123 AA;

Query Match 100.0%; Score 538; DB 24; Length 123;

Best Local Similarity 100.0%; Pred. No. 7 4e-53;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 LDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYRSSEDDHRRADIP 60  
 Db 25 LDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYRSSEDDHRRADIP 84  
 Qy 61 DRFSAKDEAHNACVLTISPVQPEDDADYVCVGYGFSP 99  
 Db 85 DRFSAKDEAHNACVLTISPVQPEDDADYVCVGYGFSP 123

# RESULT 10

ABUS9071  
 ID ABUS9071 standard; Protein; 123 AA.

XX AC ABUS9071;

XX DT 28-APR-2003 (first entry)

XX DE Novel human secreted or transmembrane protein PRO619.

XX KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
 KW cardiac insufficiency disorder; cancer; tumour; immune response;  
 KW adrenal cortical capillary endothelial growth; c-fos induction;  
 KW vascular endothelial growth factor inhibition; VEGF inhibition;  
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
 KW retinal neurons cell survival; rod photoreceptor cell survival;  
 KW retinal disorder; retinitis pigmentosa; kidney disease;  
 KW mammalian kidney mesangial cell proliferation; Berger disease;  
 KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
 KW chondrocyte redifferentiation; sports injury; arthritis.

XX OS Homo sapiens.

XX PN US2002132252-A1.

XX PD 19-SEP-2002.

XX PF 14-NOV-2001; 2001US-0990442.

XX PR 05-NOV-1997; 97WO-US20069.

XX PR 16-SEP-1998; 98WO-US19330.

XX PR 17-SEP-1998; 98WO-US19437.

XX PR 07-OCT-1998; 98WO-US21141.

XX PR 01-DEC-1998; 98WO-US25108.

XX PR 05-JAN-1999; 99WO-US00106.

XX PR 08-MAR-1999; 99WO-US05028.

XX PR 15-SEP-1999; 99WO-US21090.

XX PR 15-SEP-1999; 99WO-US21547.

XX PR 30-NOV-1999; 99WO-US28313.

XX PR 01-DEC-1999; 99WO-US28301.

XX PR 16-DEC-1999; 99WO-US28634.

XX PR 20-DEC-1999; 99WO-US30095.

XX PR 06-JAN-2000; 99WO-US30911.

XX PR 06-JAN-2000; 2000WO-US00219.

XX PR 11-FEB-2000; 2000WO-US03376.

XX PR 18-FEB-2000; 2000WO-US04341.

XX PR 22-FEB-2000; 2000WO-US04414.

XX PR 24-FEB-2000; 2000WO-US04914.

XX PR 24-FEB-2000; 2000WO-US05004.

XX PR 02-MAR-2000; 2000WO-US05841.

XX PR 10-MAR-2000; 2000WO-US06319.

XX PR 15-MAR-2000; 2000WO-US06884.

XX PR 20-MAR-2000; 2000WO-US07377.

XX PR 30-MAR-2000; 2000WO-US08439.

XX PR 15-MAY-2000; 2000WO-US13358.

XX PR 17-MAY-2000; 2000WO-US13705.

XX PR 22-MAY-2000; 2000WO-US14042.

XX PR 30-MAY-2000; 2000WO-US14941.

XX PR 02-JUN-2000; 2000WO-US15264.

R 28-JUL-2000; 2000WO-US20710.  
R 11-AUG-2000; 2000WO-US22031.  
R 23-AUG-2000; 2000WO-US23522.  
R 24-AUG-2000; 2000WO-US23328.  
R 08-NOV-2000; 2000WO-US30952.  
R 01-DEC-2000; 2000WO-US32678.  
R 28-FEB-2001; 2001WO-US06520.  
R 01-JUN-2001; 2001WO-US17800.  
R 20-JUN-2001; 2001WO-US19692.  
R 29-JUN-2001; 2001WO-US21066.  
R 09-JUL-2001; 2001WO-US21735.  
R 16-JUN-1997; 97US-049787P.  
R 17-OCT-1997; 97US-062250P.  
R 12-NOV-1997; 97US-065186P.  
R 13-NOV-1997; 97US-065311P.  
R 24-NOV-1997; 97US-066770P.  
R 25-FEB-1998; 98US-075945P.  
R 20-MAR-1998; 98US-078910P.  
R 28-APR-1998; 98US-083322P.  
R 07-MAY-1998; 98US-084600P.  
R 28-MAY-1998; 98US-087106P.  
R 02-JUN-1998; 98US-087607P.  
R 02-JUN-1998; 98US-087609P.  
R 02-JUN-1998; 98US-087759P.  
R 03-JUN-1998; 98US-087827P.  
R 04-JUN-1998; 98US-088021P.  
R 04-JUN-1998; 98US-088025P.  
R 04-JUN-1998; 98US-088026P.  
R 04-JUN-1998; 98US-088028P.  
R 04-JUN-1998; 98US-088029P.  
R 04-JUN-1998; 98US-088030P.  
R 04-JUN-1998; 98US-088033P.  
R 04-JUN-1998; 98US-088326P.  
R 05-JUN-1998; 98US-088167P.  
R 05-JUN-1998; 98US-088202P.  
R 05-JUN-1998; 98US-088212P.  
R 05-JUN-1998; 98US-088215P.  
R 09-JUN-1998; 98US-088655P.  
R 10-JUN-1998; 98US-088734P.  
R 10-JUN-1998; 98US-088738P.  
R 10-JUN-1998; 98US-088742P.  
R 10-JUN-1998; 98US-088810P.  
R 10-JUN-1998; 98US-088824P.  
R 10-JUN-1998; 98US-088826P.  
R 11-JUN-1998; 98US-088858P.  
R 11-JUN-1998; 98US-088861P.  
R 11-JUN-1998; 98US-088876P.  
R 12-JUN-1998; 98US-089105P.  
R 16-JUN-1998; 98US-089440P.  
R 16-JUN-1998; 98US-089512P.  
R 16-JUN-1998; 98US-089514P.  
R 17-JUN-1998; 98US-089532P.  
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R 17-JUN-1998; 98US-089598P.  
R 17-JUN-1998; 98US-089599P.  
R 17-JUN-1998; 98US-089600P.  
R 17-JUN-1998; 98US-089653P.  
R 18-JUN-1998; 98US-089801P.  
R 18-JUN-1998; 98US-089907P.  
R 18-JUN-1998; 98US-089908P.  
R 28-AUG-2001; 2001US-094192.

(GETH ) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Fong S, Garber H, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;

XX WPI; 2003-247083/24.  
XX N-PSDB; ABX80196.

PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
PT are therapeutically useful for enhancing immune response and in cancer  
PT treatments -  
XX Claim 12; Fig 68; 648pp; English.  
PS  
XX The invention describes an isolated human PRO polypeptide. The PRO  
XX polypeptides are useful in detecting PRO polypeptides in a sample, in  
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
CC in modulating at least one biological activity of a cell expressing a PRO  
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,  
CC PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
CC useful for treating conditions or disorders where angiogenesis would be  
CC beneficial, e.g. wound healing and antagonism of this polypeptide are  
CC useful for treating cancerous tumours. PRO12 inhibits vascular  
CC endothelial growth factor (VEGF) stimulated endothelial cell growth in  
CC cells and is thus useful for inhibiting endothelial cell growth in  
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,  
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
CC stimulated T-lymphocytes and are therapeutically useful for enhancing  
CC immune response. PRO828, PRO1068 or PRO1132 enhance survival of  
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
CC rod photoreceptor cells) and therefore are useful for treating retinal  
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813  
CC and PRO1086 induce proliferation of mammalian kidney mesangial cells,  
CC and therefore are useful for treating kidney disorders associated with  
CC decreased mesangial cell function such as Berger disease or Crohn's  
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's  
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
CC proliferation and/or redifferentiation of chondrocytes in culture and  
CC are thus useful for treating sports injuries, and arthritis. This  
CC is the amino acid sequence of a novel human PRO protein.  
XX  
XX Sequence 123 AA;

Query Match 100.0%; Score 538; DB 24; Length 123;  
Best Local Similarity 100.0%; Pred. No. 7.4e-53;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 25 LDALLVFPQVQAQLSCTLSFQHVITRDYGVSWYQORAGSAPRYLLYRSEEDHRRADIP 84  
Qy 61 DRFSAKDEAHNACVLTISPQVEDDADYVCVGYGFSP 99  
Db 85 DRFSAKDEAHNACVLTISPQVEDDADYVCVGYGFSP 123

RESULT 11

ABU59218  
ID ABU59218 standard; Protein; 123 AA.

XX AC ABU59218;

XX 22-APR-2003 (first entry)

DE Human secreted/transmembrane protein, #43.

KW Human; PRO; secreted; transmembrane; pharmaceutical;  
KW diagnostic; biosensor; bioreactor; tumour; therapeutic;  
KW Gene therapy; tumour-associated antigenic target; TAT; ADEPT;  
XX antibody-dependent enzyme mediated Prodrug therapy; cytostatic.

XX Homo sapiens.

XX OS Homo sapiens.

XX US2003027162-A1.

XX 06-FEB-2003.

XX

IF 15-NOV-2001; 2001US-0997428.  
XX 05-NOV-1997; 97WO-US200069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28304.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 02-MAR-2000; 2000WO-US05004.  
PR 10-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06319.  
PR 20-MAR-2000; 2000WO-US06884.  
PR 30-MAR-2000; 2000WO-US07377.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
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PR 28-JUL-2000; 2000WO-US20710.  
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PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30352.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-049787P.  
PR 17-OCT-1997; 97US-062250P.  
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PR 25-FEB-1998; 98US-075945P.  
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PR 18-JUN-1998; 98US-089907P.  
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PR 22-JUN-1998; 98US-090246P.  
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PR 24-JUN-1998; 98US-090444P.  
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PR 26-JUN-1998; 98US-090862P.  
PR 26-JUN-1998; 98US-090863P.  
PR 01-JUL-1998; 98US-091360P.  
PR 01-JUL-1998; 98US-091544P.  
PR 02-JUL-1998; 98US-091478P.  
PR 02-JUL-1998; 98US-091519P.  
PR 02-JUL-1998; 98US-091626P.  
PR 02-JUL-1998; 98US-091628P.  
PR 02-JUL-1998; 98US-091633P.  
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PR 02-JUL-1998; 98US-091673P.  
PR 07-JUL-1998; 98US-091978P.  
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PR 09-JUL-1998; 98US-092182P.  
PR 10-JUL-1998; 98US-092472P.  
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PR 04-AUG-1998; 98US-095282P.  
PR 04-AUG-1998; 98US-095285P.  
PR 04-AUG-1998; 98US-095301P.  
PR 04-AUG-1998; 98US-095302P.  
PR 04-AUG-1998; 98US-095318P.  
PR 04-AUG-1998; 98US-095321P.  
PR 10-AUG-1998; 98US-095325P.  
PR 10-AUG-1998; 98US-095916P.  
PR 10-AUG-1998; 98US-095929P.  
PR 10-AUG-1998; 98US-096012P.  
PR 11-AUG-1998; 98US-096143P.

R	11-AUG-1998;	98US-096146P.	XX	06-FEB-2003.
R	12-AUG-1998;	98US-096329P.	PD	
R	17-AUG-1998;	98US-096757P.	XX	
R	17-AUG-1998;	98US-096766P.	PF	
R	17-AUG-1998;	98US-096768P.	XX	
R	17-AUG-1998;	98US-096773P.	XX	
R	17-AUG-1998;	98US-096791P.	PR	14-NOV-2001; 2001US-0990562.
R	17-AUG-1998;	98US-096867P.	PR	
R	17-AUG-1998;	98US-096891P.	PR	05-NOV-1997; 97WO-US20069.
R	17-AUG-1998;	98US-096894P.	PR	16-SEP-1998; 98WO-US19330.
R	17-AUG-1998;	98US-096895P.	PR	17-SEP-1998; 98WO-US19437.
R	17-AUG-1998;	98US-096897P.	PR	07-OCT-1998; 98WO-US21141.
R	18-AUG-1998;	98US-096949P.	PR	01-DEC-1999; 98WO-US25108.
R	18-AUG-1998;	98US-096950P.	PR	05-JAN-1999; 99WO-US00106.
R	18-AUG-1998;	98US-096959P.	PR	08-MAR-1999; 99WO-US05028.
R	18-AUG-1998;	98US-097022P.	PR	02-JUN-1999; 99WO-US12252.
R	19-AUG-1998;	98US-097141P.	PR	15-SEP-1999; 99WO-US21090.
R	20-AUG-1998;	98US-097218P.	PR	15-SEP-1999; 99WO-US21547.
R	24-AUG-1998;	98US-097661P.	PR	30-NOV-1999; 99WO-US28313.
R	26-AUG-1998;	98US-097952P.	PR	01-DEC-1999; 99WO-US28301.
R	26-AUG-1998;	98US-097954P.	PR	01-DEC-1999; 99WO-US28634.
R	26-AUG-1998;	98US-097955P.	PR	16-DEC-1999; 99WO-US30095.
R	26-AUG-1998;	98US-097971P.	PR	20-DEC-1999; 99WO-US30911.
R	26-AUG-1998;	98US-097974P.	PR	05-JAN-2000; 2000WO-US00219.
R	26-AUG-1998;	98US-097978P.	PR	06-JAN-2000; 2000WO-US00376.
R	26-AUG-1998;	98US-097979P.	PR	11-FEB-2000; 2000WO-US03565.
R	26-AUG-1998;	98US-097986P.	PR	18-FEB-2000; 2000WO-US04341.
R	26-AUG-1998;	98US-098014P.	PR	22-FEB-2000; 2000WO-US04414.
R	31-AUG-1998;	98US-098525P.	PR	24-FEB-2000; 2000WO-US04914.
R	16-SEP-1998;	98US-100634P.	PR	24-FEB-2000; 2000WO-US05004.
R	17-SEP-1998;	98US-100858P.	PR	02-MAR-2000; 2000WO-US05841.
R	22-DEC-1998;	98US-113296P.	PR	10-MAR-2000; 2000WO-US06319.
R	12-MAR-1999;	99US-123957P.	PR	15-MAR-2000; 2000WO-US06884.
R	23-JUN-1999;	99US-141037P.	PR	20-MAR-2000; 2000WO-US07377.
Query Match 100.0%; Score 538; DB 24; Length 123;				
Best Local Similarity 100.0%; Pred. No. 7,4e-53;				
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
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b	25	LDALLVPPGVAQLSCTLSPOHTIYDYGVSVMYQOAGSAPRYLLAYYSSEEDHHPADIP 84	PR	11-AUG-2000; 2000WO-US22031.
Y	61	DRSAADKDEAHNACVLITISVPQEDDADYVCYGVGFSP 99	PR	23-AUG-2000; 2000WO-US23522.
b	85	DRSAADKDEAHNACVLITISVPQEDDADYVCYGVGFSP 123	PR	08-AUG-2000; 2000WO-US23328.
RESULT 12				
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AC	ABU59367;		PR	01-DEC-2000; 2000WO-US32678.
CC	ABU59367;		PR	28-FEB-2001; 2001WO-US06520.
DE	22-APR-2003 (first entry)		PR	01-JUN-2001; 2001WO-US17800.
DE	Novel human secreted or transmembrane protein PRO943.		PR	20-JUN-2001; 2001WO-US19692.
KW	Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;		PR	29-JUN-2001; 2001WO-US21066.
KW	cardiac insufficiency disorder; cancer; tumour; immune response;		PR	09-JUL-2001; 2001WO-US21735.
KW	adrenal cortical capillary endothelial growth; c-fos induction;		PR	16-JUN-1997; 97US-049787P.
KW	vascular endothelial growth factor inhibition; VEGF inhibition;		PR	17-OCT-1997; 97US-062250P.
KW	endothelial cell growth inhibitor; T-lymphocytes stimulation;		PR	13-NOV-1997; 97US-065186P.
KW	retinal neurons cell survival; rod photoreceptor cell survival;		PR	24-NOV-1997; 97US-066770P.
KW	retinal disorder; retinitis pigmentosa; kidney disease;		PR	25-FEB-1998; 98US-075945P.
KW	mammalian kidney mesangial cell proliferation; Berger disease;		PR	28-APR-1998; 98US-083322P.
KW	dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;		PR	07-MAY-1998; 98US-084600P.
XX	Chondrocyte redifferentiation; sports injury; arthritis.		PR	28-MAY-1998; 98US-087106P.
OS	Homo sapiens.		PR	02-JUN-1998; 98US-087607P.
XX			PR	02-JUN-1998; 98US-087609P.
XX			PR	02-JUN-1998; 98US-087759P.
PN	US2003027985-A1.		PR	03-JUN-1998; 98US-087827P.

PR 05-JUN-1998; 98US-088217P.  
PR 09-JUN-1998; 98US-088655P.  
PR 10-JUN-1998; 98US-088734P.  
PR 10-JUN-1998; 98US-088738P.  
PR 10-JUN-1998; 98US-088742P.  
PR 10-JUN-1998; 98US-088810P.  
PR 10-JUN-1998; 98US-088824P.  
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PR 11-JUN-1998; 98US-088856P.  
PR 11-JUN-1998; 98US-088861P.  
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PR 16-JUN-1998; 98US-089440P.  
PR 16-JUN-1998; 98US-089512P.  
PR 16-JUN-1998; 98US-089514P.  
PR 17-JUN-1998; 98US-089532P.  
PR 17-JUN-1998; 98US-089536P.  
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PR 18-JUN-1998; 98US-089801P.  
PR 18-JUN-1998; 98US-089907P.  
PR 18-JUN-1998; 98US-089908P.  
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Query Match 100.0%; Score 538; DB 24; Length 123;

Best Local Similarity 100.0%; Pred. No. 7.4e-53;

Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 25 LDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYYRSEEDHRRPADIP 84  
Qy 61 DRFSAKDEAHNACVLTISPVEDDADYICSVGVGFSP 99  
Db 85 DRFSAKDEAHNACVLTISPVEDDADYICSVGVGFSP 123

# RESULT 13

ABU60502  
ID ABU60502 standard; Protein; 123 AA.

XX AC ABU60502;

XX DT 01-MAY-2003 (first entry)

XX DE Human secreted/transmembrane protein, #43.

XX KW Human; PRO; secreted; transmembrane; signal peptide;  
pharmaceutical; diagnostic; therapeutic; gene therapy.

XX OS Homo sapiens.

XX PN US20002160384-A1.

XX PD 31-OCT-2002.

XX PF 14-NOV-2001; 2001US-0992598.

XX PR 05-NOV-1997; 97WO-US20069.

PR 16-SEP-1988; 98WO-US19330.

PR 17-SEP-1998; 98WO-US19437.

PR 07-OCT-1998; 98WO-US21141.

PR 01-DEC-1998; 98WO-US25108.

PR 05-JAN-1999; 99WO-US00106.

3 08-MAR-1999; 99WO-US05028.  
 4 02-JUN-1999; 99WO-US12252.  
 5 15-SEP-1999; 99WO-US21090.  
 6 15-SEP-1999; 99WO-US21547.  
 7 30-NOV-1999; 99WO-US28313.  
 8 01-DEC-1999; 99WO-US28301.  
 9 01-DEC-1999; 99WO-US28634.  
 10 16-DEC-1999; 99WO-US30095.  
 11 20-DEC-1999; 99WO-US30911.  
 12 05-JAN-2000; 2000WO-US00219.  
 13 06-JAN-2000; 2000WO-US00376.  
 14 11-FEB-2000; 2000WO-US03565.  
 15 22-FEB-2000; 2000WO-US04341.  
 16 22-FEB-2000; 2000WO-US04414.  
 17 24-FEB-2000; 2000WO-US04914.  
 18 02-MAR-2000; 2000WO-US05004.  
 19 02-MAR-2000; 2000WO-US05841.  
 20 10-MAR-2000; 2000WO-US06319.  
 21 15-MAR-2000; 2000WO-US06884.  
 22 20-MAR-2000; 2000WO-US07377.  
 23 30-MAR-2000; 2000WO-US08439.  
 24 15-MAY-2000; 2000WO-US13358.  
 25 17-MAY-2000; 2000WO-US13705.  
 26 22-MAY-2000; 2000WO-US14042.  
 27 30-MAY-2000; 2000WO-US14941.  
 28 02-JUN-2000; 2000WO-US15264.  
 29 28-JUL-2000; 2000WO-US20710.  
 30 11-AUG-2000; 2000WO-US22031.  
 31 23-AUG-2000; 2000WO-US23522.  
 32 24-AUG-2000; 2000WO-US23328.  
 33 08-NOV-2000; 2000WO-US30952.  
 34 01-DEC-2000; 2000WO-US32678.  
 35 28-FEB-2001; 2001WO-US06520.  
 36 01-JUN-2001; 2001WO-US17800.  
 37 29-JUN-2001; 2001WO-US19692.  
 38 09-JUL-2001; 2001WO-US21066.  
 39 16-JUN-1997; 97US-049787F.  
 40 17-OCT-1997; 97US-062250F.  
 41 12-NOV-1997; 97US-065186P.  
 42 13-NOV-1997; 97US-065311P.  
 43 24-NOV-1997; 97US-066770P.  
 44 25-FEB-1998; 98US-075945P.  
 45 20-MAR-1998; 98US-078910P.  
 46 28-APR-1998; 98US-083322P.  
 47 07-MAY-1998; 98US-084600P.  
 48 28-MAY-1998; 98US-087106P.  
 49 02-JUN-1998; 98US-087607P.  
 50 02-JUN-1998; 98US-087609P.  
 51 02-JUN-1998; 98US-087759P.  
 52 03-JUN-1998; 98US-087827P.  
 53 04-JUN-1998; 98US-088021P.  
 54 04-JUN-1998; 98US-088025P.  
 55 04-JUN-1998; 98US-088026P.  
 56 04-JUN-1998; 98US-088028P.  
 57 04-JUN-1998; 98US-088029P.  
 58 04-JUN-1998; 98US-088030P.  
 59 04-JUN-1998; 98US-088033P.  
 60 04-JUN-1998; 98US-088326P.  
 61 05-JUN-1998; 98US-088167P.  
 62 05-JUN-1998; 98US-088202P.  
 63 05-JUN-1998; 98US-088212P.  
 64 05-JUN-1998; 98US-088217P.  
 65 09-JUN-1998; 98US-088655P.  
 66 10-JUN-1998; 98US-088734P.  
 67 10-JUN-1998; 98US-088738P.  
 68 10-JUN-1998; 98US-088742P.  
 69 10-JUN-1998; 98US-088810P.  
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 73 11-JUN-1998; 98US-088861P.  
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 PR 18-JUN-1998; 98US-089801P.  
 PR 18-JUN-1998; 98US-089807P.  
 PR 18-JUN-1998; 98US-089908P.  
 PR 28-AUG-2001; 2001US-0941992.

(GETH ) GENENTECH INC.

PI Aahkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,  
 PI Grimaldi JC, Gurney AL, Kljavin IU, Napier MA, Pan J, Paoni NF,  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
 PI Zhang Z;

DR WPI: 2003-288106/28.  
 DR N-PSDB; ABX90174.

PT New transmembrane polypeptides and nucleic acids encoding the  
 PT polypeptides, useful in gene therapy, in chromosome identification, as  
 PT chromosome markers, or in generating probes -  
 PS Claim 12; Fig 68; 650pp; English.

CC The invention discloses isolated PRO secreted/transmembrane polypeptides  
 CC comprising a sequence without signal peptide and the nucleic acid  
 CC encoding them. The polypeptides can be used to raise antibodies that  
 CC specifically bind to the PRO polypeptide, for linking a bioactive  
 CC molecule to a cell expressing a PRO protein and for modulating at least  
 CC one biological activity of a cell. The PRO polypeptides or  
 CC polynucleotides are also useful in gene therapy, in chromosome  
 CC identification, as chromosome markers, or in generating probes. The PRO  
 CC polypeptides are useful as molecular markers for protein  
 CC electrophoresis, and the isolated nucleic acids may be used for  
 CC recombinantly expressing those markers. The PRO polypeptides and nucleic  
 CC acids may also be used in tissue typing. Anti-PRO antibodies are useful  
 CC in diagnostic assays for PRO, and in affinity purification of PRO from  
 CC recombinant cell culture or natural sources. The sequences presented in  
 CC ABU60478-ABU60624 are the PRO polynucleotides of the invention.  
 CC Note: The sequence data for this patent is also available in electronic  
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

SQ Sequence 123 AA;

Query Match 100.0%; Score 538; DB 24; Length 123;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-53;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 25 LDALLVFGQVAQLSCTLSPOHVTIRYGVSWYQORAGSAPRYLLYVRSEEDHRRADIP 84  
 QY 61 DRFSAAKDEAHNACVLTISPVQPEDDADYTCVGVGFSP 99  
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RESULT 14

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 DT 14-APR-2003 (first entry)  
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Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;  
horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;  
antibody-dependent enzyme mediated prodrug therapy.  
Homo sapiens.  
US2003027163-A1.  
06-FEB-2003.  
15-NOV-2001; 2001US-0397666.  
05-NOV-1997; 97WO-US200069.  
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08-MAR-1999; 99WO-US05028.  
02-JUN-1999; 99WO-US12252.  
15-SEP-1999; 99WO-US21090.  
15-SEP-1999; 99WO-US21547.  
30-NOV-1999; 99WO-US28313.  
01-DEC-1999; 99WO-US28301.  
01-DEC-1999; 99WO-US28634.  
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20-DEC-1999; 99WO-US30911.  
05-JAN-2000; 2000WO-US00219.  
06-JAN-2000; 2000WO-US00376.  
11-FEB-2000; 2000WO-US03565.  
18-FEB-2000; 2000WO-US04341.  
22-FEB-2000; 2000WO-US04414.  
24-FEB-2000; 2000WO-US04914.  
24-FEB-2000; 2000WO-US05004.  
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24-JUN-1998; 98US-090435P.  
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24-JUN-1998; 98US-090445P.  
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24-JUN-1998; 98US-090557P.  
25-JUN-1998; 98US-090676P.  
25-JUN-1998; 98US-090678P.  
25-JUN-1998; 98US-090690P.  
25-JUN-1998; 98US-090694P.  
25-JUN-1998; 98US-090695P.  
25-JUN-1998; 98US-090696P.  
26-JUN-1998; 98US-090862P.  
26-JUN-1998; 98US-090863P.  
01-JUL-1998; 98US-091360P.  
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02-JUL-1998; 98US-091519P.  
02-JUL-1998; 98US-091626P.  
02-JUL-1998; 98US-091628P.  
02-JUL-1998; 98US-091633P.  
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02-JUL-1998; 98US-091673P.  
07-JUL-1998; 98US-091978P.  
07-JUL-1998; 98US-091982P.  
09-JUL-1998; 98US-092182P.  
10-JUL-1998; 98US-092472P.  
20-JUL-1998; 98US-093339P.

pharmaceutical; diagnostic; biosensor; bioreactor; tumour; therapeutic;  
colon cancer; lung cancer; breast cancer; cancer; gene therapy.

Homo sapiens.

US2002142961-A1.

03-OCT-2002.

19-NOV-2001; 2001US-0969721.

05-NOV-1997; 97WO-US20069.

17-SEP-1998; 98WO-US19437.

07-OCT-1998; 98WO-US21141.

01-DEC-1998; 98WO-US25108.

05-JAN-1999; 99WO-US00106.

08-MAR-1999; 99WO-US05028.

02-JUN-1999; 99WO-US12252.

15-SEP-1998; 99WO-US21090.

13-SEP-1998; 99WO-US21547.

30-NOV-1999; 99WO-US28313.

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16-DEC-1999; 99WO-US30095.

05-DEC-1999; 99WO-US30911.

20-JAN-2000; 2000WO-US00219.

06-JAN-2000; 2000WO-US00376.

11-FEB-2000; 2000WO-US03565.

18-FEB-2000; 2000WO-US04341.

22-FEB-2000; 2000WO-US04414.

24-FEB-2000; 2000WO-US04914.

02-MAR-2000; 2000WO-US05004.

10-MAR-2000; 2000WO-US05841.

15-MAR-2000; 2000WO-US06319.

15-MAR-2000; 2000WO-US06884.

30-MAR-2000; 2000WO-US07377.

15-MAY-2000; 2000WO-US08439.

17-MAY-2000; 2000WO-US13358.

22-MAY-2000; 2000WO-US13705.

30-MAY-2000; 2000WO-US14042.

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28-JUL-2000; 2000WO-US15264.

11-AUG-2000; 2000WO-US20710.

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24-AUG-2000; 2000WO-US23522.

08-NOV-2000; 2000WO-US23328.

01-DEC-2000; 2000WO-US30952.

28-FEB-2001; 2000WO-US32678.

01-JUN-2001; 2001WO-US06520.

KW	pharmaceutical; diagnostic; biosensor; bioreactor; tumour; therapeutic;
KW	colon cancer; lung cancer; breast cancer; cancer; gene therapy.
XX	Homo sapiens.
OS	US2002142961-A1.
XX	03-OCT-2002.
XX	19-NOV-2001; 2001US-0969721.
XX	05-NOV-1997; 97WO-US20069.
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PR	01-DEC-1998; 98WO-US25108.
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PR	08-MAR-1999; 99WO-US05028.
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PR	16-DEC-1999; 99WO-US30095.
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PR	17-MAY-2000; 2000WO-US13358.
PR	22-MAY-2000; 2000WO-US13705.
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PR	28-JUL-2000; 2000WO-US15264.
PR	11-AUG-2000; 2000WO-US20710.
PR	23-AUG-2000; 2000WO-US22031.
PR	24-AUG-2000; 2000WO-US23522.
PR	08-NOV-2000; 2000WO-US23328.
PR	01-DEC-2000; 2000WO-US30952.
PR	28-FEB-2001; 2000WO-US32678.
PR	01-JUN-2001; 2001WO-US06520.
PR	20-JUN-2001; 2001WO-US19692.
PR	29-JUN-2001; 2001WO-US21066.
PR	09-JUL-2001; 2001WO-US21735.
PR	16-JUN-1997; 97US-049787P.
PR	17-OCT-1997; 97US-062250P.
PR	12-NOV-1997; 97US-065186P.
PR	13-NOV-1997; 97US-065311P.
PR	24-NOV-1997; 97US-066770P.
PR	25-FEB-1998; 98US-075945P.
PR	28-MAR-1998; 98US-078910P.
PR	28-APR-1998; 98US-083322P.
PR	07-MAY-1998; 98US-084600P.
PR	28-MAY-1998; 98US-087106P.
PR	02-JUN-1998; 98US-087607P.
PR	02-JUN-1998; 98US-087609P.
PR	02-JUN-1998; 98US-087759P.
PR	03-JUN-1998; 98US-087827P.
PR	04-JUN-1998; 98US-088021P.
PR	04-JUN-1998; 98US-088025P.
PR	04-JUN-1998; 98US-088026P.
PR	04-JUN-1998; 98US-088028P.
PR	04-JUN-1998; 98US-088029P.
PR	04-JUN-1998; 98US-088030P.

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ID ABUS8924 standard; Protein; 123 AA.  
XX AC ABUS8924;  
XX DT 16-APR-2003 (first entry)  
XX DE Human secreted/transmembrane protein, #43.  
XX KW Human; PRO; secreted; transmembrane; signal peptide;



PR 04-JUN-1998; 98US-088033P.  
PR 04-JUN-1998; 98US-088326P.  
PR 05-JUN-1998; 98US-088167P.  
PR 05-JUN-1998; 98US-088202P.  
PR 05-JUN-1998; 98US-088212P.  
PR 05-JUN-1998; 98US-088217P.  
PR 09-JUN-1998; 98US-088655P.  
PR 10-JUN-1998; 98US-088734P.  
PR 10-JUN-1998; 98US-088738P.  
PR 10-JUN-1998; 98US-088742P.  
PR 10-JUN-1998; 98US-088810P.  
PR 10-JUN-1998; 98US-088824P.  
PR 10-JUN-1998; 98US-088826P.  
PR 11-JUN-1998; 98US-088859P.  
PR 11-JUN-1998; 98US-088861P.  
PR 11-JUN-1998; 98US-088876P.  
PR 12-JUN-1998; 98US-089105P.  
PR 16-JUN-1998; 98US-089440P.  
PR 16-JUN-1998; 98US-089512P.  
PR 16-JUN-1998; 98US-089514P.  
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PR 17-JUN-1998; 98US-089600P.  
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PR 18-JUN-1998; 98US-089801P.  
PR 18-JUN-1998; 98US-089907P.  
PR 18-JUN-1998; 98US-089908P.  
PR 28-AUG-2001; 2001US-094199P.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
XX Perrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
XX Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
XX Zhang Z;  
XX WPI; 2003-155950/15.  
XX  
XX New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184,  
XX PRO361 or PRO846) useful as targets for therapeutic intervention in  
XX cancers (e.g. lung or breast cancers), or for diagnosing these cancers  
XX  
XX Claim 12; Fig 68; 647pp; English.  
XX  
XX The invention discloses isolated PRO secreted/transmembrane polypeptides  
XX comprising a sequence without signal peptide and the nucleic acid  
XX encoding them. The polypeptides can be used to raise antibodies that  
XX specifically bind to the PRO polypeptide, for linking a bioactive  
XX molecule to a cell expressing a PRO protein and for modulating at least  
XX one biological activity of a cell. The PRO polypeptides or  
XX polynucleotides are also useful as pharmaceuticals, diagnostics,  
XX biosensors or bioreactors, for detecting or treating e.g. tumours in  
XX mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or  
XX rabbits as targets for therapeutic intervention in certain cancers (e.g.  
XX colon, lung or breast cancers). The PRO polypeptides are also useful as  
XX presence of these cancers. The PRO polypeptides are also useful as  
XX molecular weight markers or for chromosome identification. The PRO genes  
XX are useful as hybridisation probes or for screening libraries of human  
XX cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene  
XX therapy, particularly for replacing a defective gene. The sequences  
XX presented in ASU58900-ABU59046 are the PRO polypeptides of the invention.  
XX  
XX Sequence 123 AA;  
XX  
XX Query Match 100.0%; Score 538; DB 24; Length 123;  
XX Best Local Similarity 100.0%; Pred. No. 7.4e-53;  
XX Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 25 LDALLVFFGQVAQLSCTLSFQHVITRDYGVSWYQQRAGSAPRYLLYRSEEDHHRPADIP 84  
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Db 85 DRFSAAKDEAHNACVLTISPVQPEDDADYICSVGYGFSP 123  
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Job time : 32.7703 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

M protein - protein search, using sw model

run on: February 9, 2004, 12:47:07 ; Search time 28.9865 seconds  
(without alignments)  
715.121 Million cell updates/sec

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perfect score: 538  
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scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

searched: 801455 seqs, 20932283 residues 801455

total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pcp.\*
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- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pcp.\*
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- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pcp.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	538	100.0	123	9	US-09-989-723-117
3	538	100.0	123	9	US-09-989-279-117
4	538	100.0	123	9	US-09-989-727-117
5	538	100.0	123	10	US-09-989-731-117
6	538	100.0	123	10	US-09-989-732-117
7	538	100.0	123	10	US-09-991-073-117
8	538	100.0	123	10	US-09-990-442-117
9	538	100.0	123	10	US-09-991-163-117
10	538	100.0	123	10	US-09-993-604-117
11	538	100.0	123	10	US-09-990-456-117
12	538	100.0	123	10	US-09-989-721-117
13	538	100.0	123	10	US-09-992-598-117
14	538	100.0	123	10	US-09-981-876-200
15	538	100.0	123	10	US-09-989-293A-117

- 16 US-09-989-735-117
- 17 US-09-990-444-117
- 18 US-09-991-181-117
- 19 US-09-989-730-117
- 20 US-09-990-436-117
- 21 US-09-993-687-117
- 22 US-09-989-734-117
- 23 US-09-997-653-117
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- 25 US-09-148-545-200
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- 32 US-09-998-156-117
- 33 US-09-990-437-117
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- 35 US-09-997-514-117
- 36 US-09-991-172-117
- 37 US-09-990-726-117
- 38 US-09-997-559-117
- 39 US-09-997-601-117
- 40 US-09-990-443-117
- 41 US-09-991-854-117
- 42 US-09-997-628-117
- 43 US-09-987-683-117
- 44 US-09-989-729A-117
- 45 US-09-989-729A-117

ALIGNMENTS

RESULT 1  
US-09-989-722-117  
; Sequence 117, Application US/09989722  
; Patent No. US20020072067A1  
; GENERAL INFORMATION:

- APPLICANT: Ashkenazi, Avi J.
  - APPLICANT: Baker, Kevin P.
  - APPLICANT: Botstein, David
  - APPLICANT: Desnoyers, Luc
  - APPLICANT: Eaton, Dan L.
  - APPLICANT: Ferrara, Napoleone
  - APPLICANT: Fong, Sherman
  - APPLICANT: Garber, Hanspeter
  - APPLICANT: Gerritsen, Mary E.
  - APPLICANT: Goddard, Audrey
  - APPLICANT: Godowski, Paul J.
  - APPLICANT: Grimaldi, J. Christopher
  - APPLICANT: Gurney, Austin L.
  - APPLICANT: Kijavini, Ivar J.
  - APPLICANT: Napier, Mary A.
  - APPLICANT: Pan, James
  - APPLICANT: Paoni, Nicholas F.
  - APPLICANT: Roy, Margaret Ann
  - APPLICANT: Stewart, Timothy A.
  - APPLICANT: Tamas, Daniel
  - APPLICANT: Watanabe, Colin K.
  - APPLICANT: Williams, P. Mickey
  - APPLICANT: Wood, William I.
  - APPLICANT: Zhang, Zemin
- TITLE OF INVENTION: Secreted and Transmembrane Polypeptides, and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C63  
CURRENT APPLICATION NUMBER: US/09/989, 722  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17

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PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
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PRIOR FILING DATE: 1998-07-07  
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PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 538; DB 9; Length 123;  
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b 25 LDALLVFGQVAQLSCTSPQHVIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIP 84  
Y 61 DRFSAKDEAHNAACVLTISVPQEDDADYCVSGYGSP 99  
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RESULT 2  
IS-09-989-723-117  
Sequence 117, Application US/09989723  
Patent No. US20030072092A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC62  
CURRENT APPLICATION NUMBER: US/09/989,723  
CURRENT FILING DATE: 2001-11-19  
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PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478

PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 538; DB 9; Length 123;

Best Local Similarity 100.0%; Pred. No. 5e-51;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDALLVPGQVAQLSCTLSPPQHVTTIRYGVSWYQORAGSAPRYLLYYRSEDDHRRPADIP 60  
DB 25 LDALLVPGQVAQLSCTLSPPQHVTTIRYGVSWYQORAGSAPRYLLYYRSEDDHRRPADIP 84  
QY 61 DRESAAKDEAHNACVLTISPQVEDDADYVCVGVGFSP 99  
DB 85 DRESAAKDEAHNACVLTISPQVEDDADYVCVGVGFSP 123

## RESULT 3

US-09-989-279-117

; Sequence 117, Application US/09989279

; Patent No. US20020072496A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tunas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P27301C56

; CURRENT APPLICATION NUMBER: US/09/989,279

; CURRENT FILING DATE: 2001-11-19

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186

; PRIOR FILING DATE: 1997-11-12

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066770

; PRIOR FILING DATE: 1997-11-24

PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089598
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089599
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089600
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089653
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PRIOR FILING DATE:	1998-06-18
PRIOR APPLICATION NUMBER:	60/089907
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PRIOR FILING DATE:	1998-06-26
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PRIOR FILING DATE:	1998-07-01
PRIOR APPLICATION NUMBER:	60/091478
PRIOR FILING DATE:	1998-07-02
PRIOR APPLICATION NUMBER:	60/091544
PRIOR FILING DATE:	1998-07-02

;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 538; DB 9; Length 123;  
Best Local Similarity 100.0%; Pred. No. 5e-51;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 LDALLVFGQVAQLSCTLSFQHTVIRYGYSWVQORAGSAPRYLLYRSEEDHHRPADIP 60  
DB 25 LDALLVFGQVAQLSCTLSFQHTVIRYGYSWVQORAGSAPRYLLYRSEEDHHRPADIP 84  
  
QY 61 DRFSAKDEAHNACVLTISVPQEDDADYICSVGYGFSP 99  
DB 85 DRFSAKDEAHNACVLTISVPQEDDADYICSVGYGFSP 123

RESULT 4  
US-09-989-727-117  
Sequence 117, Application US/09989727  
Patent No. US20020072497A1  
GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerritsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Kljavin, Ivar J.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE OF INVENTION: Acids Encoding the Same  
;; FILE REFERENCE: P2730PIC65  
;; CURRENT APPLICATION NUMBER: US/09/989,727  
;; CURRENT FILING DATE: 2003-11-19  
;; PRIOR APPLICATION NUMBER: 60/049787  
;; PRIOR FILING DATE: 1997-06-16  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/065186  
;; PRIOR FILING DATE: 1997-11-12  
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;; PRIOR FILING DATE: 1997-11-13  
;; PRIOR APPLICATION NUMBER: 60/066770  
;; PRIOR FILING DATE: 1997-11-24  
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;; PRIOR FILING DATE: 1998-02-25  
;; PRIOR APPLICATION NUMBER: 60/078910

;; PRIOR FILING DATE: 1998-03-20  
;; PRIOR APPLICATION NUMBER: 60/083322  
;; PRIOR FILING DATE: 1998-04-28  
;; PRIOR APPLICATION NUMBER: 60/084600  
;; PRIOR FILING DATE: 1998-05-07  
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;; PRIOR FILING DATE: 1998-05-28  
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;; PRIOR FILING DATE: 1998-06-02  
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PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626

PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 538; DB 9; Length 123;  
Best Local Similarity 100.0%; Pred.No. 5e-51;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDALLVFPQVAQLSCTLSPOHVTIRYGVSWYQORAGSAPRYLLYVSSEDDHRRPADIP 60  
DB 25 LDALLVFPQVAQLSCTLSPOHVTIRYGVSWYQORAGSAPRYLLYVSSEDDHRRPADIP 84  
QY 61 DRFSAKDEAHNACVLTISPQPEDDADYCVSGVGFSP 99  
DB 85 DRFSAKDEAHNACVLTISPQPEDDADYCVSGVGFSP 123

RESULT 5  
US-09-989-731-117  
Sequence 117, Application US/09989731  
Patent No. US20020103125A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2730P1C70  
CURRENT APPLICATION NUMBER: US/09/989,731  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28



PRIOR FILING DATE:	1998-06-17
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PRIOR FILING DATE:	1998-06-24
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PRIOR FILING DATE:	1998-06-26
PRIOR APPLICATION NUMBER:	60/091360
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PRIOR APPLICATION NUMBER:	60/091478
PRIOR FILING DATE:	1998-07-02
PRIOR APPLICATION NUMBER:	60/091544
PRIOR FILING DATE:	1998-07-01
PRIOR APPLICATION NUMBER:	60/091519
PRIOR FILING DATE:	1998-07-02
PRIOR APPLICATION NUMBER:	60/091626
PRIOR FILING DATE:	1998-07-02
PRIOR APPLICATION NUMBER:	60/091633
PRIOR FILING DATE:	1998-07-02

PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 538; DB 10; Length 123;  
Best Local Similarity 100.0%; Pred. No. 5e-51;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
y 1 LDALLVPPQVQLSCTISQHWIRYDGVSWYQORAGSAPRYLLYYRSEEDHRRADIP 60  
b 25 LDALLVPPQVQLSCTISQHWIRYDGVSWYQORAGSAPRYLLYYRSEEDHRRADIP 84  
y 61 DRESAAKDEAHNACVLITSPVQPEDADYICSVGVGFSP 99  
b 85 DRESAAKDEAHNACVLITSPVQPEDADYICSVGVGFSP 123

## RESULT 6

JS-09-989-732-117  
Sequence 117, Application US/09989732

Patent No. US20020123463A1

## GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P27301C57

CURRENT APPLICATION NUMBER: US/09/989,732

PRIOR FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

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;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
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;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09  
  
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Best Local Similarity 100.0%; Pred. No. Se-51;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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DB 25 LDALLVPPGQVACLSTLSPQHVTIRDYGVSWVQORAGSAPRYLLYYRSEDDHRRPADIP 84  
  
QY 61 DRFSAAKDEAHNAACVLTISFVQPEDDADYYICVSGYGFSP 99  
DB 85 DRFSAAKDEAHNAACVLTISFVQPEDDADYYICVSGYGFSP 123  
  
RESULT 7  
US-09-991-073-117  
; Sequence 117, Application US/09991073  
; Patent No. US20020127576A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tamas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C15  
; CURRENT APPLICATION NUMBER: US/09/991,073  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
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; PRIOR FILING DATE: 1997-11-13  
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; PRIOR FILING DATE: 1997-11-24  
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; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
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; PRIOR FILING DATE: 1998-04-28  
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; PRIOR FILING DATE: 1998-05-07  
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PRIOR FILING DATE:	1998-07-07
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PRIOR FILING DATE:	1998-07-09

Query Match 100.0%; Score 538; DB 10; Length 123;  
Best Local Similarity 100.0%; Pred. No. 5e-51;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 25 LDALLVFPQVAQSCTLSPOHVTIRDYGVSWYQQRAGSAPRYLLYRSEEDHRRPADIP 84

QY 61 DRFSAKDEARNACVLLTSPVQPEDDADYCSVGYGFSF 99  
DB 85 DRFSAKDEARNACVLLTSPVQPEDDADYCSVGYGFSF 123

RESULT 8  
US-09-990-442-117  
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Patent No. US20020132252A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C8  
CURRENT APPLICATION NUMBER: US/09/990,442  
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PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 538; DB 10; Length 123;  
Best Local Similarity 100.0%; Pred. No. 5e-51;

Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 25 LDALLVFFGQVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYYRSEDDHRRPADIP 84  
QY 61 DEFSAAKDEAHNACVLTITSPVQPEDDADYYCISVGVGFSP 99  
Db 85 DEFSAAKDEAHNACVLTITSPVQPEDDADYYCISVGVGFSP 123  
RESULT 9  
US-09-991-163-117  
; Sequence 117, Application US/09991163  
; Patent No. US20020132253A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Destroyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C17  
; CURRENT APPLICATION NUMBER: US/09/991,163  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
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QY

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Db 85 DRFSAKDEAHNACVLTSPVQPEDDADYICSVGYGFSP 123

RESULT 10  
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Sequence 117, Application US/09993604  
Patent No. US20020137075A1  
GENERAL INFORMATION:  
APPLICANT: Ashtenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC25  
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 ; Patent No. US20020137890A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnovers, Luc  
 ; APPLICANT: Eaton, Dan L.  
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 ; APPLICANT: Godowski, Paul J.  
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 ; APPLICANT: Gurney, Austin L.  
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 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE REFERENCE: P27301C22  
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PRIOR FILING DATE: 1998-07-02  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 538; DB 10; Length 123;  
Best Local Similarity 100.0%; Pred. No. 5e-51;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDALLVPGQVAQLSCTLSPQHTTIRDYGVSWYQORAGSAPRYLLYYRSEEDHHRPADIP 60  
DB 25 LDALLVPGQVAQLSCTLSPQHTTIRDYGVSWYQORAGSAPRYLLYYRSEEDHHRPADIP 84  
QY 61 DRFSAAKDEAHNAACVLITISFPQEDDADYYCSVGYGFPSP 99  
DB 85 DRFSAAKDEAHNAACVLITISFPQEDDADYYCSVGYGFPSP 123

## RESULT 12

US-09-989-721-117  
Sequence 117, Application US/09898721  
Patent No. US20020142961A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deanoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertschen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C55  
CURRENT APPLICATION NUMBER: US/09/989,721  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.08; Score 538; DB 10; Length 123;  
Best Local Similarity 100.08; Pred. No. 5e-51;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 25 LDALLVFFQVQAQLSCTLSQPHVTIRDYGVSWYQORAGSAPRYLLYYRSEDDHRRPADIP 84  
QY 61 DRFSAKDEAHNACVLTISPVPEDDADYICSVGVGSP 99  
DB 85 DRFSAKDEAHNACVLTISPVPEDDADYICSVGVGSP 123

RESULT 13

US-09-992-598-117  
Sequence 117, Application US/09992598  
Patent No. US20020160384A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
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APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC20  
CURRENT APPLICATION NUMBER: US/09/992,598  
CURRENT FILING DATE: 2001-11-14  
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Query Match 100.0%; Score 538; DB 10; Length 123;

Best Local Similarity 100.0%; Pred. No. 5e-51;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 25 LDALLVFGQVAQLSCTLSPQVTRIDYGVSWYQORAGSAPRYLLYRSEEDHHRPADIP 84  
Qy 61 DRFSAKOEHNACVLTISPQPEDDADYCVGVGFRSP 99  
Db 85 DRFSAKOEHNACVLTISPQPEDDADYCVGVGFRSP 123

RESULT 14  
US-09-981-876-200  
; Sequence 200, Application US/09981876  
; Patent No. US20020164669A1

GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 70 Human Secreted Proteins  
FILE REFERENCE: P200121  
CURRENT APPLICATION NUMBER: US/09/981,876  
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GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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Job time : 29.9865 secs



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M protein - protein search, using sw model

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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; Patent No. 6478825  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tamas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730F1C13  
; CURRENT APPLICATION NUMBER: US/09/996,243  
; CURRENT FILING DATE: 2001-11-14  
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62	PRIOR FILING DATE: 1998-06-16
63	PRIOR APPLICATION NUMBER: 60/089514
64	PRIOR FILING DATE: 1998-06-16
65	PRIOR APPLICATION NUMBER: 60/089532
66	PRIOR FILING DATE: 1998-06-17
67	PRIOR APPLICATION NUMBER: 60/089538
68	PRIOR FILING DATE: 1998-06-17
69	PRIOR APPLICATION NUMBER: 60/089598
70	PRIOR FILING DATE: 1998-06-17
71	PRIOR APPLICATION NUMBER: 60/089599
72	PRIOR FILING DATE: 1998-06-17
73	PRIOR APPLICATION NUMBER: 60/089500

PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089653
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089801
PRIOR FILING DATE:	1998-06-18
PRIOR APPLICATION NUMBER:	60/089907
PRIOR FILING DATE:	1998-06-18
PRIOR APPLICATION NUMBER:	60/089908
PRIOR FILING DATE:	1998-06-18
PRIOR APPLICATION NUMBER:	60/089947
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/089948
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/089952
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/090246
PRIOR FILING DATE:	1998-06-22
PRIOR APPLICATION NUMBER:	60/090252
PRIOR FILING DATE:	1998-06-22
PRIOR APPLICATION NUMBER:	60/090254
PRIOR FILING DATE:	1998-06-22
PRIOR APPLICATION NUMBER:	60/090349
PRIOR FILING DATE:	1998-06-23
PRIOR APPLICATION NUMBER:	60/090355
PRIOR FILING DATE:	1998-06-23
PRIOR APPLICATION NUMBER:	60/090429
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090431
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090435
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090444
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090445
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090472
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090535
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090540
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090542
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090557
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090676
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090678
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090690
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090694
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090695
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090696
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090862
PRIOR FILING DATE:	1998-06-26
PRIOR APPLICATION NUMBER:	60/090863
PRIOR FILING DATE:	1998-06-26
PRIOR APPLICATION NUMBER:	60/091360
PRIOR FILING DATE:	1998-07-01
PRIOR APPLICATION NUMBER:	60/091478
PRIOR FILING DATE:	1998-07-02
PRIOR APPLICATION NUMBER:	60/091544
PRIOR FILING DATE:	1998-07-01
PRIOR APPLICATION NUMBER:	60/091519
PRIOR FILING DATE:	1998-07-02
PRIOR APPLICATION NUMBER:	60/091626
PRIOR FILING DATE:	1998-07-02
PRIOR APPLICATION NUMBER:	60/091633
PRIOR FILING DATE:	1998-07-02

PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 538; DB 4; Length 123;  
Best Local Similarity 100.0%; Pred. No. 2.4e-52;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 1 LDALLVPPGVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYRSEEDHHRPADIP 60  
DB 25 LDALLVPPGVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYRSEEDHHRPADIP 84  
2Y 61 DRFSAAXDEAHNACVLITSPVQPEDDADYYC SVGVGFSP 99  
DB 85 DRFSAAXDEAHNACVLITSPVQPEDDADYYC SVGVGFSP 123

RESULT 2  
US-07-988-925-16  
Sequence 16, Application US/07988925  
Patent No. 5585097

GENERAL INFORMATION:  
APPLICANT: Bolt, Sarah L.  
APPLICANT: Clark, Michael R.  
APPLICANT: Gorman, Scott D.  
APPLICANT: Routledge, Edward G.  
APPLICANT: Waldmann, Herman  
TITLE OF INVENTION: antibody preparation  
NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon and Vanderhye pc  
STREET: 11th Floor, 1100 No. 5585097th Glebe Road  
CITY: Arlington  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22201

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/988.925  
FILING DATE:

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206422.9  
FILING DATE: 24-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/GB92/01933  
FILING DATE: 21-OCT-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Mitchard, Leonard C  
REGISTRATION NUMBER: 29009

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 7038164000  
TELEFAX: 7038164100  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 110 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-07-988-925-16  
Query Match 35.1%; Score 189; DB 1; Length 110;  
Best Local Similarity 46.4%; Pred. No. 9.1e-14;  
Matches 39; Conservative 14; Mismatches 25; Indels 6; Gaps 2;

QY 8 PQOVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYRSEEDHHRPADIPDRFSAAX 67  
DB 14 PGKTVIISCTLSG--IENNYVHWYQORPGAPTTFVIF-----DDDKRPGVDRFSGSI 67  
QY 68 DEAHNACVLITSPVQPEDDADYYC 91  
DB 68 DRSSNSASLTISGLQTEDEADYYC 91

RESULT 3  
US-08-362-780-16  
Sequence 16, Application US/08362780  
Patent No. 5968509  
GENERAL INFORMATION:  
APPLICANT: Gorman, Scott D.  
APPLICANT: Routledge, Edward G.  
APPLICANT: Waldmann, Herman  
TITLE OF INVENTION: Antibody Preparation  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon and Vanderhye pc  
STREET: 8th Floor, 1100 No. 5968509th Glebe Road  
CITY: Arlington  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22201

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/362,780  
FILING DATE:

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/862,543  
FILING DATE: 23-JUNE-1992  
APPLICATION NUMBER: GB 9021679.7  
FILING DATE: 05-OCT-1990

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/GB91/01726  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Mitchard, Leonard C  
REGISTRATION NUMBER: 29009  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 7038164000  
TELEFAX: 7038164100

INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 110 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-362-780-16  
Query Match 35.1%; Score 189; DB 2; Length 110;  
Best Local Similarity 46.4%; Pred. No. 9.1e-14;  
Matches 39; Conservative 14; Mismatches 25; Indels 6; Gaps 2;

QY 8 PQOVAQLSCTLSPOHVTIRDYGVSWYQORAGSAPRYLLYRSEEDHHRPADIPDRFSAAX 67  
DB 14 PGKTVIISCTLSG--IENNYVHWYQORPGAPTTFVIF-----DDDKRPGVDRFSGSI 67  
QY 68 DEAHNACVLITSPVQPEDDADYYC 91  
DB 68 DRSSNSASLTISGLQTEDEADYYC 91

RESULT 4  
US-08-918-148-74

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; Sequence 74, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Gendly, Brian M.
; APPLICANT: Guiney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 74
; LENGTH: 249
; TYPE: PRT
; ORGANISM: artificial
; US-08-918-148-74

Query Match 35.0%; Score 188.5; DB 4; Length 249;
Best Local Similarity 49.4%; Pred. No. 2.7e-13;
Matches 42; Conservative 13; Mismatches 23; Indels 7; Gaps 3;

QY 8 PQGVAQLSCTSPQHVTRDYGVSQYQORAGSAPRYLLYRSEEDHRRPADIPDRFSAK 67
Db 150 PQGVTISCTGSSGVGYNY-VSWYQCHPKAPKLIYGN-----NRSGVDFRFSK 204
QY 68 DEAHNACVLTISPQVEDDADYCS 92
Db 205 --SGNTASLTISGLQAEDEADYFCS 227

RESULT 5
US-09-157-370-5
; Sequence 5, Application US/09157370A
; Patent No. 6262238
; GENERAL INFORMATION:
; APPLICANT: STEINBACHER, Stefan
; APPLICANT: STEINBACHER, Boris
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES
; CURRENT APPLICATION NUMBER: US/09/157,370A
; CURRENT FILING DATE: 1998-09-21
; EARLIER FILING DATE: 1997-01-14
; EARLIER FILING DATE: 1997-01-14
; EARLIER FILING DATE: 1995-07-06
; EARLIER FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-157-370-5

Query Match 34.2%; Score 184; DB 3; Length 109;
Best Local Similarity 43.3%; Pred. No. 3.2e-13;
Matches 42; Conservative 15; Mismatches 24; Indels 16; Gaps 4;

QY 6 VFPGVAQLSCTSPQHVTRDYGVSQYQORAGSAPRYLLYRSEEDHRRPADIPDRFSA 65
Db 12 VSPGQTVTISCSGDSLGIGY----VSWYQKPGQAPKLIY----DDNKRPSGIDRFSG 63
QY 66 AKDEAHNACVLTISPQVEDDADYCYC-----SVGYG 96
Db 64 SK--SGNTASLTISGLQAEDEADYICOSWDSVSVVFG 98

RESULT 6
US-10-039-785-42
; Sequence 42, Application US/10039785
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; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: P550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 42
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T1014A04 scFv
; US-10-039-785-42

Query Match 33.9%; Score 182.5; DB 4; Length 245;
Best Local Similarity 45.9%; Pred. No. 1.2e-12;
Matches 39; Conservative 15; Mismatches 24; Indels 7; Gaps 3;

QY 8 PQGVAQLSCTSPQHVTRDYGVSQYQORAGSAPRYLLYRSEEDHRRPADIPDRFSAK 67
Db 148 PQGVTISCTGTTSDVGYNV-VSWYQCHPKAPKLIYGVNQ----RPSGVDFRFSK 202
QY 68 DEAHNACVLTISPQVEDDADYCS 92
Db 203 --SGNTASLTISGLQAEDEADYCS 225

RESULT 7
US-09-240-274-63
; Sequence 63, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER FILING DATE: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER FILING DATE: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 63
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain O01
; US-09-240-274-63
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Query Match 33.7%; Score 181.5; DB 3; Length 110;  
Best Local Similarity 44.0%; Pred. No. 6.1e-13;  
Matches 37; Conservative 17; Mismatches 23; Indels 7; Gaps 3;  
  
QY 8 PQGVAQLSCTLSPOHVTIRYGVSWYQQRAGSAPRYLLYYRSEEDHRRPADIPDRFSAK 67  
DB 13 PGQRTVTSCTSSNIG-APGVHWYQPPGTAPKLVIY----NDNRRPSGVDRFSGSK 67  
  
QY 68 DEAHNAACVLITSPVQPEDDADYVC 91  
DB 68 --SGTSASLAITGLQAEADYVC 89

RESULT 8  
US-09-025-769B-34  
; Sequence 34, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION NUMBER: EP 95 11 3021.0  
; APPLICATION DATE: 18-AUG-1995  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 34:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-025-769B-34

Query Match 33.6%; Score 181; DB 4; Length 107;  
Best Local Similarity 42.6%; Pred. No. 6.8e-13;  
Matches 40; Conservative 13; Mismatches 31; Indels 10; Gaps 3;  
  
QY 6 VFGQVAQLSCTLSPOHVTIRYGVSWYQQRAGSAPRYLLYYRSEEDHRRPADIPDRFSA 65  
DB 12 VAPGQTARISCGD----ALGDKYASWYQKPGQAPLVIIY----DDSDRPSGIPERFSG 63  
  
QY 66 AKDEAHNAACVLITSPVQPEDDADYVC 99  
DB 64 S--NSGNTATITISGTAQAEADYVCQHHTTPP 95

RESULT 9  
US-09-025-769B-55  
; Sequence 55, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION NUMBER: EP 95 11 3021.0  
; APPLICATION DATE: 18-AUG-1995  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 55:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-025-769B-55

Query Match 33.6%; Score 181; DB 4; Length 107;  
Best Local Similarity 42.6%; Pred. No. 6.8e-13;  
Matches 40; Conservative 13; Mismatches 31; Indels 10; Gaps 3;

QY 6 VFGQVAQLSCTLSPOHVTIRYGVSWYQQRAGSAPRYLLYYRSEEDHRRPADIPDRFSA 65  
DB 12 VAPGQTARISCGD----ALGDKYASWYQKPGQAPLVIIY----DDSDRPSGIPERFSG 63  
  
QY 66 AKDEAHNAACVLITSPVQPEDDADYVC 99  
DB 64 S--NSGNTATITISGTAQAEADYVCQHHTTPP 95

RESULT 10  
US-10-039-785-48  
; Sequence 48, Application US/10039785  
; Patent No. 6538938  
; GENERAL INFORMATION:  
; APPLICANT: Salcedo et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: PF550  
; CURRENT APPLICATION NUMBER: US/10/039,785  
; CURRENT FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: 60/369,860  
; PRIOR FILING DATE: 2002-04-05

[illegible]

COUNTRY: USA  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25 (BPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/958,201  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/028,897  
FILING DATE: 21-OCT-1996  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 111 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: 1C/2D  
US-08-958-201-14

Query Match 32.8%; Score 176.5; DB 2; Length 111;  
Best Local Similarity 45.9%; Pred. No. 2.2e-12;  
Matches 39; Conservative 14; Mismatches 25; Indels 7; Gaps 3;  
Y 8 PGQVQLSCTLSFQHVITRDYGVSWYQORAGSAPRYLLYRSEEDHRRPADIPDRPSAAK 67  
b 14 PGQVITISCTGSSDVGGYKY-VSWYQHPGKAPKLMIF-----EVENRPSGVNRFSGSK 68  
Y 68 DEAHNACVLITISFVQPEDDADYYC 92  
b 69 --SGNTASLTISGLQAEDEADYYC 91

RESULT 14  
US-09-240-274-64  
Sequence 64, Application US/09240274  
Patent No. 6255455  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
FILE REFERENCE: 09596-42U2  
CURRENT APPLICATION NUMBER: US/09/240,274  
CURRENT FILING DATE: 1999-01-29  
EARLIER APPLICATION NUMBER: 60/081,380  
EARLIER FILING DATE: 1998-04-10  
EARLIER APPLICATION NUMBER: 60/028,550  
EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 64  
LENGTH: 112  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) chain 002  
US-09-240-274-64

Query Match 32.8%; Score 176.5; DB 3; Length 112;  
Best Local Similarity 42.9%; Pred. No. 2.2e-12;  
Matches 36; Conservative 16; Mismatches 25; Indels 7; Gaps 3;  
Y 8 PGQVQLSCTLSFQHVITRDYGVSWYQORAGSAPRYLLYRSEEDHRRPADIPDRPSAAK 67  
b 13 PGQVITISCTGSSSSIGAR-YDVHWYQLPGTAPKLLIY----GNENRPSGVNRFSGSK 67  
Y 68 DEAHNACVLITISFVQPEDDADYYC 91  
b 69 --SGTASLAIITGLQAEDEADYYC 89

RESULT 15  
US-09-240-274-65  
Sequence 65, Application US/09240274  
Patent No. 6255455  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
FILE REFERENCE: 09596-42U2  
CURRENT APPLICATION NUMBER: US/09/240,274  
CURRENT FILING DATE: 1999-01-29  
EARLIER APPLICATION NUMBER: 60/081,380  
EARLIER FILING DATE: 1998-04-10  
EARLIER APPLICATION NUMBER: 60/028,550  
EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 65  
LENGTH: 110  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) chain 003  
US-09-240-274-65

Query Match 32.6%; Score 175.5; DB 3; Length 110;  
Best Local Similarity 44.0%; Pred. No. 2.8e-12;  
Matches 37; Conservative 15; Mismatches 25; Indels 7; Gaps 3;  
Y 8 PGQVQLSCTLSFQHVITRDYGVSWYQORAGSAPRYLLYRSEEDHRRPADIPDRPSAAK 67  
b 11 PGQVITISCTGSSSSNIG-AGYDVHWYQLPGTAPKLLIYGN-----NRPSGVNRFSGSK 65  
Y 68 DEAHNACVLITISFVQPEDDADYYC 91  
b 66 --SGTSASLAIITGLQAEDEADYYC 87

Search completed: February 9, 2004, 12:49:05  
Job time: 13.4865 secs

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OM protein - protein search, using sw model

Run on: February 9, 2004, 12:55:12 / Search time 25 Seconds

(without alignments)  
473.150 Million cell updates/sec

Title: US-09-981-876-200

Perfect score: 123

Sequence: 1 MACRLSFLMGFTLSVSQT.....PQPEDDADYCSGVGFSPP 123

Scoring table: OLIGO

Gapop 60.0, Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database: PIR.76:\*

1: Pirl:\*

2: Pirl:\*

3: Pirl:\*

4: Pirl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	8.9	123	2 S35302	B-cell protein 8HS
2	9	7.3	900	2 C71339	probable DNA misa
3	8	6.5	104	2 H90411	hypothetical prote
4	8	6.5	526	2 T21811	hypothetical prote
5	7	5.7	87	2 S16841	Ig kappa chain V r
6	7	5.7	93	2 T45245	hypothetical prote
7	7	5.7	109	2 S17381	hypothetical prote
8	7	5.7	123	2 I38311	T-cell receptor be
9	7	5.7	123	2 S26264	T-cell receptor be
10	7	5.7	145	2 C83370	cytochrome c oxida
11	7	5.7	191	2 C72411	Holliday junction
12	7	5.7	243	2 S27555	Ig lambda chain -
13	7	5.7	258	2 AB2317	hypothetical prote
14	7	5.7	265	2 B89837	hypothetical prote
15	7	5.7	272	2 JQ125	spermidine/putresc
16	7	5.7	298	2 JQ125	regulatory protein
17	7	5.7	322	1 S31087	phosphoprotein pho
18	7	5.7	340	1 C96665	permease (imported
19	7	5.7	371	2 G86851	histidyl-tRNA synt
20	7	5.7	375	2 AH2659	hypothetical prote
21	7	5.7	375	2 F97441	probable membrane
22	7	5.7	401	2 B64877	probable oxidoredu
23	7	5.7	401	2 D08561	probable oxidoredu
24	7	5.7	401	2 A85758	D-amino acid dehyd
25	7	5.7	418	2 A81228	probable kynurenin
26	7	5.7	462	2 F75588	probable membrane
27	7	5.7	464	2 AF0214	catalase (EC 1.11.
28	7	5.7	480	2 JC7672	hypothetical prote
29	7	5.7	484	2 B84254	hypothetical prote

30	7	5.7	518	2 E90944	probable transport
31	7	5.7	518	2 A85793	probable transport
32	7	5.7	518	2 H64942	hypothetical prote
33	7	5.7	519	2 AE0726	probable membrane
34	7	5.7	521	2 G84967	hypothetical prote
35	7	5.7	526	2 AD0770	probable membrane
36	7	5.7	528	2 AC0186	probable membrane
37	7	5.7	549	2 D90987	probable transport
38	7	5.7	549	2 G85832	probable transport
39	7	5.7	549	2 F64972	hypothetical prote
40	7	5.7	553	2 T27245	hypothetical prote
41	7	5.7	568	2 H88904	protein Y57GALC.9
42	7	5.7	659	2 T27246	hypothetical prote
43	7	5.7	837	1 S51680	fructose phosphor
44	7	5.7	934	2 I64819	DNA mismatch repai
45	7	5.7	934	2 B71612	hypothetical prote
46	6	4.9	51	2 S01870	hypothetical prote
47	6	4.9	54	2 S40381	Ig kappa chain V r
48	6	4.9	54	2 A25521	Ig kappa chain V r
49	6	4.9	60	2 A24626	Ig lambda chain V-
50	6	4.9	64	2 S17384	T-cell receptor be
51	6	4.9	72	2 T06599	disease resistance
52	6	4.9	77	2 D30502	Ig kappa chain V r
53	6	4.9	78	2 A47243	T-cell receptor be
54	6	4.9	78	2 C49039	T-cell receptor be
55	6	4.9	80	2 F75598	hypothetical prote
56	6	4.9	81	2 D83433	hypothetical prote
57	6	4.9	83	2 I30607	Ig kappa chain V-I
58	6	4.9	84	2 B28340	Ig kappa chain V r
59	6	4.9	87	2 S78490	Ig kappa chain V r
60	6	4.9	87	2 S16843	Ig kappa chain V r
61	6	4.9	87	2 S16823	Ig kappa chain V r
62	6	4.9	87	2 S16823	Ig kappa chain V r
63	6	4.9	89	2 S34096	Ig kappa chain V r
64	6	4.9	91	2 PH1071	Ig light chain V r
65	6	4.9	91	2 S37520	Ig kappa chain V r
66	6	4.9	91	2 S67340	Ig kappa chain V r
67	6	4.9	92	2 S37524	Ig kappa chain V r
68	6	4.9	92	2 S37513	Ig kappa chain V r
69	6	4.9	92	2 S37519	Ig kappa chain V r
70	6	4.9	92	2 S37517	Ig kappa chain V r
71	6	4.9	92	2 S37507	Ig kappa chain V r
72	6	4.9	92	2 S37502	Ig kappa chain V r
73	6	4.9	92	2 S37514	Ig kappa chain V r
74	6	4.9	92	2 S37510	Ig kappa chain V r
75	6	4.9	92	2 S37503	Ig kappa chain V r
76	6	4.9	92	2 S37518	Ig kappa chain V r
77	6	4.9	93	2 S37508	Ig kappa chain V r
78	6	4.9	93	2 S37526	Ig kappa chain V r
79	6	4.9	93	2 S37528	Ig kappa chain V r
80	6	4.9	93	2 S37501	Ig kappa chain V r
81	6	4.9	94	2 A70732	probable rpmB prot
82	6	4.9	95	2 F95332	hypothetical prote
83	6	4.9	96	2 S36060	hypothetical prote
84	6	4.9	96	2 PH1070	Ig lambda chain -
85	6	4.9	96	2 B49442	Ig light chain V r
86	6	4.9	96	2 A30601	Ig kappa chain V-I
87	6	4.9	98	2 S36068	Ig lambda chain -
88	6	4.9	98	2 S36050	Ig lambda chain -
89	6	4.9	99	1 W7WL35	E7 protein - human
90	6	4.9	99	2 S36055	Ig lambda chain -
91	6	4.9	99	2 S36056	Ig lambda chain -
92	6	4.9	99	2 S36057	Ig lambda chain -
93	6	4.9	99	2 S36058	Ig lambda chain -
94	6	4.9	99	2 JH0429	Ig kappa chain V-I
95	6	4.9	99	2 T37093	hypothetical prote
96	6	4.9	100	1 K3HUNG	Ig kappa chain pre
97	6	4.9	101	2 PH1057	Ig kappa chain V r
98	6	4.9	103	2 A38923	Ig light chain V r
99	6	4.9	103	2 PH1056	AL type amyloid fi
100	6	4.9	103	2 F70976	Ig light chain V r
					hypothetical prote



## ALIGNMENTS

## RESULT 1

S35302  
B-cell protein SHS-20 precursor - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 31-Dec-1993 #sequence\_revision 02-Jun-1994 #text\_change 20-Jun-2000  
C/Accession: S35302  
R/Shirasawa, T.; Ohnishi, K.; Hagiwara, S.; Shigemoto, K.; Takebe, Y.; Rajewsky, K.; Takemoto, J.; 1827-1834, 1993  
A/Title: A novel gene product associated with mu chains in immature B cells.  
A/Reference number: S35302; MUID:93259124; PMID:8491176  
A/Accession: S35302  
A/Molecule type: DNA  
A/Residues: 1-123 <SH>  
A/Cross-references: EMBL:D13208; NID:G286064; PIDN:BAA02495.1; PID:G286065  
C/Genetics:  
A/Introns: 18/1  
A/Gene: SHS-20  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: B-cell  
F:1-19/Domain: signal sequence #status Predicted <SIG>  
F:20-123/Product: B-cell protein SHS-20 #status Predicted <MAT>

Query Match 8.9%; Score 11; DB 2; Length 123;  
Best Local Similarity 100.0%; Pred. No. 0.00081;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 RPADIPDRFSA 89

Db 79 RPADIPDRFSA 89

## RESULT 2

C71339  
probable DNA mismatch repair protein (mutS) - syphilis spirochete  
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)  
C>Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 05-Nov-1999  
C/Accession: C71339  
R/Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwinther, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDevitt, L.; Weidman, J.; Smith, H.O.; Venter, J.C.  
Science 281, 375-388, 1998  
A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.  
A/Reference number: A71250; MUID:98332770; PMID:9665876  
A/Accession: C71339  
A/Status: Preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-900 <COL>  
A/Cross-references: GB:AE001212; GB:AE000520; NID:G3322597; PIDN:AAC65315.1; PID:G332260  
A/Experimental source: strain Nichols  
C/Genetics:  
A/Gene: TP0328  
C/Superfamily: DNA mismatch repair protein mutS

Query Match 7.3%; Score 9; DB 2; Length 900;  
Best Local Similarity 100.0%; Pred. No. 0.49;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 QQRAGSAPR 66

Db 807 QQRAGSAPR 815

## RESULT 3

H90411  
hypothetical protein SSO2405 [imported] - Sulfolobus solfataricus  
C:Species: Sulfolobus solfataricus  
C/Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 24-May-2001  
C/Accession: H90411  
R/She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, H.

arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A/Description: Sulfolobus solfataricus complete genome.  
A/Reference number: A39139  
A/Accession: H90411  
A/Status: Preliminary  
A/Molecule type: DNA  
A/Residues: 1-104 <KUR>  
A/Cross-references: GB:AE006641; NID:G13615709; PIDN:AAK42551.1; GSPDB:GN00155  
C/Genetics:  
A/Gene: SSO2405

Query Match 6.5%; Score 8; DB 2; Length 104;  
Best Local Similarity 100.0%; Pred. No. 0.93; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 0;

QY 23 AQLDALLY 30

Db 70 AQLDALLY 77

## RESULT 4

T21811  
hypothetical protein F35G12.12 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000  
C/Accession: T21811  
R/Chui, C.  
submitted to the EMBL Data Library, October 1994  
A/Reference number: Z19473  
A/Accession: T21811  
A/Status: Preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-526 <WIL>  
A/Cross-references: EMBL:Z46242; PIDN:CRA86334.1; GSPDB:GN00021; CESP:F35G12.12  
A/Experimental source: clone F35G12  
C/Genetics:  
A/Gene: CESP:F35G12.12  
A/Map position: 3  
A/Introns: 12/3; 45/2; 82/3; 176/3; 240/3; 260/1; 381/1  
C/Superfamily: Caenorhabditis elegans hypothetical protein F35G12.12

Query Match 6.5%; Score 8; DB 2; Length 526;  
Best Local Similarity 100.0%; Pred. No. 3.5;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 VLAQDAL 28

Db 208 VLAQDAL 215

## RESULT 5

S16841  
IG kappa chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C/Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C/Accession: S16841  
R/Riason, G.; Kuntz, J.L.; Pasquali, J.L.  
Eur. J. Immunol. 21, 1221-1227, 1991  
A/Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid factor.  
A/Reference number: S16823; MUID:91243737; PMID:1903706  
A/Accession: S16841  
A/Status: Preliminary; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-97 <BLA>  
A/Cross-references: EMBL:X54839  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F:7-82/Domain: immunoglobulin homology <IMM>

Query Match 5.7%; Score 7; DB 2; Length 87;  
Best Local Similarity 100.0%; Pred. No. 8.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 82 DIPDRFS 88  
 |||||  
 b 49 DIPDRFS 55

RESULT 6  
 45245  
 Hypothetical protein MLCB1610.18 [imported] - Mycobacterium leprae  
 ;Species: Mycobacterium leprae  
 ;Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jan-2000  
 ;Accession: T45245  
 ;James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
 submitted to the EMBL Data Library, March 1999  
 ;Reference number: Z22949  
 ;Accession: T45245  
 ;Status: preliminary; translated from GB/EMBL/DBDJ  
 ;Molecule type: DNA  
 ;Residues: 1-93 <JAW>  
 ;Cross-references: EMBL:AL049913; PIDN:CA843164.1  
 ;Experimental source: cosmid H1610  
 ;Genetics:  
 ;Note: MLCB1610.18

Query Match 5.7%; Score 7; DB 2; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 9.3; 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 62 GSAPRYL 68  
 |||||  
 b 23 GSAPRYL 29

RESULT 7  
 17381  
 T-cell receptor beta chain V region (clone IGRB04) - human (fragment)  
 ;Species: Homo sapiens (man)  
 ;Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
 ;Accession: S17381  
 ;Ferradini, L.; Roman-Roman, S.; Azocar, J.; Michalaki, H.; Triebel, F.; Hercend, T.  
 Eur. J. Immunol. 21, 935-942, 1991  
 ;Title: Studies on the human T cell receptor alpha/beta variable region genes. II. Ident  
 ;Reference number: S17378; MUID:91209402; PMID:1826889  
 ;Accession: S17381  
 ;Status: preliminary  
 ;Molecule type: mRNA  
 ;Residues: 1-109 <PER>  
 ;Cross-references: EMBL:X58799; NID:g33531; PIDN:CA841605.1; PID:g312241  
 ;Superfamily: immunoglobulin V region; immunoglobulin homology  
 ;Keywords: T-cell receptor  
 ;32-108/Domain: immunoglobulin homology <IMM>

Query Match 5.7%; Score 7; DB 2; Length 109;  
 Best Local Similarity 100.0%; Pred. No. 11; 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 83 IPDRFSA 89  
 |||||  
 b 75 IPDRFSA 81

RESULT 8  
 S26264  
 T-cell receptor beta chain V region 5.5 precursor (clone HT183) - human (fragment)  
 ;Species: Homo sapiens (man)  
 ;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000  
 ;Accession: S26264  
 ;Plaza, A.; Kono, D.H.; Theofilopoulos, A.N.  
 J. Immunol. 147, 4360-4365, 1991  
 ;Title: New human V-beta genes and polymorphic variants.  
 ;Reference number: S26255; MUID:92091749; PMID:1684376  
 ;Accession: S26264  
 ;Molecule type: mRNA

A;Residues: 1-123 <PLA>  
 A;Cross-references: EMBL:X57613; NID:g37622; PIDN:CAA40839.1; PID:g37623  
 A;Experimental source: clone HT183  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: T-cell receptor  
 F;46-122/Domain: immunoglobulin homology <IMM>

Query Match 5.7%; Score 7; DB 2; Length 123;  
 Best Local Similarity 100.0%; Pred. No. 12; 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 83 IPDRFSA 89  
 |||||  
 b 89 IPDRFSA 95

RESULT 9

I38311  
 T-cell receptor beta chain V region (V-beta 23, germline) precursor - human (fragment)  
 ;Species: Homo sapiens (man)  
 ;Date: 16-Feb-1996 #sequence\_revision 16-Feb-1996 #text\_change 21-Jan-2000  
 ;Accession: I38311  
 ;Slightom, J.L.; Siemieniak, D.R.; Sieu, L.C.; Koop, B.F.; Hood, L.  
 Genomics 20, 149-168, 1994  
 A;Title: Nucleotide sequence analysis of 77.7 kb of the human V beta T-cell receptor ge  
 A;Reference number: A54302; MUID:94292194; PMID:8020962  
 ;Accession: I38311  
 ;Status: preliminary  
 ;Molecule type: DNA  
 A;Residues: 1-123 <RES>  
 A;Cross-references: EMBL:U03115; NID:g467918; PIDN:AAA17710.1; PID:g467920  
 C;Genetics:  
 A;Gene: TCRBV23S1  
 A;Introns: 27/1  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: T-cell receptor  
 F;46-122/Domain: immunoglobulin homology <IMM>

Query Match 5.7%; Score 7; DB 2; Length 123;  
 Best Local Similarity 100.0%; Pred. No. 12; 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 83 IPDRFSA 89  
 |||||  
 b 89 IPDRFSA 95

RESULT 10

C84370  
 cytochrome c oxidase subunit II [imported] - Halobacterium sp. NRC-1  
 ;Species: Halobacterium sp. NRC-1  
 ;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
 ;Accession: C84370  
 ;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.  
 ;Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jable  
 ; Jung, K.H.; Alam, M.; Freitas, T.  
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
 A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L  
 A;Title: Genome sequence of Halobacterium species NRC-1.  
 A;Reference number: A84160; MUID:20504483; PMID:11018550  
 ;Accession: C84370  
 ;Status: preliminary  
 ;Molecule type: DNA  
 A;Residues: 1-145 <STO>  
 A;Cross-references: GB:AE004437; NID:g10581612; PIDN:AAG20327.1; GSPDB:GN00138  
 C;Genetics:  
 A;Gene: coxB2

Query Match 5.7%; Score 7; DB 2; Length 145;  
 Best Local Similarity 100.0%; Pred. No. 13; 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 32 PGQVAQL 38

```

Db      86 PQVAQL 92
|||||
RESULT 11
C72411
Holliday junction DNA helicase - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: C72411
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: C72411
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-191 <ARN>
A:Cross-references: GB:AE001701; GB:AE000512; NID:G4980648; PIDN:AAD35258.1; PID:G498065
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TW0165
C:Superfamily: holliday junction DNA helicase ruva

Query Match      5.7%; Score 7; DB 2; Length 191;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 TFLVSQ 19
      |||||
Db      52 TFLVSQ 58

RESULT 12
S25755
IG lambda chain - human
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25755
R:Combrato, G.; Klobbeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(lambda) and J(lambda) gene segments of the human immunoglobulin lam
A:Reference number: S16439; MUID:91257162; PMID:1904362
A:Accession: S25755
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-243 <COM>
A:Cross-references: EMBL:X57820; NID:G33739; PIDN:CAA40957.1; PID:G33740
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:158-226/Domain: immunoglobulin homology <IMV>

Query Match      5.7%; Score 7; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      65 PRYLXY 71
      |||||
Db      65 PRYLXY 71

RESULT 13
AB2317
hypothetical protein all4089 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AB2317
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuriitz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AB2317
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <KUR>
A:Cross-references: GB:BA000019; PIDN:BAW5788.1; PID:gl7133224; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all4089

Query Match      5.7%; Score 7; DB 2; Length 258;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      19 QTVLAQL 25
      |||||
Db      92 QTVLAQL 98

RESULT 14
B89837
hypothetical protein SA0620 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: B89837
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu
ma, A.; Mizutani-Ti, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: B89837
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-265 <KUR>
A:Cross-references: GB:BA000018; PID:gl3700556; PIDN:BAW41853.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA0620

Query Match      5.7%; Score 7; DB 2; Length 265;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      29 LVFPQGV 35
      |||||
Db      61 LVFPQGV 67

RESULT 15
F75412
spermidine/putrescine ABC transporter, permease protein - Deinococcus radiodurans (stra
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: F75412
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vanathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: F75412
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-272 <WHI>
A:Cross-references: GB:AE001977; GB:AE000513; NID:G6459045; PIDN:AAF10873.1; PID:G64590
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1303
A:Map position: 1
C:Superfamily: spermidine/putrescine transport system permease protein poth

```

Query Match 5.7%; Score 7; DB 2; Length 272;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 6 LSFLMG 12  
|||||  
244 LSFLMG 250

Db

RESULT 16

702125  
regulatory protein trpI - Pseudomonas syringae  
C:Species: Pseudomonas syringae  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 08-Oct-1999  
C:Accession: JQ2125  
R:Auerbach, S.; Gao, J.; Gussin, G.N.  
Gene 123, 25-32, 1993  
A:Title: Nucleotide sequences of the trpI, trpB, and trpA genes of Pseudomonas syringae  
A:Reference number: JQ2125; MUID:93138427; PMID:8423001  
A:Accession: JQ2125  
A:Molecule type: DNA  
A:Residues: 1-298 <AUE>  
A:Cross-references: GB:M95710; NID:g151618; PIDN:AAA26015.1; PID:g151621  
C:Genetics:  
A:Gene: trpI  
C:Superfamily: regulatory protein ampr  
C:Keywords: DNA binding; transcription regulation

Query Match 5.7%; Score 7; DB 2; Length 298;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 25 LDALLVF 31  
|||||  
141 LDALLVF 147

Db

RESULT 17

S31087  
phosphoprotein phosphatase (EC 3.1.3.16) 1 (clone TOPP3) [similarity] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Nov-2001  
C:Accession: S31087  
R:Smith, R.D.; Walker, J.C.  
Plant Mol. Biol. 21, 307-316, 1993  
A:Title: Expression of multiple type 1 phosphoprotein phosphatases in Arabidopsis thaliana  
A:Reference number: S31085; MUID:93144705; PMID:7678768  
A:Accession: S31087  
A:Molecule type: mRNA  
A:Residues: 1-322 <SMI>  
A:Cross-references: EMBL:M93410; NID:g166798; PIDN:AAA32838.1; PID:g166799  
C:Superfamily: phosphoprotein phosphatase; phosphoesterase core homology; phosphoprotein  
C:Keywords: iron; metalloprotein; phosphoric monoester hydrolase; serine/threonine-speci  
F:27-286/Domain: phosphoprotein phosphatase homology <PPP>  
F:55-123/Domain: phosphoesterase core homology <PEC>  
F:61,63,89/Binding site: iron (Asp, His, Asp) #status predicted  
F:89,121,170,245/Binding site: zinc (Asp, Asn, His, His) #status predicted  
F:92,122,269/Active site: Asp, His, Tyr #status predicted  
F:93,218/Binding site: substrate phosphate (Arg) #status predicted

Query Match 5.7%; Score 7; DB 1; Length 322;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 RPADIPD 85  
|||||  
188 RPADIPD 194

Db

RESULT 18

C96665  
phosphoprotein phosphatase (EC 3.1.3.16) 1 F22C12.20 [similarity] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Nov-2001  
C:Accession: C96665  
R:Theologas, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: C96665  
A:Molecule type: DNA  
A:Residues: 1-340 <STO>  
A:Cross-references: GB:AE005173; NID:g6692101; PIDN:AAF24566.1; GSPDB:GN00141  
C:Genetics:  
A:Gene: F22C12.20  
A:Map position: 1  
C:Superfamily: phosphoprotein phosphatase; phosphoesterase core homology; phosphoprotein  
C:Keywords: iron; metalloprotein; phosphoric monoester hydrolase; serine/threonine-spec  
F:27-296/Domain: phosphoprotein phosphatase homology <PPP>  
F:55-123/Domain: phosphoesterase core homology <PEC>  
F:61,63,89/Binding site: iron (Asp, His, Asp) #status predicted  
F:89,121,170,245/Binding site: zinc (Asp, Asn, His, His) #status predicted  
F:92,122,279/Active site: Asp, His, Tyr #status predicted  
F:93,218/Binding site: substrate phosphate (Arg) #status predicted

Query Match 5.7%; Score 7; DB 1; Length 340;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 RPADIPD 85  
|||||  
188 RPADIPD 194

Db

RESULT 19

G86851  
parmease [imported] - Lactococcus lactis subsp. lactis (strain IL1403)  
C:Species: Lactococcus lactis subsp. lactis  
C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001  
C:Accession: G86851  
R:Bolotin, A.; Wincker, P.; Mauder, S.; Jaillon, O.; Malarre, K.; Weissenbach, J.; Ehrh  
Genome Res. 11, 731-753, 2001  
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s  
A:Reference number: A86625; MUID:21235186; PMID:11337471  
A:Accession: G86851  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-371 <STO>  
A:Cross-references: GB:AE005176; PID:g12724842; PIDN:AAK05913.1; GSPDB:GN00146  
A:Experimental source: strain IL1403  
C:Genetics:  
A:Gene: ysiB

Query Match 5.7%; Score 7; DB 2; Length 371;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 LDALLVF 31  
|||||  
229 LDALLVF 235

Db

RESULT 20

AH2659  
histidyl-tRNA synthetase hiss [imported] - Agrobacterium tumefaciens (strain C58, Dupont  
C:Species: Agrobacterium tumefaciens  
C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002  
C:Accession: AH2659  
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, P.; Romero, P.; Zhang, S.  
 Science 294, 2317-2323, 2001  
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, J.E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
 A:Reference number: AB2577; MUID:21608550; PMID:11743193

A:Accession: AH2659  
 A:Status: preliminary  
 A:Molecule type: DNA

A:Residues: 1-375 <KUR>

A:Cross-references: GB:AE008688; PIDN:AA141694.1; PID:g17739040; GSPDB:GN00186

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: hisS

A:Map position: circular chromosome

Query Match 5.7%; Score 7; DB 2; Length 375;

Best Local Similarity 100.0%; Pred. No. 29;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQLDALL 29

DB 173 AQLDALL 179

RESULT 21

F97441

probable hypothetical protein AGR\_C\_1214 [imported] - Agrobacterium tumefaciens (strain C58, Cere)  
 C:Species: Agrobacterium tumefaciens

C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 18-Nov-2002

A:Accession: F97441

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,

A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A:Reference number: A97359; MUID:21608551; PMID:11743194

A:Accession: F97441

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-375 <KUR>

A:Cross-references: GB:AE007869; PIDN:AAK86487.1; PID:g15155637; GSPDB:GN00169

C:Genetics:

A:Gene: AGR\_C\_1214

A:Map position: circular chromosome

Query Match 5.7%; Score 7; DB 2; Length 375;

Best Local Similarity 100.0%; Pred. No. 29;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQLDALL 29

DB 173 AQLDALL 179

RESULT 22

B64877

probable membrane protein yciW - Escherichia coli (strain K-12)

C:Species: Escherichia coli

C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002

A:Accession: B64877

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: B64877

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-401 <BLAT>

A:Cross-references: GB:AE000227; GB:U00096; NID:g1787543; PIDN:AACT4369.1; PID:g1787544;

A:Experimental source: strain K-12, substrain MG1655

C:Genetics:

A:Gene: yciW  
 C:Superfamily: Escherichia coli probable membrane protein yciW  
 C:Keywords: transmembrane protein  
 F:181-197/Domain: transmembrane #status predicted <TM>

Query Match 5.7%; Score 7; DB 2; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 31;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 PDRFSAA 90

DB 356 PDRFSAA 362

RESULT 23

D90861

probable oxidoreductase ECs1860 [imported] - Escherichia coli (strain O157:H7, substra)

C:Species: Escherichia coli

C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 03-Aug-2001

A:Accession: D90861

R:Havashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen

A:Reference number: A99629; MUID:21156231; PMID:11286796

A:Accession: D90861

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-401 <HAY>

A:Cross-references: GB:BA000007; PIDN:BA835283.1; PID:g13361325; GSPDB:GN00154

A:Experimental source: strain O157:H7, substrain RIMD 0509952

C:Genetics:

A:Gene: ECs1860

C:Superfamily: Escherichia coli probable membrane protein yciW

Query Match 5.7%; Score 7; DB 2; Length 401;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 PDRFSAA 90

DB 356 PDRFSAA 362

RESULT 24

A85758

probable oxidoreductase yciW [imported] - Escherichia coli (strain O157:H7, substrain E

C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001

A:Accession: A85758

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: A85758

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-401 <STC>

A:Cross-references: GB:AE005174; NID:g12515501; PIDN:AA056525.1; GSPDB:GN00145; UWGP:Z2

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: yciW

C:Superfamily: Escherichia coli probable membrane protein yciW

Query Match 5.7%; Score 7; DB 2; Length 401;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 PDRFSAA 90

DB 356 PDRFSAA 362

```

RESULT 25
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AF0214
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-464 <NUR>
A:Cross-references: GB:AL590842; PIDN:CA90578.1; PID:gl5979786; GSPDB:GN00175
A:Gene: YP01759

Query Match 5.7%; Score 7; DB 2; Length 464;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CLSFLIM 11
DB 139 CLSFLIM 145

RESULT 28
JC7672
catalase (EC 1.11.1.6) - Desulfovibrio vulgaris
C:Species: Desulfovibrio vulgaris
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C:Accession: JC7672
R:Kitamura, M.; Nakamishi, T.; Kojima, S.; Kumagai, I.; Inoue, H.
J. Biochem. 129, 357-364, 2001
A:Title: Cloning and expression of the catalase gene from the anaerobic bacterium Desul-
A:Reference number: JC7672; MUID:21125589; PMID:11226874
A:Accession: JC7672
A:Molecule type: DNA
A:Residues: 1-480 <KIT>
A:Cross-references: DDBJ:AB020341
C:Comment: This enzyme, one of the hemoproteins, located in the cytoplasm, functions as
C:Genetics:
A:Gene: kat
C:Superfamily: catalase
C:Keywords: oxidoreductase

Query Match 5.7%; Score 7; DB 2; Length 480;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 EDDADYY 114
DB 414 EDDADYY 420

RESULT 29
EB4254
hypothetical protein Vng0983c [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: EB4254
R:Ng, W.V.; Kennedy, S.P.; Mahaitas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.;
Lethausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablonski,
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: EB4254
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-484 <STC>
A:Cross-references: GB:AE004437; NID:gl0590537; PIDN:AA019401.1; GSPDB:GN00138
C:Genetics:
A:Gene: VNG0983C
C:Superfamily: hypothetical protein MJ1633

Query Match 5.7%; Score 7; DB 2; Length 484;
Best Local Similarity 100.0%; Pred. No. 36;

RESULT 26
P75588
probable kynureninase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: P75588
R:White, O.; Eisen, J.A.; Heideberg, J.P.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zaleski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: P75588
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-462 <WHI>
A:Cross-references: GB:AE001863; GB:AE001825; NID:g6460670; PIDN:AAF12444.1; PID:g646073
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRA0338
A:Map position: 2
C:Superfamily: nifs protein

Query Match 5.7%; Score 7; DB 2; Length 462;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 LAQLDAL 28
DB 62 LAQLDAL 58

RESULT 27
AF0214
probable membrane protein YP01759 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AF0214
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell,
```

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LSVSQTV 21  
|||||

Db 287 LSVSQTV 293

RESULT 30  
E90944  
C:Species: Escherichia coli  
C:Title: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 18-Jul-2001  
C:Accession: E90944  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurakawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome  
A:Reference number: A99629; MUID:21156231; PMID:11258796  
A:Accession: E90944  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-518 <HAY>  
A:Cross-references: GB:BA000007; PIDN:BA035948.1; PID:gl3361992; GSPDB:GN00154  
A:Experimental source: strain O157:H7, substrain RMD 050952  
C:Genetics:  
A:Gene: ECs2525

Query Match 5.7%; Score 7; DB 2; Length 518;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CLSFLM 11  
|||||

Db 189 CLSFLM 195

RESULT 31  
E95793  
C:Species: Escherichia coli  
C:Title: Probable transport protein yoeE [imported] - Escherichia coli (strain O157:H7, substrain  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C:Accession: A85793  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: A85793  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-518 <STO>  
A:Cross-references: GB:AE005174; NID:gl2515859; PIDN:AGS56805.1; GSPDB:GN00145; UWGP:Z28  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: yoeE

Query Match 5.7%; Score 7; DB 2; Length 518;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CLSFLM 11  
|||||

Db 189 CLSFLM 195

RESULT 32  
H64942  
C:Species: Escherichia coli  
C:Title: Hypothetical protein b1816 - Escherichia coli (strain K-12)  
C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002  
C:Accession: H64942  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617; PMID:9278503  
A:Accession: H64942  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-518 <BLAT>  
A:Cross-references: GB:AE000276; GB:U00096; NID:gl788117; PIDN:AAC74886.1; PID:gl788119  
A:Experimental source: strain K-12, substrain MG1655

Query Match 5.7%; Score 7; DB 2; Length 518;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CLSFLM 11  
|||||

Db 189 CLSFLM 195

RESULT 33  
AE0726  
C:Species: Salmonella enterica subsp. enterica serovar Typhi  
C:Title: Probable membrane protein STY1958 [imported] - Salmonella enterica subsp. enterica sero  
A:Note: This species has also been called Salmonella typhi  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C:Accession: AE0726  
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher  
th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar  
S.; Moulé, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A:Authors: Farry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K  
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero  
A:Reference number: AB0502; MUID:21534947; PMID:11677608  
A:Accession: AE0726  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-519 <PAR>  
A:Cross-references: GB:AL513382; PIDN:CAD05511.1; PID:gl6503015; GSPDB:GN00176  
C:Genetics:  
A:Gene: STY1958

Query Match 5.7%; Score 7; DB 2; Length 519;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CLSFLM 11  
|||||

Db 189 CLSFLM 195

RESULT 34  
GB4967  
C:Species: Buchnera sp.  
C:Title: Hypothetical protein [imported] - Buchnera sp. (strain APS)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 02-Mar-2001  
C:Accession: GB4967  
R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.  
Nature 407, 81-86, 2000  
A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.  
A:Reference number: A84930; MUID:20445173; PMID:10993077  
A:Accession: GB4967  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-521 <STO>  
A:Cross-references: GB:AP000398; GSPDB:GN00144  
A:Experimental source: strain APS  
C:Genetics:  
A:Gene: yoeB; BU323

Query Match 5.7%; Score 7; DB 2; Length 521;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Y      5 CLSFLM 11
b      189 CLSFLM 195

RESULT 35
D0770
robable membrane protein yegH [imported] - Salmonella enterica subsp. enterica serovar
;Species: Salmonella enterica subsp. enterica serovar Typhi
;Note: this species has also been called Salmonella typhi
;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
;Accession: AD0770
;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
h. T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
ature 413, 848-852, 2001
;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
;Reference number: AB0502; MUID:21534947; PMID:11677608
;Accession: AD0770
;Status: preliminary
;Molecule type: DNA
;Residues: 1-526 <FAR>
;Cross-references: GB:AL513382; PIDN:CAD02482.1; PID:gl6503346; GSPDB:GN00176
;Genetics:
;Gene: yegH

Query Match      5.7%; Score 7; DB 2; Length 526;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      5 CLSFLM 11
b      189 CLSFLM 195

RESULT 36
AC0186
probable membrane protein YPO1527 [imported] - Yersinia pestis (strain CO92)
;Species: Yersinia pestis
;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
;Accession: AC0186
;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
;eno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
l, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
;Reference number: AB0001; MUID:21470413; PMID:11586360
;Accession: AC0186
;Status: preliminary
;Molecule type: DNA
;Residues: 1-528 <KUR>
;Cross-references: GB:AL590842; PIDN:CAC90350.1; PID:gl5979569; GSPDB:GN00175
;Genetics:
;Gene: YPO1527

Query Match      5.7%; Score 7; DB 2; Length 528;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      5 CLSFLM 11
b      189 CLSFLM 195

RESULT 37
D90987
probable transport protein ECs2868 [imported] - Escherichia coli (strain O157:H7, substra
;Species: Escherichia coli
;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
;Accession: D90987
;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.-G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: D90987
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-549 <HAY>
A;Cross-references: GB:BA000007; PIDN:BA836291.1; PID:gl3362337; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 050952
C;Genetics:
A;Gene: ECs2868

Query Match      5.7%; Score 7; DB 2; Length 549;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      5 CLSFLM 11
b      211 CLSFLM 217

RESULT 38
G85832
probable transport protein yegH [imported] - Escherichia coli (strain O157:H7, substrain
;Species: Escherichia coli
;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
;Accession: G85832
;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85832
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-549 <STO>
A;Cross-references: GB:AE005174; NID:gl2516260; PIDN:AGS7123.1; GSPDB:GN00145; UWGP:Z3.
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: yegH

Query Match      5.7%; Score 7; DB 2; Length 549;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      5 CLSFLM 11
b      211 CLSFLM 217

RESULT 39
F64972
hypothetical protein b2063 - Escherichia coli (strain K-12)
;Species: Escherichia coli
;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
;Accession: F64972
;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: F64972
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-549 <BLAT>
A;Cross-references: GB:AE000296; GB:U00096; NID:gl788373; PIDN:AACT5124.1; PID:gl788377,
A;Experimental source: strain K-12, substrain MG1655

Query Match      5.7%; Score 7; DB 2; Length 549;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      5 CLSFLM 11

```



DB 211 CLSFLM 217  
|||||  
RESULT 40  
T27245  
Hypothetical protein Y57G11C.9a - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C/Accession: T27245  
R/McMurray, A.  
submitted to the EMBL Data Library, September 1997  
A/Reference number: Z20330  
A/Accession: T27245  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-553 <WIL>  
A/Cross-references: EMBL:Z99281; PIDN:CA854457.1; GSPDB:GN00022; CESP:Y57G11C.9a  
A/Experimental source: clone Y57G11C  
C/Genetics:  
A/Gene: CESP:Y57G11C.9a  
A/Map position: 4  
A/Introns: 67/2; 109/2; 382/1; 418/2; 447/1; 496/3  
Query Match 5.7%; Score 7; DB 2; Length 553;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 24 QLDALLV 30  
|||||  
DB 545 QLDALLV 551  
RESULT 41  
H88904  
protein Y57G11C.9 [imported] - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001  
C/Accession: H88904  
R/anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biological processes  
A/Reference number: A75000; MUID:199069613; PMID:9851916  
A/Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_elegans/  
A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 283, 2103, 1999  
A/Accession: H88904  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-568 <STO>  
A/Cross-references: GB:chr\_IV; PIDN:CA816531.1; PID:G3981206; GSPDB:GN00022; CESP:Y57G11C.9  
C/Genetics:  
A/Gene: Y57G11C.9  
A/Map position: 4  
Query Match 5.7%; Score 7; DB 2; Length 568;  
Best Local Similarity 100.0%; Pred. No. 41;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 24 QLDALLV 30  
|||||  
DB 560 QLDALLV 566  
RESULT 42  
T27246  
Hypothetical protein Y57G11C.9b - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C/Accession: T27246  
R/McMurray, A.  
submitted to the EMBL Data Library, September 1997  
A/Reference number: Z20330  
A/Accession: T27246

A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-659 <WIL>  
A/Cross-references: EMBL:Z99281; PIDN:CA854458.1; GSPDB:GN00022; CESP:Y57G11C.9b  
A/Experimental source: clone Y57G11C  
C/Genetics:  
A/Gene: CESP:Y57G11C.9b  
A/Map position: 4  
A/Introns: 67/2; 109/2; 382/1; 418/2; 524/2; 553/1; 602/3  
Query Match 5.7%; Score 7; DB 2; Length 659;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 24 QLDALLV 30  
|||||  
DB 651 QLDALLV 657  
RESULT 43  
S51680  
fructose phosphotransferase multiphosphoryltransfer protein - Xanthomonas campestris  
N/Contains: phosphocarrier protein HPr; phosphotransferase system enzyme I (EC 2.7.3.9)  
C/Species: Xanthomonas campestris  
C/Date: 07-May-1995 #sequence\_revision 31-Jan-1997 #text\_change 11-Jun-1999  
C/Accession: S51680  
R/De Crecy-Lagard, V.; Panchin, A.  
submitted to the EMBL Data Library, September 1994  
A/Description: Phosphotransferase system of Xanthomonas campestris pv. campestris : cha  
A/Reference number: S51680  
A/Accession: S51680  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-837 <DEC>  
A/Cross-references: EMBL:Z37113; NID:G603896; PIDN:CA854482.1; PID:G603897  
C/Genetics:  
A/Gene: frub  
A/Start codon: TTG  
C/Superfamily: fructose phosphotransferase multiphosphoryltransfer protein; phosphotran  
sphtotransferase system phosphohistidine-containing protein homology  
C/Keywords: phosphocarrier protein; phosphohistidine; phosphoprotein; phosphotransferas  
F:122-145/Domain: phosphotransferase system mannitol-specific enzyme II factor Iii homol  
F:168-244/Domain: phosphotransferase system phosphohistidine-containing protein homology  
F:175-825/Domain: phosphotransferase system enzyme I homology <PTI>  
F:175/Active site: His (phosphohistidine intermediate) #status predicted  
F:206/Binding site: phosphate (Ser) (covalent) #status predicted  
Query Match 5.7%; Score 7; DB 1; Length 837;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 21 VLAQLDA 27  
|||||  
DB 406 VLAQLDA 412  
RESULT 44  
I64819  
DNA mismatch repair protein - human  
N/Alternate names: mismatch recognition protein MSH2;hereditary nonpolyposis cancer pro  
C/Species: Homo sapiens (man)  
C/Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 17-Nov-2000  
R/Wijnjen, J.; Vasen, H.; Khan, P.M.; Menko, F.H.; van der Klift, H.; van Leeuwen, C.; V  
Cats, A.; Kleibuker, J.; Varesco, L.; Bertario, L.; Bisgaard, M.L.; Mohr, J.; Podde, R  
Am. J. Hum. Genet. 56, 1060-1066, 1995  
A/Title: Seven new mutations in hMSH2, an HNPCC gene, identified by denaturing gradient  
A/Reference number: I51878; MUID:95243220; PMID:7726159  
A/Accession: I64819  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-934 <RES>  
A/Cross-references: GB:L47582; NID:G1000868; PIDN:AAB59565.1; PID:G1000869

A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-54 <RUE>

A;Status: translation not known  
A;Molecule type: mRNA  
A;Residues: 1-54 <KLE>

A;Cross-references: EMBL:X72491; NID:9441450; PIDN:CAA51159.1; PID:G441451  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 4.9%; Score 6; DB 2; Length 54;  
Best Local Similarity 100.0%; Pred. No. 66;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88  
DB 17 IPDRFS 22

## RESULT 48

A25521  
Ig kappa chain V region (321) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 21-May-1988 #sequence\_revision 21-May-1990 #text\_change 09-May-1997  
C;Accession: A25521  
R;Chen, P.P.; Albrandt, K.; Orida, N.K.; Radoux, V.; Chen, E.Y.; Schrantz, R.; Liu, F.T.  
Proc. Natl. Acad. Sci. U.S.A. 83, 8318-8322, 1986  
A;Title: Genetic basis for the cross-reactive idiotypes on the light chains of human IGM  
A;Reference number: A94135; MUID:87041448; PMID:3095834  
A;Accession: A25521  
A;Molecule type: DNA  
A;Residues: 1-54 <CHE>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 4.9%; Score 6; DB 2; Length 54;  
Best Local Similarity 100.0%; Pred. No. 66;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88  
DB 17 IPDRFS 22

## RESULT 49

A24626  
Ig lambda chain V-II region (Har) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 25-Oct-1987 #sequence\_revision 25-Oct-1987 #text\_change 16-Aug-1996  
C;Accession: A24626  
R;Sulitz, M.; Linke, R.  
Biol. Chem. Hoppe-Seyler 366, 907-915, 1985  
A;Title: Amyloid fibrils derived from V-region together with C-region fragments from a I  
A;Reference number: A24626; MUID:86077295; PMID:3935132  
A;Accession: A24626  
A;Molecule type: Protein  
A;Residues: 1-60 <EUL>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 4.9%; Score 6; DB 2; Length 60;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 VSWYQQ 59  
DB 28 VSWYQQ 33

## RESULT 50

S17384  
T-cell receptor beta chain V region (clone IGRb07) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S17384  
R;Ferradini, L.; Roman-Roman, S.; Azocar, J.; Michalaki, H.; Triebel, F.; Hercend, T.  
Eur. J. Immunol. 21, 935-942, 1991  
A;Title: Studies on the human T cell receptor alpha/beta variable region genes. II. Idet  
A;Reference number: S17378; MUID:91209402; PMID:1826889

A;Accession: S17384  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-64 <FER>  
A;Cross-references: EMBL:X58804; NID:933535; PIDN:CAA41610.1; PID:G33536  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: T-cell receptor

Query Match 4.9%; Score 6; DB 2; Length 64;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 VSWYQQ 59  
DB 2 VSWYQQ 7

## RESULT 51

T06599  
disease resistance response protein 230 - garden pea  
C;Species: Pisum sativum (garden pea)  
C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jun-2000  
C;Accession: T06599  
R;Chiang, C.C.; Hadwiger, L.A.  
Mol. Plant Microbe Interact. 4, 324-331, 1991  
A;Title: The Fusarium solani-induced expression of a pea gene family encoding high cyst  
A;Reference number: Z15787; MUID:92190628; PMID:1799696  
A;Accession: T06599  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-72 <CHI>  
A;Cross-references: EMBL:L01578; NID:G169073; PIDN:AAA79117.1; PID:G169074  
A;Experimental source: cv. Alaska  
C;Genetics:  
A;Gene: DRR230-a  
C;Superfamily: gamma-thionin

Query Match 4.9%; Score 6; DB 2; Length 72;  
Best Local Similarity 100.0%; Pred. No. 83;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CLSFL 10  
DB 8 CLSFL 13

## RESULT 52

D30502  
Ig kappa chain V region (D44) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 03-Nov-1988 #sequence\_revision 03-Aug-1992 #text\_change 23-Jul-1999  
C;Accession: D30502  
R;Eilat, D.; Webster, D.M.; Rees, A.R.  
J. Immunol. 141, 1745-1753, 1988  
A;Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 m.  
A;Reference number: A30502; MUID:88315787; PMID:2457627  
A;Accession: D30502  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-77 <EIL>  
A;Cross-references: GB:M21908; NID:G197073; PIDN:AAA38908.1; PID:G197074  
A;Note: the authors translated the codon CAG for residue 48 as Pro  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 4.9%; Score 6; DB 2; Length 77;  
Best Local Similarity 100.0%; Pred. No. 88;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 VSWYQQ 59  
DB 2 VSWYQQ 7



```
RESULT 58
E28840
IG kappa chain V region (HP20) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 23-Jul-1999
C:Accession: E28840; L25114
R:Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.
EMBL: J. 4, 3681-3698, 1985
A:Title: The idiotypic network and the internal image: possible regulation of a germ-line
A:Reference number: A91028; MUID:86136012; PMID:13937730
A:Accession: E28840
A:Molecule type: mRNA
A:Residues: 1-84 <OLL>
A:Cross-references: GB:X03385; NID:G52161; PIDN:CAA27112.1; PID:G52162
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 4.9%; Score 6; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 SWYQQR 60
Db 17 SWYQQR 22

RESULT 59
S78490
IG kappa chain V region (patient 31) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Apr-1998 #sequence_revision 08-May-1998 #text_change 21-Jan-2000
C:Accession: S78490; S34103
R:Wagner, S.
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
submitted to the EMBL Data Library, July 1992
A:Reference number: S78488
A:Accession: S78490
A:Molecule type: DNA
A:Residues: 1-87 <WAG>
A:Cross-references: EMBL:X67187
A:Experimental source: patient 31
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34103
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-49, 'L', '51-61', 'YF', '64-75', 'A', '77-87' <WAW>
A:Cross-references: EMBL:X67187
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;7-82/Domain: immunoglobulin homology <IMM>

Query Match 4.9%; Score 6; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88
Db 50 IPDRFS 55

RESULT 60
S16843
IG kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16843
R:Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fa
A:Reference number: S16823; MUID:91243737; PMID:1903706
A:Accession: S16843
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-87 <BLA>
A:Cross-references: EMBL:X54841
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;7-82/Domain: immunoglobulin homology <IMM>

Query Match 4.9%; Score 6; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88
Db 50 IPDRFS 55

RESULT 61
S16842
IG kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16842
R:Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fa
A:Reference number: S16823; MUID:91243737; PMID:1903706
A:Accession: S16842
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-87 <BLA>
A:Cross-references: EMBL:X54840
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;7-82/Domain: immunoglobulin homology <IMM>

Query Match 4.9%; Score 6; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88
Db 50 IPDRFS 55

RESULT 62
S16823
IG kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16823
R:Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fa
A:Reference number: S16823; MUID:91243737; PMID:1903706
A:Accession: S16823
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-87 <BLA>
A:Cross-references: EMBL:X54821
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;7-82/Domain: immunoglobulin homology <IMM>

Query Match 4.9%; Score 6; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88
Db 50 IPDRFS 55
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RESULT 63
S34096
I; kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S34096
Wagner, S.D.; Luzzatto, L.
J. Immunol. 23, 391-397, 1993
Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
Reference number: S34076; MUID:93170387; PMID:8436174
Accession: S34096
Status: preliminary
Molecule type: DNA
Residues: 1-89 <WAG>
Cross-references: EMBL:X67180
Superfamily: immunoglobulin V region; immunoglobulin homology
Keywords: heterotetramer; immunoglobulin
9-84/Domain: immunoglobulin homology <IMM>

Query Match 4.9%; Score 6; DB 2; Length 89;
Best Local Similarity 100.0%; Pred.No. 99;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88
DB 52 IPDRFS 57

RESULT 64
PH1071
Ig light chain V region (clone 165.3m) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1071
Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
Title: Both IgM and Igg anti-DNA antibodies are the products of clonally selective B c
Reference number: PH0971; MUID:92381444; PMID:1512540
Accession: PH1071
Status: nucleic acid sequence not shown
Molecule type: mRNA
Residues: 1-91 <TILL>
Experimental source: B cell, strain [NZB x NZW]F1
Superfamily: immunoglobulin V region; immunoglobulin homology
Keywords: immunoglobulin
F.10-83/Domain: immunoglobulin homology <IMM>

Query Match 4.9%; Score 5; DB 2; Length 91;
Best Local Similarity 100.0%; Pred.No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 VSWYQQ 59
DB 27 VSWYQQ 32

RESULT 65
S37520
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37520
Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
Description: Human IgM(+)IGD(+) cells, the major B cell subset in the peripheral blood
Reference number: S37501
Accession: S37520
Status: preliminary
Molecule type: mRNA
Residues: 1-91 <KLE>
Cross-references: EMBL:Z26612; NID:G405682; PIDN:CAA91365.1; PID:G405683
Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
```

C;Keywords: heterotetramer; immunoglobulin

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Query Match 4.9%; Score 6; DB 2; Length 91;
Best Local Similarity 100.0%; Pred.No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88
DB 42 IPDRFS 47

RESULT 66
S67940
Ig kappa chain V region, subgroup III (clone MH52) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Mar-1997 #sequence_revision 09-May-1997 #text_change 20-Mar-1998
C;Accession: S67940
R;Hexham, J.M.; Furmaniak, J.; Pegg, C.; Burton, D.R.; Smith, B.R.
Autoimmunity 12, 135-141, 1992
Title: Cloning of a human autoimmune response: preparation and sequencing of a human
Reference number: S67940; MUID:92314301; PMID:1617110
Accession: S67940
Status: preliminary
Molecule type: mRNA
Residues: 1-91 <HEX>
Cross-references: EMBL:X73852
Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 4.9%; Score 6; DB 2; Length 91;
Best Local Similarity 100.0%; Pred.No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88
DB 40 IPDRFS 45

RESULT 67
S37524
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37524
Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
Description: Human IgM(+)IGD(+) cells, the major B cell subset in the peripheral blood
Reference number: S37501
Accession: S37524
Status: preliminary
Molecule type: mRNA
Residues: 1-92 <KLE>
Cross-references: EMBL:Z26620; NID:G405690; PIDN:CAA81373.1; PID:G405691
Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 4.9%; Score 6; DB 2; Length 92;
Best Local Similarity 100.0%; Pred.No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88
DB 42 IPDRFS 47

RESULT 68
S37513
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37513
Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
Description: Human IgM(+)IGD(+) cells, the major B cell subset in the peripheral blood
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S37501  
I;Reference number: S37501  
A;Accession: S37513  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-92 <KLE>  
A;Cross-references: EMBL:Z26598; NID:g405668; PIDN:CAA81352.1; PID:g405669  
A;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 4.9%; Score 6; DB 2; Length 92;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88  
DB 42 IPDRFS 47

RESULT 69  
S37519  
Ig kappa chain V region (V-kappa 3) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
A;Accession: S37519  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-92 <KLE>  
A;Cross-references: EMBL:Z26613; NID:g405680; PIDN:CAA81366.1; PID:g405681  
A;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 4.9%; Score 6; DB 2; Length 92;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88  
DB 42 IPDRFS 47

RESULT 70  
S37517  
Ig kappa chain V region (V-kappa 3) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
A;Accession: S37517  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-92 <KLE>  
A;Cross-references: EMBL:Z26615; NID:g405676; PIDN:CAA81368.1; PID:g405677  
A;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 4.9%; Score 6; DB 2; Length 92;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88  
DB 42 IPDRFS 47

RESULT 71

S37507  
Ig kappa chain V region (V-kappa 3) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
A;Accession: S37507  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-92 <KLE>  
A;Cross-references: EMBL:Z26605; NID:g405655; PIDN:CAA81358.1; PID:g405656  
A;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 4.9%; Score 6; DB 2; Length 92;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88  
DB 42 IPDRFS 47

RESULT 72  
S37502  
Ig kappa chain V region (V-kappa 3) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
A;Accession: S37502  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-92 <KLE>  
A;Cross-references: EMBL:Z26610; NID:g405645; PIDN:CAA81363.1; PID:g405646  
A;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 4.9%; Score 6; DB 2; Length 92;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88  
DB 42 IPDRFS 47

RESULT 73  
S37514  
Ig kappa chain V region (V-kappa 3) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
A;Accession: S37514  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-92 <KLE>  
A;Cross-references: EMBL:Z26597; NID:g405670; PIDN:CAA81351.1; PID:g405671  
A;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 4.9%; Score 6; DB 2; Length 92;  
Best Local Similarity 100.0%; Pred. No. 1e+02;

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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y      83 IPDRFS 88
      |||||
b      42 IPDRFS 47

RESULT 74
37510
g kappa chain V region (V-kappa 3) - human (fragment)
;Species: Homo sapiens (man)
;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
;Accession: S37510
;Klein, U.; Kuipers, R.; Rajewsky, K.
;Submitted to the EMBL Data Library, September 1993
;Description: Human IGM(+)IGD(+) cells, the major B cell subset in the peripheral blood
;Reference number: S37501
;Accession: S37510
;Status: preliminary
;Molecule type: mRNA
;Residues: 1-92 <KLE>
;Cross-references: EMBL:Z26601; NID:G405662; PIDN:CAA81355.1; PID:G405663
;Superfamily: immunoglobulin V region; immunoglobulin homology
;Keywords: heterotrimer; immunoglobulin

Query Match 4.9%; Score 6; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y      83 IPDRFS 88
      |||||
b      42 IPDRFS 47

RESULT 75
37503
g kappa chain V region (V-kappa 3) - human (fragment)
;Species: Homo sapiens (man)
;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
;Accession: S37503
;Klein, U.; Kuipers, R.; Rajewsky, K.
;Submitted to the EMBL Data Library, September 1993
;Description: Human IGM(+)IGD(+) cells, the major B cell subset in the peripheral blood
;Reference number: S37501
;Accession: S37503
;Status: preliminary
;Molecule type: mRNA
;Residues: 1-92 <KLE>
;Cross-references: EMBL:Z26609; NID:G405647; PIDN:CAA81362.1; PID:G405648
;Superfamily: immunoglobulin V region; immunoglobulin homology
;Keywords: heterotrimer; immunoglobulin

Query Match 4.9%; Score 6; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y      83 IPDRFS 88
      |||||
b      42 IPDRFS 47

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Search completed: February 9, 2004, 12:59:34  
 Job time : 32 secs



GenCore version 5.1.6  
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M protein - protein search, using sw model

Run on: February 9, 2004, 12:49:12 ; Search time 18 Seconds  
(without alignments)  
321.349 Million cell updates/sec

Title: US-09-981-876-200

Perfect score: 123  
Sequence: 1 MACRCLSLMGFLFSLVSQT.....FVQPEDDADYCSVGVGFSP 123

Scoring table:

OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

result	No.	Score	Query Match	Length	DB ID	Description
1	123	100.0	123	1	VPR3 HUMAN	O9uk13 homo sapien
2	9	7.3	900	1	MUTS TREPA	O83348 treponema p
3	7	5.7	188	1	ROVA THEMA	O9wy12 thermotoga
4	7	5.7	298	1	TRPI PSESY	F34818 pseudomonas
5	7	5.7	320	1	YC19 KLEPN	O48445 klebsiella
6	7	5.7	322	1	PP13 ARATH	P48483 arabidopsis
7	7	5.7	401	1	YCIW ECOLI	P76035 escherichia
8	7	5.7	418	1	DADA NEIMB	O9klh5 neisseria m
9	7	5.7	515	1	V314 BUCAP	O8k9m0 buchnera ap
10	7	5.7	518	1	YOAE ECOLI	P76262 escherichia
11	7	5.7	521	1	Y323 BUCAI	P57408 buchnera ap
12	7	5.7	527	1	YEGH ECOLI	P43246 escherichia
13	7	5.7	934	1	MSH2 HUMAN	P18924 bacterioph
14	6	4.9	51	1	AC BFT4	O01783 pisum sativ
15	6	4.9	72	1	D230 PEA	Q10879 mycobacteri
16	6	4.9	94	1	R28A MYCTU	P40368 trypanosoma
17	6	4.9	97	1	HLC2 TRCYR	P27230 human papil
18	6	4.9	99	1	V57 HPV35	P01621 homo sapien
19	6	4.9	100	1	KV3C HUMAN	P01619 homo sapien
20	6	4.9	108	1	KV3A HUMAN	P01714 homo sapien
21	6	4.9	108	1	KV3A HUMAN	P01620 homo sapien
22	6	4.9	109	1	KV3D HUMAN	P01622 homo sapien
23	6	4.9	109	1	KV3E HUMAN	P01623 homo sapien
24	6	4.9	109	1	KV3G HUMAN	P04206 homo sapien
25	6	4.9	109	1	KV3H HUMAN	P06888 homo sapien
26	6	4.9	109	1	KV3I HUMAN	P01708 homo sapien
27	6	4.9	109	1	KV3J HUMAN	P01713 homo sapien
28	6	4.9	110	1	KV3K HUMAN	P01702 homo sapien
29	6	4.9	111	1	KV3L HUMAN	P01704 homo sapien
30	6	4.9	111	1	KV3M HUMAN	P01705 homo sapien
31	6	4.9	111	1	KV3N HUMAN	P01706 homo sapien
32	6	4.9	111	1	KV3O HUMAN	P01707 homo sapien
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RESULT 1

#### ALIGNMENTS

34	6	4.9	111	1	LV2F HUMAN	P01709 homo sapien
35	6	4.9	111	1	LV2G HUMAN	P01710 homo sapien
36	6	4.9	111	1	LV2H HUMAN	P01711 homo sapien
37	6	4.9	111	1	LV2I HUMAN	P01712 homo sapien
38	6	4.9	111	1	LV2L HUMAN	P04222 homo sapien
39	6	4.9	112	1	LV1H HUMAN	P06887 homo sapien
40	6	4.9	112	1	LV2K HUMAN	P04209 homo sapien
41	6	4.9	121	1	RNPA COXBU	P45648 coxiella bu
42	6	4.9	126	1	PCD5 MOUSE	P56812 mus musculus
43	6	4.9	128	1	KV3K HUMAN	P06311 homo sapien
44	6	4.9	129	1	KV3L HUMAN	P18135 homo sapien
45	6	4.9	129	1	KV3M HUMAN	P18136 homo sapien
46	6	4.9	130	1	LV1G HUMAN	P06316 homo sapien
47	6	4.9	136	1	KV5B MOUSE	P01634 mus musculus
48	6	4.9	142	1	VPR1 MOUSE	P13372 mus musculus
49	6	4.9	142	1	VPR2 MOUSE	P13373 mus musculus
50	6	4.9	169	1	RST1 AVESA	P50695 avena sativ
51	6	4.9	169	1	RST2 AVESA	P50696 avena sativ
52	6	4.9	169	1	RST3 AVESA	P50697 avena sativ
53	6	4.9	169	1	RST4 AVESA	P50698 avena sativ
54	6	4.9	172	1	PHCB SYN7	P06539 synechococc
55	6	4.9	173	1	HSIV YERPE	O8zjj4 yersinia pe
56	6	4.9	174	1	VNSC PHODV	P35940 phocine dis
57	6	4.9	177	1	TLP OYSA	P31110 oryza sativ
58	6	4.9	189	1	CYOC BUCAP	O8k995 buchnera ap
59	6	4.9	190	1	APOM MOUSE	Q9z1r3 mus musculus
60	6	4.9	190	1	APOM RAT	P14630 rattus norv
61	6	4.9	191	1	I18B MOUSE	Q920m9 mus musculus
62	6	4.9	199	1	VG66 B2MD2	O64258 mycobacteri
63	6	4.9	210	1	URK D3IRA	O9rxz5 deinococcus
64	6	4.9	218	1	TRPF SYN3	P74435 synechocyst
65	6	4.9	234	1	GLNA DUNSA	P11600 dunaliella
66	6	4.9	234	1	YMFE ECOLI	P75968 escherichia
67	6	4.9	236	1	H184 RHOC	Q30725 rhodobacter
68	6	4.9	236	1	SPSH STRPY	O9xsc8 streptococc
69	6	4.9	237	1	NRL HUMAN	P54845 homo sapien
70	6	4.9	237	1	NRL MOUSE	P54846 mus musculus
71	6	4.9	237	1	UPK THEMA	Q9wz25 thermotoga
72	6	4.9	238	1	PSB6 MOUSE	Q60692 mus musculus
73	6	4.9	243	1	H184 BRUME	Q8ye36 bruceella me
74	6	4.9	243	1	H184 BRUSU	Q8y790 bruceella su
75	6	4.9	247	1	H184 AGRT5	P58790 agrobacteri
76	6	4.9	250	1	NGN2 HUMAN	Q9h2a3 homo sapien
77	6	4.9	251	1	C10B HUMAN	P02746 homo sapien
78	6	4.9	253	1	BTUD YERPE	O8zdx6 yersinia pe
79	6	4.9	254	1	MODA HRAIN	P45323 haemophilus
80	6	4.9	256	1	TPIS VIBPA	Q87c31 vibrio para
81	6	4.9	259	1	Y128 CHLPN	Q92953 chlamydia p
82	6	4.9	262	1	END8 ECO57	Q8x9c6 escherichia
83	6	4.9	262	1	END8 ECOLI	P50465 escherichia
84	6	4.9	263	1	NGN2 MOUSE	P70447 mus musculus
85	6	4.9	265	1	COX3 MYTED	P41775 mytilus edu
86	6	4.9	277	1	HEMK ECOLI	P37186 escherichia
87	6	4.9	280	1	LPXC ANASP	Q8yurs anabaena sp
88	6	4.9	280	1	MDCB KLEPN	P71422 klebsiella
89	6	4.9	283	1	PANC OCEIH	Q8cx59 oceanobacil
90	6	4.9	285	1	GSPC ERWCA	P31699 erwinia car
91	6	4.9	286	1	PPNK NEIMA	Q9jql9 neisseria m
92	6	4.9	302	1	YGBJ ECOLI	Q46888 escherichia
93	6	4.9	302	1	TAL EUCAI	P57194 buchnera ap
94	6	4.9	316	1	TAL BUCAP	O8ka27 buchnera ap
95	6	4.9	326	1	BLAA STCPN	P33651 scryptomyce
96	6	4.9	329	1	YE57 MYCPN	P75326 mycoplasma
97	6	4.9	333	1	MAUG METFL	Q50426 methylobact
98	6	4.9	336	1	NADA HELPJ	Q9zjnl helicobacte
99	6	4.9	341	1	Y33B MYCGE	Q9zb73 mycoplasma
100	6	4.9	344	1	ASTA ECOLI	P76218 escherichia

PR3 HUMAN STANDARD; PRT; 123 AA.  
D VPR3\_HUMAN  
C Q9UK3; 2001 (Rel. 40, Created)  
T 16-OCT-2001 (Rel. 40, Last sequence update)  
T 16-OCT-2001 (Rel. 40, Last sequence update)  
T 15-SEP-2003 (Rel. 42, Last annotation update)  
E Pre-B lymphocyte protein 3 precursor (VpreB3 protein) (N27C7-2).  
N VPREB3.  
S Homo sapiens (Human).  
C Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
X NCBI\_TaxID=9606;  
N [1]  
N SEQUENCE FROM N.A.  
P MEDLINE=20169186; PubMed=10702669;  
A Rosnet O., Mattei M.-G., Delattre O., Schiff C.;  
T "VPREB3: cDNA characterization and expression in human and chromosome  
T mapping in human and mouse";  
L Cytogenet. Cell Genet. 87:205-208 (1999).  
N [2]  
N SEQUENCE FROM N.A.  
P Shimizu N., Minosima S., Kawasaki K., Sasaki T., Hosono K.;  
A "Molecular cloning of N27C7-2 gene";  
T Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
N [3]  
N SEQUENCE FROM N.A.  
P TISSUE=Testis;  
X MEDLINE=22388257; PubMed=12477932;  
A Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
A Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,  
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
A Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
A Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullány S.J.,  
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
A Faney J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
A Rodriguez A.C., Grinnwood J., Schmutz J., Myers R.M.,  
A Butterfield V.S.N., Kryzwicki M.I., Skalska U., Smalilus D.E.,  
A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
T "Generation and initial analysis of more than 15,000 full-length  
T human and mouse cDNA sequences";  
R Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RL  
C -!- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR  
C COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS.  
C -!- TISSUE SPECIFICITY: EXPRESSED IN B CELL PRECURSORS. EXPRESSED IN  
C FETAL LIVER, BONE MARROW, SPLEEN, AND LYMPH NODE.  
C -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
C -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
C  
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C  
C EMBL; AF163825; AAF09451.1; -  
C EMBL; AB050772; BAB83034.1; -  
C EMBL; BC020666; AAB20666.1; -  
C HSSP; P01709; 2MCG.  
C Genew; HGNC:12710; VPREB3.  
C MIM; 605017;  
C InterPro; IPR007110; Ig-like.  
C InterPro; IPR003006; Ig MHC.  
C InterPro; IPR003596; Ig\_v.  
C Pfam; PF00047; Ig; 1.

DR SMART; SMO0406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
KW Immunoglobulin domain; B-cell; Signal.  
FT SIGNAL 1 20 POTENTIAL.  
FT CHAIN 21 123 PRE-B LYMPHOCYTE PROTEIN 3.  
FT DOMAIN 21 123 IG-LIKE.  
FT DISULFID 40 115 BY SIMILARITY.  
SQ SEQUENCE 123 AA; 13710 MW; BF09AC5196059E85 CRC64;  
  
Query Match 100.0%; Score 123; DB 1; Length 123;  
Best Local Similarity 100.0%; Pred. NO. 1.3e-118; Indels 0; Gaps 0;  
Matches 123; Conservative 0; Mismatches 0;  
  
QY 1 MACRCLSFLMGTFLSVQTVLAQDALLVFPQVQVQLSCTLSPOHVTIRDYGVSWYQQR 60  
DB 1 MACRCLSFLMGTFLSVQTVLAQDALLVFPQVQVQLSCTLSPOHVTIRDYGVSWYQQR 60  
QY 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISVPQEDDADYYCSYGYG 120  
DB 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISVPQEDDADYYCSYGYG 120  
QY 121 FSP 123  
DB 121 FSP 123  
  
RESULT 2  
MUTS\_TREPA STANDARD; PRT; 900 AA.  
ID MUTS\_TREPA  
AC O83348; 1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE DNA mismatch repair protein mutS.  
GN MUTS OR TP0328  
OS Treponema pallidum.  
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.  
OX NCBI\_TaxID=160;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Nichols;  
RX MEDLINE=98327770; PubMed=9665876;  
RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,  
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,  
RA Sodergren E., Hardnam J.W., McLeod M.P., Salzberg S., Peterson J.,  
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Uetebach T.,  
RA McDonald L., Artach P., Bowman C., Cotton M.D., Fujii C., Garland S.,  
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,  
RA Venter J.C.;  
R "Complete genome sequence of Treponema pallidum, the syphilis  
R spirochete";  
RL Science 281:375-388 (1998).  
CC -!- FUNCTION: This protein is involved in the repair of mismatches in  
CC DNA. It is possible that it carries out the mismatch recognition  
CC step. This protein has a weak ATPase activity (By similarity).  
CC -!- SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTS FAMILY.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; AE001212; AAC65315.1; -  
CC PIR; C71339; C71339.  
CC TIGR; TP0328; -  
CC HAMAP; MF 00096; 1.  
CC InterPro; IPR005748; Muts1.  
CC InterPro; IPR000432; Muts\_C.  
CC InterPro; IPR002863; Muts\_N.  
CC Pfam; PF01624; Muts\_1; 1.

R Pfam; PF05188; Muts II; 1.  
R Pfam; PF05192; Muts III; 1.  
R Pfam; PF05190; Muts IV; 1.  
R Pfam; PF00488; Muts V; 1.  
R Pfam; PF001263; Muts C; 1.  
R ProDom; PD001263; Muts C; 1.  
R SMART; SM00533; MUTSd; 1.  
R SMART; SM00533; MUTSd; 1.  
R TIGRFAMs; TIGR01070; mutS1; 1.  
R PROSITE; PS00486; DNA Mismatch Repair 2; 1.  
R DNA repair; ATP-binding; DNA-binding; Complete proteome.  
I NP\_BIND 626 633 ATP (POTENTIAL)  
C SEQUENCE 900 AA; 99704 MW; 0972F3B6C8C088FE CRC64;  
  
Query Match 7.3%; Score 9; DB 1; Length 900;  
Best Local Similarity 100.0%; Pred. No. 0.31;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Y 58 QQRAGSAPR 66  
|||||  
b 807 QQRAGSAPR 815  
  
EVAL 3  
UVA THEME STANDARD; PRT; 188 AA.  
D -RUVA\_THEME STANDARD; PRT; 188 AA.  
C QWY12;  
T 30-MAY-2000 (Rel. 39, Created)  
T 30-MAY-2000 (Rel. 39, Last sequence update)  
T 28-FEB-2003 (Rel. 41, Last annotation update)  
E Holliday junction DNA helicase ruva.  
N RUVA OR TM0165.  
S Thermotoga maritima.  
X Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.  
X NCBI\_TaxID=2336;  
N [1]  
P SEQUENCE FROM N.A.  
C STRAIN=MSB8 / DSM 3109;  
X MEDLINE=9267315; PubMed=10360571;  
A Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,  
A Hart D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,  
A McDonald L., Utterback T.R., Malek J.A., Linder K.D., Garrett M.M.,  
A Stewart A.M., Sutton M.D., Pratt M.S., Phillips C.A., Richardson D.,  
A Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,  
A Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;  
T "Evidence for lateral gene transfer between Archaea and Bacteria from  
genome sequence of Thermotoga maritima";  
I Nature 399:323-329(1999).  
C -!- FUNCTION: THE RUVA-RUVB COMPLEX IN THE PRESENCE OF ATP RENATURALIZES  
CRUCIFORM STRUCTURE IN SUPERCOILED DNA WITH PALINDROMIC SEQUENCE,  
INDICATING THAT IT MAY PROMOTE STRAND EXCHANGE REACTIONS IN  
HOMOLOGOUS RECOMBINATION. RUVAB IS AN HELICASE THAT MEDIATES THE  
HOLLIDAY JUNCTION MIGRATION BY LOCALIZED DENATURATION AND  
REANNEALING. RUVB STIMULATES, IN THE PRESENCE OF DNA, THE WEAK  
ATPASE ACTIVITY OF RUVB (BY SIMILARITY).  
C -!- SUBUNIT: FORMS A COMPLEX WITH RUVB.  
C -!- SIMILARITY: BELONGS TO THE RUVA FAMILY.  
-----  
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-----  
C EMBL; AE001701; AA035258.1; -.  
C HSP; P40832; 1BVS.  
C TIGR; TM0165; -.  
C HAMAP; MF\_00031; -; 1.  
C InterPro; IPR003583; HHH 1.  
C InterPro; IPR000085; Ruva.  
C Pfam; PF01330; Ruva; 1.  
C ProDom; PD006268; Ruva; 1.

DR SMART; SM00278; HHH1; 2.  
DR TIGRFAMs; TIGR00084; ruva; 1.  
KW DNA repair; SOS response; DNA-binding; DNA recombination; Helicase;  
KW Complete proteome.  
SQ SEQUENCE 188 AA; 20818 MW; 28E7F39D67FD61DD CRC64;  
  
Query Match 5.7%; Score 7; DB 1; Length 188;  
Best Local Similarity 100.0%; Pred. No. 9.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 13 TFLSVSQ 19  
|||||  
DB 49 TFLSVSQ 55  
  
RESULT 4  
TRPI\_PSESY STANDARD; PRT; 298 AA.  
ID TRPI\_PSESY STANDARD; PRT; 298 AA.  
AC P34818;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 01-JUN-1994 (Rel. 23, Last annotation update)  
DE TrpBA operon transcriptional activator.  
GN TRPI.  
OS Pseudomonas syringae (pv. syringae).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=321;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93138427; PubMed=8423001;  
RA Auerbach S., Gao J., Gussin G.N.;  
RT "Nucleotide sequences of the trpI, trpB, and trpA genes of  
Pseudomonas syringae: positive control unique to fluorescent  
pseudomonads";  
RL Gene 123:25-32(1993).  
CC -!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPEA GENES ENCODING  
THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE  
INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE  
TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.  
CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL  
REGULATORS.  
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-----  
C EMBL; M95710; AA26015.1; -.  
C PIR; JQ2125; JQ2125.  
C InterPro; IPR000847; HTH Lysr.  
C InterPro; IPR005119; Lysr\_subst.  
C Pfam; PF00126; HTH 1; 1.  
C Pfam; PF03466; Lysr\_substrate; 1.  
C PRINTS; PR00039; HTHLYSR.  
C PROSITE; PS00044; HTH\_LYSR\_FAMILY; 1.  
C Tryptophan biosynthesis; Transcription regulation; Activator;  
KW DNA-binding.  
FT DNA\_BIND 23 42 H-T-H MOTIF (POTENTIAL).  
SQ SEQUENCE 298 AA; 32416 MW; 52D65FC34C15996B CRC64;  
  
Query Match 5.7%; Score 7; DB 1; Length 298;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 25 LDALLVF 31  
|||||  
DB 141 LDALLVF 147

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RESULT 5
YC19_KLEPN STANDARD; PRT; 320 AA.
AC Q48445;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in CFS region (ORF19) (Fragment).
DS Klebsiella pneumoniae
JC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
JC Enterobacteriaceae; Klebsiella.
XX NCBI_TaxID=573;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Chedi;
RX MEDLINE=95204345; PubMed=7896702;
RA Arakawa Y., Wacharotayankun R., Negatsuka T., Ito H., Kato N.,
RA Ohta M.,
RT "Genomic organization of the Klebsiella pneumoniae cps region
RT responsible for serotype K2 capsular polysaccharide synthesis in the
RT virulent strain Chedi."
RL J. Bacteriol. 177:1788-1796(1995).
CC -!- SIMILARITY: BELONGS TO THE UPF0053 FAMILY.
CC -!- SIMILARITY: Contains 2 CBS domains.
CC -----
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CC -----
CC EMBL; D21242; BAA21009.1;
CC InterPro; IPR000644; CBS_domain.
CC InterPro; IPR005170; CorC_HlyC.
CC InterPro; IPR005496; Terc.
CC Pfam; PF00571; CBS; 2.
CC Pfam; PF03471; CorC_HlyC; 1.
CC Pfam; PF03741; Terc; 1.
CC SMART; SM00116; CBS; 2.
KW Hypothetical protein; CBS domain; Repeat; Transmembrane.
FT TRANSMEM 24 POTENTIAL.
FT NON_TER 320 320
SQ SEQUENCE 320 AA; 36281 MW; 23F964B82E058D72 CRC64;

Query Match 5.7%; Score 7; DB 1; Length 320;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CLSFLIM 11
DB 4 CLSFLIM 10

RESULT 6
PP13_ARATH STANDARD; PRT; 322 AA.
AC P48483; Q9SH54;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine protein phosphatase PP1 isozyme 3 (EC 3.1.3.16).
GN TOPP3 OR ATIG64040 OR F22C12.20.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotsids II; Brassicales; Brassicaceae; Arabidopsids.
XX NCBI_TaxID=3702;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=93144705; PubMed=7678768;
RA Smith R.D., Walker J.C.;

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RT "Expression of multiple type 1 phosphoprotein phosphatases in
RT Arabidopsis thaliana."
RL Plant Mol. Biol. 21:307-316(1993).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altieri H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Chung M.K., Conn L., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Dunn P., Egtu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Lagin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Militscher J., Miran M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vayaberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana."
RL Nature 408:816-820(2000).
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -!- SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES. PP-1
CC SUBFAMILY.
CC -!- CAUTION: Ref.2 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
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CC -----
CC EMBL; M93410; AAA32838.1;
CC EMBL; AC007764; AAP24566.1; ALT_SEQ.
CC FIR; S31087; S31087.
CC HSPF; P08129; IFJM.
CC InterPro; IPR004843; M-peptidase.
CC InterPro; IPR006185; S/T phosphatase.
CC InterPro; IPR006186; T_phtase_apah.
CC Pfam; PR00149; Metallophos; 1.
CC PRINTS; PR00114; STPHPTASE.
CC ProDom; PD000252; t_phtase_apah; 1.
CC SMART; SM00156; PP2AC; 1.
CC PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.
KW Hydrolase; Iron; Manganese; Multigene family.
FT METAL 61 61 IRON (BY SIMILARITY).
FT METAL 63 63 IRON AND MANGANESE (BY SIMILARITY).
FT METAL 89 89 MANGANESE (BY SIMILARITY).
FT METAL 121 121 MANGANESE (BY SIMILARITY).
FT ACT_SITE 122 122 GENERAL ACID (BY SIMILARITY).
FT METAL 170 170 MANGANESE (BY SIMILARITY).
FT METAL 245 245 MANGANESE (BY SIMILARITY).
SQ SEQUENCE 322 AA; 36215 MW; 644A70BB9F63215C CRC64;

Query Match 5.7%; Score 7; DB 1; Length 322;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 RPADIPD 85
DB 188 RPADIPD 194

RESULT 7

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C1W ECOLI
D YCIW_ECOLI STANDARD; PRT; 401 AA.
C P76035;
T 15-JUL-1998 (Rel. 36, Created)
T 15-JUL-1998 (Rel. 36, Last sequence update)
T 16-OCT-2001 (Rel. 40, Last annotation update)
T E Hypothetical protein yciW.
N YCIW OR E1287.
S Escherichia coli.
C Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
C Enterobacteriaceae; Escherichia.
X NCBI_TaxID=562;
[1]
N P SEQUENCE FROM N.A.
C STRAIN=K12 / MG1655;
X MEDLINE=97426617; PubMed=9278503;
A Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
A Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.P.,
A Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
A Mau B., Shao Y.;
T "The complete genome sequence of Escherichia coli K-12.";
L Science 277:1453-1474 (1997).
C -----
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C -----
R EMBL; AE000227; AAC74369.1; -.
R PIR; B64877; B64877.
R EcoGene; EG14262; yciW.
W Hypothetical protein; Complete proteome.
Q SEQUENCE 401 AA; 45130 MW; 1DFAFDCEEB9362B7 CRC64;

Query Match 5.7%; Score 7; DB 1; Length 401;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 84 PDRFSAA 90
b 356 PDRFSAA 362
|||||

RESULT 8
D DADA_NEIMB STANDARD; PRT; 418 AA.
C Q9K1H5;
Y 28-FEB-2003 (Rel. 41, Created)
Y 28-FEB-2003 (Rel. 41, Last sequence update)
Y 28-FEB-2003 (Rel. 41, Last annotation update)
DE D-amino acid dehydrogenase small subunit (EC 1.4.99.1).
N DADA OR NMB0176.
S Neisseria meningitidis (serogroup B).
C Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
C Neisseriaceae; Neisseria.
X NCBI_TaxID=491;
[1]
N P SEQUENCE FROM N.A.
R STRAIN=MC58 / Serogroup B;
C MEDLINE=20175755; PubMed=10710307;
X Tetelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
X Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
X Nelson W.C., Gwin M.L., DeBoy R., Peterson J.D., Hickey E.K.,
X Hart D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
X Mason T., Ciecko A., Parksey D.S., Blair E., Ciftone H., Clark E.B.,
X Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
X Gill J., Scarlato V., Maignani V., Pizzo M., Grandi G., Sun L.,
X Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
X "Complete genome sequence of Neisseria meningitidis serogroup B strain
X MC58.";
```

```

RL Science 287:1809-1815 (2000).
CC -!- FUNCTION: Oxidative deamination of D-amino acids (By similarity).
CC -!- CATALYTIC ACTIVITY: A D-amino acid + H(2)O + acceptor = a 2-oxo
CC acid + NH(3) + reduced acceptor.
CC -!- COFACTOR: FAD (By similarity).
CC -!- SUBUNIT: Heterodimer of a small and a large subunit (By
CC similarity).
CC -!- SIMILARITY: BELONGS TO THE DADA FAMILY OF OXIDOREDUCTASES.
CC -----
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CC -----
R EMBL; AE002375; AAF40633.1; -.
R PIR; A81228; A81228.
R TIGR; NMB0176; -.
R HAMAP; MF_01202; -.
R InterPro; IPR006076; IPR006076.
R InterPro; IPR00205; NAD_binding.
R Pfam; PF01266; DAO; 1.
KW Oxidoreductase; Flavoprotein; FAD; Complete proteome.
FT NP_BIND 3 17
SQ SEQUENCE 418 AA; 46355 MW; B50C13F9DFBC214D CRC64;

Query Match 5.7%; Score 7; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 TVLAQLD 26
Db 259 TVLAQLD 265
|||||

RESULT 9
Y314_BUCAP STANDARD; PRT; 515 AA.
ID Y314_BUCAP
AC Q8K9NC;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein BUSG314.
GN BUSG314.
OS Buchnera aphidicola (subsp. Schizaphis graminum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=98794;
[1]
N P SEQUENCE FROM N.A.
R MEDLINE=22084549; PubMed=12089438;
R Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,
R Werngreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.;
R "50 million years of genomic stasis in endosymbiotic bacteria.";
RT Science 296:2376-2379 (2002).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE UPF0053 FAMILY. STRONG, TO E.COLI YOAE.
CC -!- SIMILARITY: Contains 2 CBS domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
R EMBL; AE014108; AAM67868.1; -.
R InterPro; IPR000644; CBS domain.
R InterPro; IPR005170; CoxC_HlyC.
R InterPro; IPR005496; Terc.
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SEQUENCE FROM N.A.
RC STRAIN=0157:H7 / EDL933 / ATCC 700927;
RC MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RC "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
RC Nature 409:529-533(2001).
RL [5]
RC SEQUENCE FROM N.A.
RC STRAIN=0157:H7 / RIMD 0509952;
RC MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Takagi T., Makino K., Ohnishi M., Kurokawa K., Murata T., Tanaka M., Tobe T.,
RA Han C.-G., Ohtsubo E., Nakayama K., Sasaki K., Ogasawara N., Yasunaga T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kubura S., Shiba T., Hattori M., Shinagawa H.;
RC "Complete genome sequence of enterohemorrhagic Escherichia coli
RC O157:H7 and genomic comparison with a laboratory strain K-12";
RC DNA Res. 8:11-22(2001).
RL [-]
RC SUBCELLULAR LOCATION: Integral membrane protein (Potential).
RC SIMILARITY: BELONGS TO THE UPF0053 FAMILY.
RC SIMILARITY: Contains 2 CBS domains.
CC [-]
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CC [-]
CC EMBL; AE000276; AAC74886.1; -
CC EMBL; D90825; BAA15623.1; -
CC EMBL; D90826; BAA15628.1; -
CC EMBL; AE016761; AAK80681.1; -
CC EMBL; AE005404; AAG56805.1; -
CC EMBL; AF002558; BAE35948.1; -
CC PIR; E90944; E90944.
CC PIR; H64942; H64942.
CC EcoGene; EG13517; YoaE.
CC InterPro; IPR000644; CBS domain.
CC InterPro; IPR005170; CorC_HLYC.
CC InterPro; IPR005496; TerC.
CC Pfam; PF00571; CBS; 2.
CC Pfam; PF03471; CorC_HLYC; 1.
CC Pfam; PF03741; TerC; 1.
CC Hypothetical protein; CBS domain; Repeat; Transmembrane;
CC Complete proteome.
KW Complete proteome.
FT TRANSMEM 14 34 POTENTIAL.
FT TRANSMEM 49 69 POTENTIAL.
FT TRANSMEM 79 99 POTENTIAL.
FT TRANSMEM 125 145 POTENTIAL.
FT TRANSMEM 150 170 POTENTIAL.
FT TRANSMEM 185 205 POTENTIAL.
FT TRANSMEM 207 227 POTENTIAL.
FT TRANSMEM 355 375 POTENTIAL.
SQ SEQUENCE 518 AA; 56527 MW; 90DF7C9A092F1ECC CRC64;

Query Match 5.7%; Score 7; DB 1; Length 518;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 5 CLSFLIM 11
DB 189 CLSFLIM 195
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RESULT 11
Y323_BUCAI
ID Y323_BUCAI STANDARD; PRT; 521 AA.

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PC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.X., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shaq Y.;  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474 (1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=97251358; PubMed=9097040;  
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,  
RA Iseno K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,  
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,  
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,  
RA Saito N., Sampaio G., Seki Y., Sivasubramanian S., Tagami H.,  
RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horuchi T.;  
RT "A 460-Kb DNA sequence of the Escherichia coli K-12 genome  
corresponding to the 40.1-50.0 min region on the linkage map.";  
RL DNA Res. 3:379-392 (1996).  
CC -|- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -|- SIMILARITY: BELONGS TO THE UPF0053 FAMILY.  
CC -|- SIMILARITY: Contains 2 CBS domains.  
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CC -----  
CC EMBL; AF001119; BAB13031.1; -  
CC InterPro; IPR000644; CBS domain.  
CC InterPro; IPR005170; CorC\_HlyC.  
CC Pfam; PF00571; CBS; 2.  
CC Pfam; PF03471; CorC\_HlyC; 1.  
CC Pfam; PF03741; TerC; 1.  
CC Hypothetical protein; CBS domain; Repeat; Transmembrane;  
CC Complete proteome.  
CC TRANSMEM 13 33 POTENTIAL.  
CC TRANSMEM 49 69 POTENTIAL.  
CC TRANSMEM 80 100 POTENTIAL.  
CC TRANSMEM 125 145 POTENTIAL.  
CC TRANSMEM 150 170 POTENTIAL.  
CC TRANSMEM 185 205 POTENTIAL.  
CC TRANSMEM 207 227 POTENTIAL.  
CC SEQUENCE 521 AA; 58722 MW; 56D9E406600DD958 CRC64;  
Query Match 5.7%; Score 7; DB 1; Length 521;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Y 5 CLSFLM 11  
D 189 CLSFLM 195  
RESULT 12  
ID YEGH\_ECOLI STANDARD; PRT; 527 AA.  
AC P76389; P94756;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein yegh.  
EN YEGH OR B2063.  
SS Escherichia coli.  
SC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
CC Enterobacteriaceae; Escherichia.  
XX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.

PC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.X., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shaq Y.;  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474 (1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=97251358; PubMed=9097040;  
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,  
RA Iseno K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,  
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,  
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,  
RA Saito N., Sampaio G., Seki Y., Sivasubramanian S., Tagami H.,  
RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horuchi T.;  
RT "A 460-Kb DNA sequence of the Escherichia coli K-12 genome  
corresponding to the 40.1-50.0 min region on the linkage map.";  
RL DNA Res. 3:379-392 (1996).  
CC -|- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -|- SIMILARITY: BELONGS TO THE UPF0053 FAMILY.  
CC -|- SIMILARITY: Contains 2 CBS domains.  
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CC -----  
CC EMBL; AF000296; AAC75124.1; ALT INIT.  
CC EMBL; D80844; BAA15916.1; ALT\_INIT.  
CC EcoGene; EG14051; yegh.  
CC InterPro; IPR000644; CBS domain.  
CC InterPro; IPR005170; CorC\_HlyC.  
CC InterPro; IPR005496; TerC.  
CC Pfam; PF00571; CBS; 2.  
CC Pfam; PF03471; CorC\_HlyC; 1.  
CC Pfam; PF03741; TerC; 1.  
CC SMART; SM00116; CBS; 2.  
CC Hypothetical protein; CBS domain; Repeat; Transmembrane;  
CC Complete proteome.  
CC TRANSMEM 14 34 POTENTIAL.  
CC TRANSMEM 51 71 POTENTIAL.  
CC TRANSMEM 81 101 POTENTIAL.  
CC TRANSMEM 145 165 POTENTIAL.  
CC TRANSMEM 185 205 POTENTIAL.  
CC SEQUENCE 527 AA; 59450 MW; 0C211895B9A0112D CRC64;  
Query Match 5.7%; Score 7; DB 1; Length 527;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Y 5 CLSFLM 11  
D 189 CLSFLM 195  
RESULT 13  
ID MSH2\_HUMAN STANDARD; PRT; 934 AA.  
AC P43246; O75488;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE DNA mismatch repair protein Msh2.  
EN MSH2.  
SS Homo sapiens (Human).  
SC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
XX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.



X NCBI\_TaxID=9606;  
N [1]  
P SEQUENCE FROM N.A.  
X MEDLINE=94073959; PubMed=8252616;  
X Fishel R., Lescoe M., Rao M., Copeland N.G., Jenkins N.A.,  
X Garber J., Kane M.F., Kolodner R.D.;  
A "The human mutator gene homolog MSH2 and its association with  
T hereditary nonpolyposis colon cancer.";  
L Cell 75:1027-1038(1993).  
N [2]  
N ERRATUM.  
X MEDLINE=94208055; PubMed=8156592;  
X Fishel R., Lescoe M., Rao M., Copeland N.G., Jenkins N.A.,  
X Garber J., Kane M.F., Kolodner R.D.;  
L Cell 77:167-167(1994).  
N [3]  
P SEQUENCE FROM N.A. AND DISASE.  
X MEDLINE=95229152; PubMed=7713503;  
X Kolodner R.D., Hall N.R., Lipford J., Kane M.F., Rao M.R.S.,  
X Morrison P., Wirth L., Finan P., Burn J., Chapman P., Barabino C.,  
X Merchant B., Bishop D.T.;  
L "Structure of the human MSH2 locus and analysis of two Muir-Torre  
X kindreds for msh2 mutations.";  
L Genomics 24:516-526(1994).  
N [4]  
P SEQUENCE FROM N.A.  
X TISSUE=Muscle;  
X MEDLINE=22388257; PubMed=12477932;  
X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
X Klausner R.D., Collins F.S., Wagner C.M., Shenmen C.M., Schuler G.D.,  
X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,  
X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
X Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
X Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
X Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
X Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
X Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
X Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,  
X Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
X Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
X Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
X Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
X Rodriguez A.C., Grinnwood J., Schmutz J., Myers R.M.,  
X Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smailus D.E.,  
X Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
R "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
N [5]  
P SEQUENCE OF 375-425 FROM N.A.  
RC TISSUE=Blood;  
RA Corvello C.M., Bevilacqua R.A.U., Rossi B.M., Simpson A.J.G.;  
RT "A novel germline mutation at exon 7 of the hMSH2 gene (417 del G) in  
RT a large HNPCC Brazilian kindred.";  
RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.  
N [6]  
P DNA-BINDING.  
RP MEDLINE=95007585; PubMed=7923193;  
RP Fishel R., Ewel A., Lescoe M.K.;  
RT "Purified human MSH2 protein binds to DNA containing mismatched  
RT nucleotides.";  
RL Cancer Res. 54:5539-5542(1994).  
N [7]  
P IDENTIFICATION OF MSH2 AS MEMBER OF BASC.  
RX MEDLINE=20245492; PubMed=10783165;  
RX Wang Y., Cortez D., Yazdi P., Neff N., Ellledge S.J., Qin J.;  
RT "BASC, a super complex of BRCA1-associated proteins involved in the  
RT recognition and repair of aberrant DNA structures.";  
RL Genes Dev. 14:927-939(2000).  
N [8]  
P REVIEW.  
RP MEDLINE=94310688; PubMed=8036718;  
RA Jiricny J.,  
RT "Colon cancer and DNA repair: have mismatches met their match?";  
Trends Genet. 10:164-168(1994).  
N [9]  
P REVIEW ON VARIANTS.  
RX MEDLINE=97403931; PubMed=9259192;  
RX Papadopoulos N., Lindblom A.;  
RT "Molecular basis of HNPCC: mutations of MMR genes.";  
RL Hum. Mutat. 10:89-99(1997).  
N [10]  
P VARIANTS HNPCC LEU-622 AND TYR-639.  
RX MEDLINE=94084796; PubMed=8261515;  
RX Leach F.S., Nicolaides N.C., Papadopoulos N., Liu B., Jen J.,  
RX Parsons R., Peltomaki P., Sistonen P., Aaltonen L.A.,  
RX Nyström-Lahti M., Guan X.-Y., Zhang J., Meltzer P.S., Yu J.-W.,  
RX Rao F.-T., Chen D.-J., Cerosaletti K.M., Fournier R.E.K., Todd S.,  
RX Lewis T., Leach R.J., Naylor S.L., Weissenbach J., Mecklin J.-P.,  
RX Jaarvinen H., Petersen G.M., Hamilton S.R., Green J., Jass J.,  
RX Watson P., Lynch H.T., Trent J.M., de la Chapelle A., Kinzler K.W.,  
RX Vogelstein B.;  
RT "Mutations of a muts homolog in hereditary nonpolyposis colorectal  
RT cancer.";  
RL Cell 75:1215-1225(1993).  
N [11]  
P VARIANT HNPCC ASN-596 DEL.  
RX MEDLINE=95179130; PubMed=7874129;  
RX Mary J.-L., Bishop T., Kolodner R.D., Lipford J.R., Kane M.F.,  
RX Weber W., Torhorst J., Mueller H., Spycher M., Scott R.J.;  
RT "Mutation analysis of the hMSH2 gene reveals a three base pair  
RT deletion in a family predisposed to colorectal cancer development.";  
RL Hum. Mol. Genet. 3:2067-2069(1994).  
N [12]  
P VARIANT HIS-96.  
RX MEDLINE=95243220; PubMed=7726159;  
RX Wijnen J., Vassen H., Khan P.M., Menko F.H., van der Klift H.,  
RX van Leeuwen C., van den Broek M., van Leeuwen-Cornelisse I.,  
RX Ngegast F., Weijers-Heijboer A., Lindhout D., Griffioen G., Cats A.,  
RX Kleibeker J., Varesco L., Bertario L., Bisgaard M.-L., Mohr J.,  
RX Fodde R.;  
RT "Seven new mutations in hMSH2, an HNPCC gene, identified by  
RT denaturing gradient-gel electrophoresis.";  
RL Am. J. Hum. Genet. 56:1060-1066(1995).  
N [13]  
P VARIANTS PHE-390 AND LYS-419.  
RX MEDLINE=96305099; PubMed=8690195;  
RX Konishi M., Kikuchi-Yanoshita R., Tanaka K., Muraoka M., Onda A.,  
RX Okumura Y., Kishi N., Iwama T., Mori T., Koike M., Ushio K., Chiba M.,  
RX Nomizu S., Konishi F., Utsunomiya J., Miyaki M.;  
RT "Molecular nature of colon tumors in hereditary nonpolyposis colon  
RT cancer, familial polyposis, and sporadic colon cancer.";  
RL Gastroenterology 111:307-317(1996).  
N [14]  
P VARIANT ASP-322.  
RX MEDLINE=96163505; PubMed=8566964;  
RX Maliaka Y.K., Chudina A.P., Belev N.F., Alday P., Bochkov N.P.,  
RX Buerstedde J.-M.;  
RT "CpG dinucleotides in the hMSH2 and hMLH1 genes are hotspots for  
RT HNPCC mutations";  
RL Hum. Genet. 97:251-255(1996).  
N [15]  
P VARIANT HNPCC ASN-596 DEL, AND VARIANT HIS-167.  
RX MEDLINE=97026284; PubMed=8872463;  
RX Moslein G., Tester D.J., Lindor N.M., Honechel R., Cunningham J.M.,  
RX French A.J., Halling K.C., Schwab M., Gorzki P., Thibodeau S.N.;  
RT "Microsatellite instability and mutation analysis of hMSH2 and hMLH1  
RT in patients with sporadic, familial and hereditary colorectal  
RT cancer.";  
RL Hum. Mol. Genet. 5:1245-1252(1996).  
N [16]  
P VARIANT CRC TYR-506.  
RX MEDLINE=96390800; PubMed=8797773;  
RX Han H.-J., Yuan Y., Xu J.-L., Oh J.-H., Won Y.-J., Kang K.J.,  
RX Kim K.-Y., Kim S., Kim C.-Y., Kim J.-P., Oh N.-G., Lee K.H., Choe K.J.,  
RX Nakamura Y., Park J.-G.;



T "Germline mutations of hMLH1 and hMSH2 genes in Korean hereditary  
T nonpolyposis colorectal cancer."  
J Natl. Cancer Inst. 88:1317-1319(1996).  
[17]  
N VARIANT GLN-46.  
P MEDLINE=96293410; PubMed=8700523;  
X MEDLINE=96293410; PubMed=8700523;  
A Bubb V.J., Curtis L.J., Cunningham C., Dunlop M.G., Carothers A.D.,  
A Morris R.G., White S., Bird C.C., Wyllie A.H.,  
T "Microsatellite instability and the role of hMSH2 in sporadic  
T colorectal cancer."  
L Oncogene 12:2641-2649(1996).  
N [18]  
P VARIANT HNPCC THR-305; THR-834 AND ASN-596 DEL.  
X MEDLINE=97456423; PubMed=93111737;  
A Wijnen J., Khan P.M., Vasen H., van der Klift H., Mulder A.,  
A van Leeuwen-Cornelisse I., Bakker B., Losekoot M., Moeller P.,  
A Podde R.,  
T "Hereditary nonpolyposis colorectal cancer families not complying  
T with the Amsterdam Criteria show extremely low frequency of  
T mismatch-repair-gene mutations."  
L Am. J. Hum. Genet. 61:329-335(1997).  
N [19]  
P VARIANT HNPCC CYS-323.  
X MEDLINE=97382414; PubMed=9240418;  
A Akiyama Y., Teubouchi N., Yuasa Y.,  
T "Frequent somatic mutations of hMSH3 with reference to microsatellite  
T instability in hereditary nonpolyposis colorectal cancers."  
L Biochem. Biophys. Res. Commun. 236:248-252(1997).  
N [20]  
P VARIANT SER-596.  
X MEDLINE=97147120; PubMed=8993976;  
A Viel A., Genuardi M., Capozzi E., Leonardi F., Bellacosa A.,  
A Paravatou-Petsotas M., Pomponi M.G., Fornasari M., Percesepe A.,  
A Roncucci L., Tamassia M.C., Benatti P., Ponz de Leon M., Valenti A.,  
A Covino M., Anti M., Foletto M., Bolocchi M., Neri G.,  
T "Characterization of MSH2 and MLH1 mutations in Italian families with  
T hereditary nonpolyposis colorectal cancer."  
L Genes Chromosomes Cancer 18:8-18(1997).  
N [21]  
P VARIANT ASP-322.  
X MEDLINE=97242567; PubMed=9087566;  
A Wu Y., Nyström-Lanti M., Osinga J., Looman M.W.G., Peltomäki P.,  
A Aaltonen L.A., de la Chapelle A., Hofstra R.M.W., Buys C.H.C.M.,  
T "MSH2 and MLH1 mutations in sporadic replication error-positive  
Query Match 5.7%; Score 7; DB 1; Length 934;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Y 21 VLAQLDA 27  
b 598 VLAQLDA 604  
RESULT 14  
C\_BPT4 STANDARD; PRT; 51 AA.  
D AC BPT4  
C P18924;  
T 01-NOV-1990 (Rel. 16, Created)  
T 01-NOV-1990 (Rel. 16, Last sequence update)  
T 15-SEP-2003 (Rel. 42, Last annotation update)  
T Acridine resistance protein.  
N AC OR 52.2.  
S Bacteriophage T4.  
X Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;  
X T4-like viruses.  
X NCBI\_TaxID=10665;  
N [1]  
P SEQUENCE FROM N.A.  
X MEDLINE=8617248; PubMed=3280805;  
A Chapman D., Morad I., Kaufmann G., Gait M.J., Jorissen L., Snyder L.,  
T "Nucleotide and deduced amino acid sequence of stp: the bacteriophage  
T4 anticodon nuclease gene."

J. Mol. Biol. 199:373-377(1988).  
[2]  
P SEQUENCE FROM N.A.  
R Kutter E., Arisaka F., Kunisawa T., Tsugita A., Mosig G.,  
R Mesyanzhinov V., Ruger W., Stidham T., Thomas E.,  
RT "Bacteriophage T4 genome analysis."  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
N [3]  
P FUNCTION.  
R MEDLINE=98240730; PubMed=9560385;  
X Wang F.J., Ripley L.S.,  
R "The spectrum of acridine resistant mutants of bacteriophage T4  
RT reveals cryptic effects of the tBL14 DNA polymerase allele on  
RT spontaneous mutagenesis."  
RL Genetics 148:1655-1665(1998).  
C -!- FUNCTION: Mutations in the ac gene confer resistance to acridine-  
C inhibition of phage development.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; AF158101; RAD42488.1; --  
DR FIR; S01870; S01870.  
DR PROSITE; PS00013; PROKAR\_LIPOPROTEIN; UNKNOWN\_1.  
KW Antibiotic resistance.  
SQ SEQUENCE 51 AA; 5472 MW; 63FDCB0161A8B569 CRC64;  
Query Match 4.9%; Score 6; DB 1; Length 51;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 97 ACVLTI 102  
Db 18 ACVLTI 23  
RESULT 15  
D230\_PEA STANDARD; PRT; 72 AA.  
AC Q01783;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Disease resistance response protein 230 precursor.  
GN F1230.  
OS Pisum sativum (Garden pea).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.  
OX NCBI\_TaxID=3888;  
RN [1]  
P SEQUENCE FROM N.A.  
R STRAIN=cv. Alaska;  
RX MEDLINE=92190628; PubMed=1799696;  
RA Chiang C.C., Hadwiger L.A.;  
RT "The Fusarium solani-induced expression of a pea gene family encoding  
RT high cysteine content proteins."  
RL Mol. Plant Microbe Interact. 4:324-331(1991).  
CC -!- INDUCTION: UPON CONTACT WITH THE PLANT PATHOGEN FUNGUS FUSARIUM  
CC SOLANI.  
CC -!- PTM: FOUR DISULFIDE BONDS MAY BE PRESENT.  
CC -!- SIMILARITY: BELONGS TO THE PLANT DEFENSIN FAMILY.  
CC -----  
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CC -----  
DR EMBL; L01578; AAA79117.1; --  
DR PIR; T06599; T06599.  
DR InterPro; IPR002118; Gamma-thionin.  
DR InterPro; IPR003614; Kntc1.  
DR Pfam; PF00304; Gamma-thionin; 1.  
DR ProDom; PD002594; G\_Purothionin; 1.  
DR SMART; SM00505; Kntc1; 1.  
KW Plant defense; Pathogenesis-related protein; Multigene family; Signal.  
FT SIGNAL 1 27 POTENTIAL.  
FT CHAIN 28 72 DISEASE RESISTANCE RESPONSE PROTEIN 230.  
SQ SEQUENCE 72 AA; 7986 MW; 50B6A90E5FE0CE2B CRC64;  
  
Query Match 4.9%; Score 6; DB 1; Length 72;  
Best Local Similarity 100.0%; Pred. No. 43; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 CLSFLL 10  
DB 8 CLSFLL 13  
  
RESULT 16  
R28A\_MYCTU STANDARD; PRT; 94 AA.  
AC Q10879;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE 50S Ribosomal protein L28-1.  
GN RPB1 OR RPB OR RV0105C OR MT0114 OR MTCY251.24C.  
OS Mycobacterium tuberculosis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
CX NCBI\_TaxID=1773;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H37RV;  
RX MEDLINE=98295987; PubMed=9634230;  
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
RA Gordon S.V., Eigmler K., Gas S., Barry C.E. III, Tekala P.,  
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,  
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
RA Sultston J.E., Taylor K., Whitehead S., Barrell B.G.;  
RA "Deciphering the biology of Mycobacterium tuberculosis from the  
RT complete genome sequence."  
RL Nature 393:537-544(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CDC 1551 / Oshkosh;  
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,  
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
RA Delcher A., Uterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
RA Bishai W.;  
RA "Whole genome comparison of Mycobacterium tuberculosis clinical and  
RT laboratory strains."  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.  
CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
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DR EMBL; Z74410; CAA98918.1; --  
DR EMBL; AE006923; AAK44336.1; --  
DR PIR; A70752; A70752.  
DR TIGR; MT0114; --  
DR TubercuList; RV0105C; --  
DR HAMAP; MF\_00373; --; 1.  
DR InterPro; IPR001383; Ribosomal L28.  
DR Pfam; PF00830; Ribosomal L28; 1.  
DR TIGRFAMs; TIGR00009; L28; 1.  
KW Ribosomal protein; Complete proteome.  
SQ SEQUENCE 94 AA; 10530 MW; D2D927D1934C83F7 CRC64;  
  
Query Match 4.9%; Score 6; DB 1; Length 94;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 60 RAGSAP 65  
DB 72 RAGSAP 77  
  
RESULT 17  
H1C2\_TRYCR STANDARD; PRT; 97 AA.  
AC P40268;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Histone H1.C2.  
OS Trypanosoma cruzi.  
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
CX NCBI\_TaxID=5693;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Tulaneu 2;  
RX MEDLINE=95059220; PubMed=7969272;  
RA Aaslund L., Carlsson L., Henriksson J., Rydaaker M., Toro G.C.,  
RA Galanti N., Pettersson U.;  
RT "A gene family encoding heterogeneous histone H1 proteins in  
RT Trypanosoma cruzi";  
RL Mol. Biochem. Parasitol. 65:317-330(1994).  
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CC -----  
DR EMBL; L27115; AAA66478.1; --  
DR KW Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.  
SQ SEQUENCE 97 AA; 10290 MW; AA8073FDBA36121B CRC64;  
  
Query Match 4.9%; Score 6; DB 1; Length 97;  
Best Local Similarity 100.0%; Pred. No. 55;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 38 LSCYLS 43  
DB 8 LSCYLS 13  
  
RESULT 18  
VE7\_HPV35 STANDARD; PRT; 99 AA.  
AC P27230;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE E7 protein.  
GN E7.  
OS Human papillomavirus type 35.

DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; IG_V.
DR	Pfam; PF00047; Ig_1.
DR	SMART; SMO0406; IGV; 1.
DR	PROSITE; PSS0835; IG_LIKE; 1.
KW	Immunoglobulin V region; Signal; Hybridoma.
FT	NON_TER 1 1
FT	SIGNAL <1 4
FT	CHAIN 5 100
FT	DISULFID 27 93
FT	NON_TER 100 100
SSQ	SEQUENCE 100 AA; 10729 MW; 5D9AF363C52632F CRC64;
 Query Match	
Best Local Similarity 4.9%; Score 6; DB 1; Length 100;	
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	83 IPDRFS 88
DB	
	63 IPDRFS 68
 RESULT 20	
ID	KV3A_HUMAN STANDARD; PRT; 108 AA.
AC	P01619;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	Ig kappa chain V-II region B6.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI	TaxID=9606;
RN	[1]
RP	SEQUENCE.
RA	Milstein C.;
RT	"The basic sequences of immunoglobulin kappa chains: sequence studies
RL	of Bence Jones proteins Rad, Fr4 and B6.";
FEBS	Lett. 2:301-304(1969).
CC	- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR	PIR; A01891; K3HUB6.
DR	HSP; P80362; 1WTL.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003006; IG_MHC.
DR	InterPro; IPR003596; IG_V.
DR	Pfam; PF00047; Ig_1.
DR	SMART; SMO0406; IGV; 1.
DR	PROSITE; PSS0835; IG_LIKE; 1.
KW	Immunoglobulin V region; Bence-Jones protein.
FT	DISULFID 23 89
FT	NON_TER 108 108
SSQ	SEQUENCE 108 AA; 11635 MW; 8BC14FP07A419E3D CRC64;
 Query Match	
Best Local Similarity 4.9%; Score 6; DB 1; Length 108;	
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	83 IPDRFS 88
DB	
	59 IPDRFS 64
 RESULT 21	
ID	LV3A_HUMAN STANDARD; PRT; 108 AA.
AC	P01714;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	15-SEP-2003 (Rel. 42, Last annotation update)
DE	Ig lambda chain V-III region SH.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
SEQUENCE.  
MEDLINE=70166723; PubMed=4909564;  
Titani K., Wikler M., Shinoda T., Putnam F.W.;  
"The amino acid sequence of a lambda type Bence-Jones protein. 3. The  
complete amino acid sequence and the location of the disulfide  
bridges.";  
J. Biol. Chem. 245:2171-2176(1970).  
-1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
-1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
PIR: A01980; L3HUSH.  
HSSP: P80748; 2LOI.  
GO: GO:0005576; C:extracellular; NAS.  
GO: GO:0003823; F:antigen binding activity; NAS.  
GO: GO:0006955; P:immune response; NAS.  
InterPro: IPR007110; Ig-like.  
InterPro: IPR003006; Ig\_MHC.  
InterPro: IPR003596; Ig\_V.  
Pfam: PF00047; Ig; 1.  
SMART: SMO0406; IGV; 1.  
PROSITE: PS0835; IG LIKE; 1.  
Immunoglobulin V region; Bence-Jones protein.  
DOMAIN 1 97  
DISULFID 21 86  
NON TER 108 108  
SEQUENCE 108 AA; 11392 MW; E7E1229586411A56 CRC64;  
Query Match 4.9%; Score 6; DB 1; Length 108;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
2Y 83 IPDRFS 88  
| | | | |  
2D 56 IPDRFS 61  
| | | | |  
RESULT 22  
KV3E HUMAN STANDARD; PRT; 109 AA.  
AC P01620;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-III region SIE.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
SEQUENCE.  
MEDLINE=82046598; PubMed=6794615;  
Andrews D.W., Capra J.D.;  
"Amino acid sequence of the variable regions of light chains from two  
idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa  
group.";  
Biochemistry 20:5816-5822(1981).  
-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA  
GLOBULIN ACTIVITY.  
PIR: A01892; K3HUSI.  
HSSP: P80362; 1WTL.  
GO: GO:0005576; C:extracellular; NAS.  
GO: GO:0003823; F:antigen binding activity; NAS.  
GO: GO:0006955; P:immune response; NAS.  
InterPro: IPR007110; Ig-like.  
InterPro: IPR003006; Ig\_MHC.  
InterPro: IPR003596; Ig\_V.  
Pfam: PF00047; Ig; 1.  
SMART: SMO0406; IGV; 1.  
PROSITE: PS0835; IG LIKE; 1.  
Immunoglobulin V region.  
DISULFID 23 89  
BY SIMILARITY.

FT NON TER 109 109  
SQ SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;  
Query Match 4.9%; Score 6; DB 1; Length 109;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 83 IPDRFS 88  
| | | | |  
Db 59 IPDRFS 64  
| | | | |  
RESULT 23  
KV3D HUMAN STANDARD; PRT; 109 AA.  
ID KV3D HUMAN STANDARD; PRT; 109 AA.  
AC P01622;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-III region Ti.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
SEQUENCE.  
MEDLINE=72188439; PubMed=5027703;  
Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;  
"Rule of antibody structure. The primary structure of a monoclonal  
immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein  
Ti). IV. The complete amino acid sequence and its significance for  
the mechanism of antibody production.";  
Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).  
-1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
-1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
PIR: A01895; K3HUTI.  
HSSP: P80362; 1WTL.  
GO: GO:0005576; C:extracellular; NAS.  
GO: GO:0003823; F:antigen binding activity; NAS.  
GO: GO:0006955; P:immune response; NAS.  
InterPro: IPR007110; Ig-like.  
InterPro: IPR003006; Ig\_MHC.  
InterPro: IPR003596; Ig\_V.  
Pfam: PF00047; Ig; 1.  
SMART: SMO0406; IGV; 1.  
PROSITE: PS0835; IG LIKE; 1.  
Immunoglobulin V region; Bence-Jones protein.  
DISULFID 23 89  
BY SIMILARITY.  
FT NON TER 109 109  
SQ SEQUENCE 109 AA; 11788 MW; 8C35058CDC7749BC CRC64;  
Query Match 4.9%; Score 6; DB 1; Length 109;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 83 IPDRFS 88  
| | | | |  
Db 59 IPDRFS 64  
| | | | |  
RESULT 24  
KV3E HUMAN STANDARD; PRT; 109 AA.  
ID KV3E HUMAN STANDARD; PRT; 109 AA.  
AC P01623;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-III region WOL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NCBI\_TaxID=9606;  
[1]

P SEQUENCE.  
X MEDLINE=82046598; PubMed=6794615;  
A Andrews D.W., Capra J.D.;  
T "Amino acid sequence of the variable regions of light chains from two  
I idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa  
T group.";  
L Biochemistry 20:5816-5822(1981).  
L C -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA  
C GLOBULIN ACTIVITY.  
R PIR; A01896; K3HUWL.  
R HSP; P80362; LWL.  
R GO; GO:0005576; C:extracellular; NAS.  
R GO; GO:0003823; F:antigen binding activity; NAS.  
R GO; GO:0006955; P:immune response; NAS.  
R InterPro; IPR007110; IG-LIKE.  
R InterPro; IPR003006; IG\_MHC.  
R InterPro; IPR003596; IG\_V.  
R Pfam; PF00047; IG; 1.  
R SMART; SM00406; IGV; 1.  
R PROSITE; PS50835; IG-LIKE; 1.  
W Immunoglobulin V region.  
T DISULFID 23 89  
T NON TER 109 109 BY SIMILARITY.  
T Q SEQUENCE 109 AA; 11746 MW; 566C115E6B9CBEE CRC64;

Query Match 4.9%; Score 6; DB 1; Length 109;  
Best Local Similarity 100.0%; Pred.No.61;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 83 IPRFS 88  
|  
|  
|  
|  
|  
b 59 IPRFS 64

RESULT 25  
V3G HUMAN STANDARD; PRT; 109 AA.  
C P04206;  
T 20-MAR-1987 (Rel. 04, Created)  
T 20-MAR-1987 (Rel. 04, Last sequence update)  
T 15-JUL-1999 (Rel. 38, Last annotation update)  
T Ig kappa chain V-III region GOL (Rheumatoid factor).  
E Homo sapiens (Human).  
S Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
X Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
X NCBI\_TaxID=9606;  
[1]

SEQUENCE.  
X MEDLINE=86230578; PubMed=3085710;  
X Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;  
X "Amino acid sequence of a light chain variable region of a human  
X rheumatoid factor of the Wa idiotype group, in part predicted by its  
X reactivity with antipeptide antibodies.";  
X Mol. Immunol. 23:239-244(1986).  
X PIR; A01893; K3HUGO.  
X HSP; P80362; LWL.  
X GO; GO:0005576; C:extracellular; NAS.  
X GO; GO:0003823; F:antigen binding activity; NAS.  
X GO; GO:0006955; P:immune response; NAS.  
X InterPro; IPR007110; IG-LIKE.  
X InterPro; IPR003006; IG\_MHC.  
X InterPro; IPR003596; IG\_V.  
X Pfam; PF00047; IG; 1.  
X SMART; SM00406; IGV; 1.  
X PROSITE; PS50835; IG-LIKE; 1.  
W Immunoglobulin V region.  
T DISULFID 23 89  
T NON TER 109 109 BY SIMILARITY.  
T Q SEQUENCE 109 AA; 11830 MW; 9349A5B1D9358B86 CRC64;

Query Match 4.9%; Score 6; DB 1; Length 109;  
Best Local Similarity 100.0%; Pred.No.61;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPRFS 88  
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|  
Db 59 IPRFS 64

RESULT 26  
LV2E HUMAN STANDARD; PRT; 109 AA.  
ID LV2E HUMAN  
AC P06888;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-I region EPS.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=86000126; PubMed=3929803;  
RA Toft K.G., Sletten K., Husby G.;  
RT "The amino-acid sequence of the variable region of a carbohydrate-  
RT containing amyloid fibril protein EPS (immunoglobulin light chain,  
RT type lambda).";  
RL Biol. Chem. Hoppe-Seyler 366:617-625(1985).  
CC -1- MISCELLANEOUS: RESIDUES 1-2, 56-62, AND 74-78 AND THE SEQUENCED  
CC PEPTIDES WERE POSITIONED BY HOMOLOGY.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A24656; LIHURP.  
DR HSP; P01703; 7FAP.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-LIKE.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG-LIKE; 1.  
KW Immunoglobulin V region; Amyloid; Glycoprotein.  
FT DOMAIN 1 105 IG-LIKE  
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .).  
FT DISULFID 22 89 BY SIMILARITY.  
FT NON TER 109 109  
SQ SEQUENCE 109 AA; 11414 MW; 556A313E24DSAC73 CRC64;

Query Match 4.9%; Score 6; DB 1; Length 109;  
Best Local Similarity 100.0%; Pred.No.61;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPRFS 88  
|  
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|  
|  
|  
Db 59 IPRFS 64

RESULT 27  
LV2E HUMAN STANDARD; PRT; 109 AA.  
ID LV2E HUMAN  
AC P01708;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-II region BUR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=80006606; PubMed=113407;  
RA Infante A.J., Putnam F.W.;  
RT "Primary structure of a human IgM immunoglobulin. V. Amino acid

Query Match 4.9%; Score 6; DB 1; Length 109;  
Best Local Similarity 100.0%; Pred.No.61;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPRFS 88  
|  
|  
|  
|  
|  
Db 59 IPRFS 64

sequence of a human IgA lambda light chain (Bur).";  
J. Biol. Chem. 254:9006-9016(1979).  
-I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN- AND MCG-  
MARKERS.  
-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
-I- SIMILARITY: Contains 1 immunoglobulin-like domain.

QY 54 VSWYQQ 59  
DB 35 VSWYQQ 40  
PRT; 110 AA.  
RESULT 29  
LV2J HUMAN  
ID LV2J HUMAN STANDARD; PRT; 110 AA.  
AC P01703;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE IG lambda chain V-I region NIG-64.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=81215386; PubMed=6787031;  
RA Takayasu T., Takahashi N., Shinoda T., Okuyama T.,  
RA "Comparative studies on the structure of the light chains of human  
RT immunoglobulins. IV. Assignment of a subgroup.",  
RL J. Biochem. 89:421-436(1981).  
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A01979; L2HUBR.  
DR HSSP; P01709; 2MCG.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG\_1.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.  
FT MOD RES 1 1  
FT DISULFID 22 90  
FT SITE 91 91  
FT NON TER 110 110  
FT SEQUENCE 110 AA; 11506 MW; BFD8AE1C5D267FAB CRC64;

Query Match 4.9%; Score 6; DB 1; Length 109;  
Best Local Similarity 100.0%; Pred.No. 61;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
2y 54 VSWYQQ 59  
3b 35 VSWYQQ 40  
PRT; 110 AA.  
RESULT 28  
LV2J HUMAN  
ID LV2J HUMAN STANDARD; PRT; 110 AA.  
AC P01713;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE IG lambda chain V-II region NIG-58.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=81215386; PubMed=6787031;  
RA Takayasu T., Takahashi N., Shinoda T., Okuyama T., Tomioka H.,  
RA "Comparative studies on the structure of the light chains of human  
RT immunoglobulins. III. Amino acid sequence of a lambda type Bence  
RL Jones euglobulin.",  
RL J. Biochem. 89:421-436(1981).  
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A01979; L2HUBR.  
DR HSSP; P01709; 2MCG.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG\_1.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.  
FT MOD RES 1 1  
FT DISULFID 22 90  
FT SITE 91 91  
FT NON TER 110 110  
FT SEQUENCE 110 AA; 11455 MW; 76C9F4C6B20312B6 CRC64;

Query Match 4.9%; Score 6; DB 1; Length 110;  
Best Local Similarity 100.0%; Pred.No. 62;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 54 VSWYQQ 59  
DB 35 VSWYQQ 40  
PRT; 111 AA.  
RESULT 29  
LV2A HUMAN  
ID LV2A HUMAN STANDARD; PRT; 111 AA.  
AC P01702;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE IG lambda chain V-I region NIG-64.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=83186114; PubMed=6404900;  
RA Kamekuni F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,  
RA "Comparative studies on the structure of the light chains of human  
RT immunoglobulins. IV. Assignment of a subgroup.",  
RL J. Biochem. 93:421-429(1983).  
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A01965; L1HUNG.  
DR HSSP; P01703; 7FAB.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG\_1.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.  
FT MOD RES 1 1  
FT DISULFID 22 89  
FT NON TER 111 111  
FT SEQUENCE 111 AA; 11454 MW; A21C6121C18A61E0 CRC64;

Query Match 4.9%; Score 6; DB 1; Length 111;  
Best Local Similarity 100.0%; Pred.No. 62;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 54 VSWYQQ 59  
DB 34 VSWYQQ 39  
PRT; 111 AA.  
RESULT 30  
LV2A HUMAN  
ID LV2A HUMAN STANDARD; PRT; 111 AA.  
AC P01704;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE IG lambda chain V-II region TOG.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=80048495; PubMed=500108;

Query Match 4.9%; Score 6; DB 1; Length 111;  
Best Local Similarity 100.0%; Pred.No. 62;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 54 VSWYQQ 59  
DB 34 VSWYQQ 39  
PRT; 111 AA.  
RESULT 30  
LV2A HUMAN  
ID LV2A HUMAN STANDARD; PRT; 111 AA.  
AC P01704;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE IG lambda chain V-II region TOG.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=80048495; PubMed=500108;

A Nabeshima Y., Ikenaka T.;  
I "Primary structure of cyto Bence-Jones protein (Tog) from the urine  
of a patient with IgD myeloma";  
L Mol. Immunol. 16:439-444(1979).  
C -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
C -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
R R PIR; A01969; L2HUTG.  
R HSSP; P01709; 2MCG.  
R GO; GO:0005576; C:extracellular; NAS.  
R GO; GO:0003823; F:antigen binding activity; NAS.  
R GO; GO:0006955; P:immune response; NAS.  
R InterPro; IPR007110; IG-LIKE.  
R InterPro; IPR003006; IG\_MHC.  
R Pfam; PF00047; IG\_V.  
R SMART; SM00406; IGV; 1.  
R PROSITE; PS50835; IG\_LIKE; 1.  
W Immunoglobulin V region; Bence-Jones protein;  
W Pyrrolidone carboxylic acid.  
T DOMAIN 1 100 IG-LIKE.  
T MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
T DISULFID 22 90 BY SIMILARITY.  
T NON\_TER 111 111  
Q SEQUENCE 111 AA; 11713 MW; FD20AEF4CE5364E2 CRC64;  
  
Query Match 4.9%; Score 6; DB 1; Length 111;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Y 54 VSWYQQ 59  
b 35 VSWYQQ 40  
|||||  
  
RESULT 31  
V2B HUMAN STANDARD; PRT; 111 AA.  
C P01705;  
T 21-JUL-1986 (Rel. 01, Created)  
T 21-JUL-1986 (Rel. 01, Last sequence update)  
T 15-SEP-2003 (Rel. 42, Last annotation update)  
E Ig lambda chain V-II region NEI.  
S Homo sapiens (Human).  
C Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
X NCBI\_TaxID=9606;  
N [1]  
P SEQUENCE.  
X MEDLINE=72233223; PubMed=5043326;  
A Garver F.A., Hilschmann N.;  
T "The primary structure of a monoclonal human lambda-type  
immunoglobulin L-chain of subgroup II (Bence-Jones protein NEI).";  
L Eur. J. Biochem. 26:10-32(1972).  
C -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
C -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
R R PIR; A01970; L2HUNI.  
R HSSP; P01709; 2MCG.  
R GO; GO:0005576; C:extracellular; NAS.  
R GO; GO:0003823; F:antigen binding activity; NAS.  
R GO; GO:0006955; P:immune response; NAS.  
R InterPro; IPR007110; IG-LIKE.  
R InterPro; IPR003006; IG\_MHC.  
R Pfam; PF00047; IG\_V.  
R SMART; SM00406; IGV; 1.  
R PROSITE; PS50835; IG\_LIKE; 1.  
W Immunoglobulin V region; Bence-Jones protein; Glycoprotein;  
W Pyrrolidone carboxylic acid.  
T DOMAIN 1 106 IG-LIKE.  
T MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
T DISULFID 22 90 BY SIMILARITY.  
T CARBOHYD 96 96 N-LINKED (GLCNAC. . .).  
T NON\_TER 111 111

SQ SEQUENCE 111 AA; 11591 MW; AD6D156584D087EB CRC64;  
  
Query Match 4.9%; Score 6; DB 1; Length 111;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 54 VSWYQQ 59  
DB 35 VSWYQQ 40  
|||||  
  
RESULT 32  
LV2C HUMAN STANDARD; PRT; 111 AA.  
ID LV2C\_HUMAN  
AC P01706;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-II region BOH.  
DE Ig lambda chain V-II region BOH.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=75115478; PubMed=804002;  
RA Kohler H., Rudofsky S., Kluskins L.;  
RT "The primary structure of a human lambda II chain.";  
RL J. Immunol. 114:415-421(1975).  
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE O2+ MARKER.  
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A01972; L2HUBH.  
DR HSSP; P01709; 2MCG.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-LIKE.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.  
FT DOMAIN 1 106 IG-LIKE.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT DISULFID 22 90 BY SIMILARITY.  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 11650 MW; 94520309932623B8 CRC64;  
  
Query Match 4.9%; Score 6; DB 1; Length 111;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 54 VSWYQQ 59  
DB 35 VSWYQQ 40  
|||||  
  
RESULT 33  
LV2D HUMAN STANDARD; PRT; 111 AA.  
ID LV2D\_HUMAN  
AC P01707;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-II region TRO.  
DE Ig lambda chain V-II region TRO.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.

XX MEDLINE=80114123; PubMed=118915;  
YA Scholz R., Yang C., Hilschmann N.;  
IT "Rule of antibody structure. Primary structure of a human monoclonal  
IT IgA1-immunoglobulin (myeloma protein fro). VI. Amino acid sequence of  
YT the L-chain, lambda-type, subgroup II";  
YL Hoppe-Seyler's Z. Physik. Chem. 360:1903-1918(1979).  
XC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
XC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
XR PIR; A01973; L2HUTR.  
XR HSSP; P01709; 2MCG.  
XR GO; GO:0005576; C:extracellular; NAS.  
XR GO; GO:0003823; F:antigen binding activity; NAS.  
XR GO; GO:0006955; P:immune response; NAS.  
XR InterPro; IPR007110; IG-like.  
XR InterPro; IPR003006; IG\_MHC.  
XR Pfam; PF00047; IG; 1.  
XR SMART; SM00406; IGV; 1.  
XR PROSITE; PS0835; IG LIKE; 1.  
XR Immunoglobulin V region; Pyrrrolidone carboxylic acid.  
FT DOMAIN 1 106  
FT MOD\_RES 1 1  
FT DISULFID 22 90  
FT NON\_TER 111 111  
FT SEQUENCE 111 AA; 11561 MW; 99DC457A12B8F6E1 CRC64;  
Query Match 4.9%; Score 6; DB 1; Length 111;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
2Y 54 VSWYQQ 59  
Db 35 VSWYQQ 40  
RESULT 34  
LV2F HUMAN  
ID LV2F HUMAN STANDARD; PRT; 111 AA.  
AC P01709;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-II region MCG.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RX SEQUENCE  
RA Fett J.W., Deutsch H.F.;  
RL "Primary structure of the Mcg lambda chain."  
RN [2]  
RP LAMBDA CHAIN GENES.  
RX MEDLINE=75013804; PubMed=4415202;  
RA Fett J.W., Deutsch H.F.;  
RL "A new lambda-chain gene."  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
RA Edmundson A.B., Ely K.R., Abola E.E., Schiffer M.,  
RA Panagiotopoulos N.;  
RL "Rotational allomerism and divergent evolution of domains in  
RT immunoglobulin light chains."  
RL Biochemistry 14:3953-3961(1975).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY.  
RX MEDLINE=90133913; PubMed=2515285;  
RA Ely K.R., Herron J.N., Harker M., Edmundson A.B.;  
RL "Three-dimensional structure of a light chain dimer crystallized in  
RT water. Conformational flexibility of a molecule in two crystal  
RT forms."

J. Mol. Biol. 210:601-615(1989).  
-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
-!- MISCELLANEOUS: THE MCG-TYPE C REGION APPEARS TO BE CORRELATED WITH  
CC A VERY UNUSUAL V-REGION SUBSTITUTION, 103-THR ABOVE FOR GLY,  
CC SUGGESTING THAT THE V-C JOINING MECHANISM IS NOT ALWAYS RANDOM.  
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+  
CC MARKERS.  
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A90381; L2HUMC.  
DR PDB; 2MCG; 15-JUL-92.  
DR PDB; 1A8J; 17-JUN-98.  
DR PDB; 1DCL; 15-MAY-97.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG LIKE; 1.  
DR Immunoglobulin V region; Bence-Jones protein; 3D-structure;  
KW Pyrrrolidone carboxylic acid. IG-LIKE.  
FT DOMAIN 1 108  
FT MOD\_RES 1 1  
FT DISULFID 22 90  
FT STRAND 5 5  
FT STRAND 10 12  
FT STRAND 18 23  
FT TURN 26 32  
FT STRAND 36 40  
FT TURN 42 43  
FT STRAND 50 51  
FT TURN 52 54  
FT STRAND 55 55  
FT TURN 62 63  
FT STRAND 66 68  
FT STRAND 72 77  
FT HELIX 82 84  
FT STRAND 86 93  
FT STRAND 99 101  
FT STRAND 105 109  
FT NON\_TER 111 111  
FT SEQUENCE 111 AA; 11558 MW; 7CC1D6E2FA3377BA CRC64;  
Query Match 4.9%; Score 6; DB 1; Length 111;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 54 VSWYQQ 59  
Db 35 VSWYQQ 40  
RESULT 35  
LV2G HUMAN  
ID LV2G HUMAN STANDARD; PRT; 111 AA.  
AC P01710;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-II region BO.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RX SEQUENCE.  
RA MEDLINE=71103825; PubMed=5532228;  
RA Wikler M., Putnam F.W.;  
RL "Amino acid sequence of human lambda chains. 3. Tryptic peptides,  
RT chymotryptic peptides, and sequence of protein Bo."  
J. Biol. Chem. 245:4488-4507(1970).



C -I- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.  
C -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
R PIR; A01976; L2HUBO.  
R HSSP; P01709; 2MCG.  
R GO; GO:0005576; C:extracellular; NAS.  
R GO; GO:0003823; F:antigen binding activity; NAS.  
R GO; GO:0006955; P:immune response; NAS.  
R InterPro; IPR007110; IG-LIKE.  
R InterPro; IPR003006; IG-MHC.  
R InterPro; IPR003596; IG\_V.  
R Pfam; PF00047; IG; 1.  
R SMART; SM00406; IGV; 1.  
R PROSITE; PS50835; IG-LIKE; 1.  
W Immunoglobulin V region; Bence-Jones protein;  
W Pyridolone carboxylic acid.  
T DOMAIN 1 106 IG-LIKE.  
T MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
T DISULFID 22 90 BY SIMILARITY.  
T NON\_TER 111 111  
Q SEQUENCE 111 AA; 11785 MW; 925FA1BF72421BAC CRC64;  
  
Query Match 4.9%; Score 6; DB 1; Length 111;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Y 54 VSWYQQ 59  
| | | | |  
b 35 VSWYQQ 40  
  
RESULT 36  
V2H HUMAN  
D LV2H HUMAN STANDARD; PRT; 111 AA.  
C P01711;  
T 21-JUL-1986 (Rel. 01, Created)  
T 21-JUL-1986 (Rel. 01, Last sequence update)  
T 15-SEP-2003 (Rel. 42, Last annotation update)  
E IG lambda chain V-II region VII.  
S Homo sapiens (Human)  
C Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
X NCBI\_TaxID=9606;  
N [1]  
P SEQUENCE.  
X MEDLINE=71215142; PubMed=5087637;  
A Ponstingl H., Hilschmann N.;  
T "Structural rule of antibodies. Complete primary structure of a  
monoclonal immunoglobulin L chain of the lambda type, subgroup II  
(Bence Jones protein VII).";  
T Hoppe-Seyler's Z. Physiol. Chem. 352:859-877(1971).  
C -I- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.  
C -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
R PIR; A01977; L2HUVL.  
R HSSP; P01709; 2MCG.  
R GO; GO:0005576; C:extracellular; NAS.  
R GO; GO:0003823; F:antigen binding activity; NAS.  
R GO; GO:0006955; P:immune response; NAS.  
R InterPro; IPR007110; IG-LIKE.  
R InterPro; IPR003006; IG-MHC.  
R InterPro; IPR003596; IG\_V.  
R Pfam; PF00047; IG; 1.  
R SMART; SM00406; IGV; 1.  
R PROSITE; PS50835; IG-LIKE; 1.  
W Immunoglobulin V region; Bence-Jones protein.  
T DOMAIN 1 100 IG-LIKE.  
T DISULFID 22 90 BY SIMILARITY.  
T NON\_TER 111 111  
Q SEQUENCE 111 AA; 11445 MW; 3913736B3EF367E0 CRC64;  
  
Query Match 4.9%; Score 6; DB 1; Length 111;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 ADYCS 116  
| | | | |  
Db 86 ADYCS 91  
  
RESULT 37  
LV2I HUMAN  
ID LV2I HUMAN STANDARD; PRT; 111 AA.  
AC P01712;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE IG lambda chain V-II region WIN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
X NCBI\_TaxID=9606;  
N [1]  
P SEQUENCE.  
RX MEDLINE=79062503; PubMed=102365;  
RA Chen B.L., Chiu Y.-Y.H., Humphrey R.L., Poljak R.J.;  
RT "Amino acid sequence of the human myeloma lambda chain Win.";  
RL Biochim. Biophys. Acta 537:9-21(1978).  
CC -I- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.  
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A01978; L2HUVN.  
DR HSSP; P01709; 2MCG.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-LIKE.  
DR InterPro; IPR003006; IG-MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG-LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein;  
KW Pyridolone carboxylic acid.  
FT DOMAIN 1 106 IG-LIKE.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT DISULFID 22 90 BY SIMILARITY.  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 11694 MW; 8C3CB95FE721B87C CRC64;  
  
Query Match 4.9%; Score 6; DB 1; Length 111;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 54 VSWYQQ 59  
| | | | |  
Db 35 VSWYQQ 40  
  
RESULT 38  
LV2L HUMAN  
ID LV2L HUMAN STANDARD; PRT; 111 AA.  
AC P80422;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE IG gamma lambda chain V-II region DOT.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
X NCBI\_TaxID=9606;  
N [1]  
P SEQUENCE.  
RX MEDLINE=95255298; PubMed=7737190;  
RA Scoppini M., Ballotti V., Negri A., Merlini G., Garver F., Ferrini G.;  
RT "Characterization of the two unique human anti-flavin monoclonal  
immunoglobulins.";  
RL Eur. J. Biochem. 228:886-893(1995).  
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR HSSP; P01709; 2MCG.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG\_LIKE; 1.  
DR Immunoglobulin V region.  
FT DOMAIN 1 106 IG-LIKE.  
FT DISULFID 22 90 BY SIMILARITY.  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 11787 MW; F358B1EA2CD7109A CRC64;  
Query Match 4.9%; Score 6; DB 1; Length 111;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
2Y 54 VSWYQQ 59  
DB 35 VSWYQQ 40  
RESULT 39  
LV1H HUMAN  
ID LV1H HUMAN STANDARD; PRT; 112 AA.  
AC P06867;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-I region MEM.  
OS Homo sapiens (Human).  
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
CX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RA MEDLINE=85257662; PubMed=2410269;  
RA Mihaesco E., Roy J.P., Congy N., Peran-Rivat L., Mihaesco C.;  
RT "The amino acid sequence of a lambda light chain presenting abnormal  
RT physicochemical and antigenic features."  
RL Eur. J. Biochem. 150:349-357(1985).  
CC -!- MISCELLANEOUS: RESIDUES 33-36 AND SOME OF THE SEQUENCED PEPTIDES  
CC WERE POSITIONED BY HOMOLOGY.  
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE MCG+ AND KERN+  
CC MARKERS.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A25479; LIHUM.  
DR HSSP; P01703; 7FAB.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG\_LIKE; 1.  
DR Immunoglobulin V region; Monoclonal antibody;  
KW Pyridoxone carboxylic acid.  
FT DOMAIN 1 106 IG-LIKE.  
FT MOD\_RES 1 1 PYRIDOXONE CARBOXYLIC ACID.  
FT DISULFID 22 90 BY SIMILARITY.  
FT NON\_TER 112 112  
SQ SEQUENCE 112 AA; 11789 MW; 748124F079CFFB4 CRC64;  
Query Match 4.9%; Score 6; DB 1; Length 112;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 84 PDRFSA 89

Db 61 PDRFSA 66  
RESULT 40  
LV2K HUMAN  
ID LV2K HUMAN STANDARD; PRT; 112 AA.  
AC P04209;  
DT 20-MAR-1987 (Rel. 04, Created)  
DT 20-MAR-1987 (Rel. 04, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-II region NTG-84.  
OS Homo sapiens (Human).  
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
CX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RA MEDLINE=85204383; PubMed=3922791;  
RA Tonioke H., Kametani F., Hoshi A., Shinoda T., Isobe T.;  
RT "Amino acid sequence of an amyloidogenic Bence Jones protein in  
RT myeloma-associated systemic amyloidosis."  
RL FEBS Lett. 185:139-141(1985).  
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN ISOLATED FROM AN  
CC INDIVIDUAL WITH MYELOMA-ASSOCIATED SYSTEMIC AMYLOIDOSIS.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A01971; L2HUNG.  
DR HSSP; P01709; 2MCG.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG\_LIKE; 1.  
DR Immunoglobulin V region; Amyloid; Bence-Jones protein.  
KW DOMAIN 1 102 IG-LIKE.  
FT DISULFID 22 90 BY SIMILARITY.  
FT NON\_TER 112 112  
SQ SEQUENCE 112 AA; 11581 MW; 988FEF363AE1E4F3 CRC64;  
Query Match 4.9%; Score 6; DB 1; Length 112;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 54 VSWYQQ 59  
DB 35 VSWYQQ 40  
RESULT 41  
RNPA COXBU  
ID RNPA COXBU STANDARD; PRT; 121 AA.  
AC P45648;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ribonuclease P protein component (EC 3.1.26.5) (RNasep protein) (RNase  
DE P protein) (Protein C5).  
DR RNPA OR CBU1918.  
OS Coxiella burnetii.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;  
OC Coxiellaceae; Coxiella.  
CX NCBI\_TaxID=777;  
RN [1]\_taxID=777;  
RP SEQUENCE FROM N.A.  
RC STRAIN=Nine Mile Phase I / Bratislava;  
RX MEDLINE=94350801; PubMed=8071197;  
RA Suhani M., Chen S.Y., Thompson H.A., Hoover T.A., Hill A.,  
RA Williams J.C.;  
RT "Cloning and characterization of an autonomous replication sequence

from Coccidia burnettii";  
 J. Bacteriol. 176:5233-5243 (1994).  
 [2]  
 P SEQUENCE FROM N.A.  
 N STRAIN=Nine Mile phase I / RSA 493;  
 X MEDLINE=2260857; PubMed=12704232;  
 A Seshadri R., Paulsen I.T., Eisen J.A., Read T.D., Nelson K.E.,  
 A Nelson W.C., Ward N.L., Tettelin H., Davidson T.M., Beanan M.J.,  
 A DeBoy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J.,  
 A Khouri H.M., Lee K.H., Carty H.A., Scanlan D., Heinzen R.A.,  
 A Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.;  
 I "Complete genome sequence of the Q-fever pathogen, Coccidia  
 burnettii";  
 L Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460 (2003).  
 C -i- FUNCTION: RNaseP catalyzes the removal of the 5'-leader sequence  
 from pre-tRNA to produce the mature 5'-terminus. It can also  
 cleave other RNA substrates such as 4.5S RNA. The protein  
 component plays an auxiliary but essential role in vivo by binding  
 to the 5'-leader sequence and broadening the substrate specificity  
 of the ribozyme (By similarity).  
 C -i- CATALYTIC ACTIVITY: Endonucleolytic cleavage of RNA, removing 5'-  
 extra-nucleotide from tRNA precursor.  
 C -i- SUBUNIT: Consists of a catalytic RNA component (M1 or rnpB) and a  
 protein subunit (By similarity).  
 C -i- SIMILARITY: BELONGS TO THE RNPA FAMILY.  
 C -----  
 C This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 C -----  
 R EMBL: U10529; AAA56917.1; -;  
 R EMBL: AE016966; AAC91409.1; -;  
 R PIR: I40652; I40652.  
 R TIGR: CBUL198; -;  
 R HAWAP: MF\_00227; -; 1.  
 R InterPro: IPR000100; Ribonuclease\_P.  
 R Pfam: PF00825; Ribonuclease\_P; 1.  
 R ProDom: PD003629; Ribonuclease\_P; 1.  
 R TIGRfam: TIGR00189; rnpA; 1.  
 R PROSITE: PS00648; RIBONUCLEASE\_P; 1.  
 R HydroLase: Nuclease; Endonuclease; tRNA processing; RNA-binding.  
 Q SEQUENCE 121 AA; 14398 MW; E9402C3D8208FE CRC64;  
 Query Match 4.9%; Score 6; DB 1; Length 121;  
 Best Local Similarity 100.0%; Pred. No. 67;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 67 YLLYR 72  
 32 YLLYR 37

RX MEDLINE=99121216; PubMed=9920759;  
 RA Liu H.T., Wang Y.G., Zhang Y.M., Song Q.S., Di C.H., Chen G., Tang J.,  
 RA Ma D.L.;  
 RT "TFAR19, a novel apoptosis-related gene cloned from human leukemia  
 cell line TF-1, could enhance apoptosis of some tumor cells induced  
 by growth factor withdrawal";  
 RT Biochem. Biophys. Res. Commun. 254:203-210 (1999).  
 RL Biochem. Biophys. Res. Commun. 254:203-210 (1999).  
 CC -i- FUNCTION: MAY FUNCTION IN THE PROCESS OF APOPTOSIS (BY  
 CC SIMILARITY).  
 CC -i- TISSUE SPECIFICITY: Widely expressed.  
 CC -i- SIMILARITY: BELONGS TO THE PDCD5 FAMILY.  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: AF161074; AAD45607.1; -;  
 DR HSSP: O27652; 1E1J.  
 DR MGD: MGI:1913538; Pcd5.  
 DR InterPro: IPR002836; TFAR19-related.  
 DR Pfam: PF01984; dsDNA bind; 1.  
 DR ProDom: PD008148; TFAR19-related; 1.  
 KW Apoptosis.  
 SQ SEQUENCE 126 AA; 14275 MW; 05796820CD5C780B CRC64;  
 Query Match 4.9%; Score 6; DB 1; Length 126;  
 Best Local Similarity 100.0%; Pred. No. 69;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 108 EDDADY 113  
 121 EDDADY 126

RESULT 43  
 KV3K HUMAN  
 ID KV3K HUMAN STANDARD; PRT; 128 AA.  
 AC P06311;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-III region IARC/BL41 precursor.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86041852; PubMed=2997711;  
 RA Klobbeck H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;  
 RT "Human immunoglobulin kappa light chain genes of subgroups II and  
 III";  
 RL Nucleic Acids Res. 13:6499-6513 (1985).  
 CC -----  
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 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: Z00021; CAA77316.1; -;  
 DR PIR: A01899; K3HU41.  
 DR HSSP: P01607; 1REI.  
 DR GO: GO:0005576; C:extracellular; NAS.  
 DR GO: GO:0003823; F:antigen binding activity; NAS.  
 DR GO: GO:0006955; P:immune response; NAS.  
 DR InterPro: IPR007110; Ig-like.

DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IgV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20  
FT CHAIN 21 128 IG KAPPA CHAIN V-III REGION IARC/BL41.  
FT DOMAIN 21 43 FRAMEWORK-1.  
FT DOMAIN 21 43 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 44 54 FRAMEWORK-2.  
FT DOMAIN 55 69 FRAMEWORK-2.  
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 77 108 FRAMEWORK-3.  
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 118 128 JK1 SEGMENT.  
FT DISULFID 43 108 BY SIMILARITY.  
FT NON TER 128 128  
SQ SEQUENCE 128 AA; 14070 MW; CC8957FOFE3B9012 CRC64;

Query Match 4.9%; Score 6; DB 1; Length 128;

Best Local Similarity 100.0%; Pred. No. 70; Mismatches 0; Indels 0; Gaps 0;

2Y 83 IPDRFS 88  
Db 78 IPDRFS 83

## RESULT 44

KV3L HUMAN  
ID KV3L HUMAN STANDARD; PRT; 129 AA.  
AC P18135;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-III, region HAH precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88171307; PubMed=3127527;  
RA Kipps T.J.; Tomhave E.; Chen P.P.; Carson D.A.;  
RT "Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";  
RT J. Exp. Med. 167:840-852(1988).  
RL -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M  
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC  
CC LEUKEMIA.  
DR PIR; P10022; K3HUHA.  
DR HSP; P80362; 1WT.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IgV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20  
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.  
FT DOMAIN 21 43 FRAMEWORK-1.  
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 56 70 FRAMEWORK-2.  
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 78 109 FRAMEWORK-3.  
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 119 129 JK1 SEGMENT.  
FT DISULFID 43 109 BY SIMILARITY.

FT NON TER 129 129  
SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;  
Query Match 4.9%; Score 6; DB 1; Length 129;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88  
Db 79 IPDRFS 84

## RESULT 45

KV3M HUMAN  
ID KV3M HUMAN STANDARD; PRT; 129 AA.  
AC P18136;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG kappa chain V-III region HIC precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88171307; PubMed=3127527;  
RA Kipps T.J.; Tomhave E.; Chen P.P.; Carson D.A.;  
RT "Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";  
RT J. Exp. Med. 167:840-852(1988).  
RL -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M  
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC  
CC LEUKEMIA.  
DR PIR; P10021; K3HUHI.  
DR HSP; P80362; 1WT.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IgV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20  
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.  
FT DOMAIN 21 43 FRAMEWORK-1.  
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 56 70 FRAMEWORK-2.  
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 78 109 FRAMEWORK-3.  
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 119 129 JK1 SEGMENT.  
FT DISULFID 43 109 BY SIMILARITY.  
FT NON TER 129 129  
SQ SEQUENCE 129 AA; 14070 MW; 7395528A2BB74D6 CRC64;

Query Match 4.9%; Score 6; DB 1; Length 129;

Best Local Similarity 100.0%; Pred. No. 70; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88  
Db 79 IPDRFS 84

## RESULT 46

LVIG HUMAN  
ID LVIG HUMAN STANDARD; PRT; 130 AA.  
AC P06316;

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Query Match          4.9%; Score 6; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

fy      54 VSWYQQ 59
      |||||
ib      53 VSWYQQ 58

RESULT 47
KV5B_MOUSE
ID:KV5B_MOUSE STANDARD; PRT; 136 AA.
AC P01634;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
IG kappa chain V-V region MOPC 21 precursor.
DE Mus musculus (Mouse).
DS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
DC NCBI_TaxID=10090;
XX [1]
RN SEQUENCE FROM N.A.
RP
RP MEDLINE=82059477; PubMed=6170937;
XX Hamlyn P.H., Galt M.J., Milstein C.;
RT "Complete sequence of an immunoglobulin mRNA using specific priming
RT and the dideoxynucleotide method of RNA sequencing.";
RL Nucleic Acids Res. 9:4485-4494 (1981).

```

```

RESULT 48
VPRL_MOUSE
ID VPRL_MOUSE STANDARD; PRT; 142 AA.
AC P13372;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Immunoglobulin iota chain precursor (VPreB1 protein).
OS VPREB1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6 X DBA/2J;
RC MEDLINE=88023315; PubMed=3117530;
RX Kudo A., Melchers F.;
RA "A second gene, VpreB in the lambda 5 locus of the mouse, which
RT appears to be selectively expressed in pre-B lymphocytes.";
RT EMBO J. 6:12267-2272(1987).
RL -1- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR
CC COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS. THIS
CC COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE EARLY
CC STEPS OF B-CELL DIFFERENTIATION.
CC -1- TISSUE SPECIFICITY: ONLY EXPRESSED BY PRE-B-CELLS.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

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-----  
EMBL; X05556; CAA29071.1; -  
EMBL; X05557; CAA29072.1; -  
PIR; A28344; A28344.  
HSSP; P01607; IREI.  
MGD; MGI:989336; Vpreb1.  
GO; GO:0005886; C:plasma membrane; IPI.  
GO; GO:0004872; P:receptor activity; IPI.  
GO; GO:0030097; P:hemopectasis; IMP.  
GO; GO:0006955; P:immune response; IPI.  
InterPro; IPR007110; Ig-like.  
InterPro; IPR003006; Ig\_MHC.  
InterPro; IPR003596; Ig\_V.  
PFam; PF00047; Ig; 1.  
SMART; SM00406; IGV; 1.  
PROSITE; PS00835; IG LIKE; 1.  
Immunoglobulin domain; B-cell; Signal.  
SIGNAL 1 19  
CHAIN 20 142  
DOMAIN 20 41  
DOMAIN 42 56  
DOMAIN 57 70  
DOMAIN 71 81  
DOMAIN 82 115  
DOMAIN 41 115  
DISULFID 41 115  
SEQUENCE 142 AA; 16125 MW; 2E18BF963A0F448C CRC64;  
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Query Match 4.9%; Score 6; DB 1; Length 142;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
-----  
2Y 38 LSCTLS 43  
39 LSCTLS 44  
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RESULT 49  
VPR2 MOUSE  
ID VPR2 MOUSE STANDARD; PRT; 142 AA.  
AC P13373;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Immunoglobulin omega chain precursor (VpreB2 protein).  
GN VPREB2  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6 X DBA/2J;  
RX MEDLINE=88029315; PubMed=3117530;  
RA Kudo A., Melchers F.  
RT "A second gene, VpreB in the lambda 5 locus of the mouse, which appears to be selectively expressed in pre-B lymphocytes."  
RL EMBO J. 6:2267-2272(1987).  
CC -!- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS. THIS COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE EARLY STEPS OF B-CELL DIFFERENTIATION.  
CC -!- TISSUE SPECIFICITY: ONLY EXPRESSED BY PRE-B-CELLS.  
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
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-----  
EMBL; X05563; CAA29077.1; -  
PIR; B28344; B28344.  
HSSP; P01607; IREI.  
MGD; MGI:98937; Vpreb2.  
InterPro; IPR007110; Ig-like.  
InterPro; IPR003006; Ig\_MHC.  
InterPro; IPR003596; Ig\_V.  
PFam; PF00047; Ig; 1.  
SMART; SM00406; IGV; 1.  
PROSITE; PS00835; IG LIKE; 1.  
Immunoglobulin domain; B-cell; Signal.  
SIGNAL 1 19  
CHAIN 20 142  
DOMAIN 20 41  
DOMAIN 42 56  
DOMAIN 57 70  
DOMAIN 71 81  
DOMAIN 82 115  
DOMAIN 41 115  
DISULFID 41 115  
SEQUENCE 142 AA; 16052 MW; 7EA7128A4E63D920 CRC64;  
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Query Match 4.9%; Score 6; DB 1; Length 142;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 38 LSCTLS 43  
39 LSCTLS 44  
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RESULT 50  
RST1 AVESA  
ID RST1 AVESA STANDARD; PRT; 169 AA.  
AC PS0695;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Thaumatin-like pathogenesis-related protein 1 precursor.  
GN RASTL-1.  
OS Avena sativa (Oat).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Avenaeae; Avena.  
OX NCBI\_TaxID=4498;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Rodney;  
RX MEDLINE=96303536; PubMed=8755626;  
RA Lin K.C., Bushnell W.R., Szabo L.J., Smith A.G.;  
RT "Isolation and expression of a host response gene family encoding thaumatin-like proteins in incompatible oat-stem rust fungus interactions."  
RL Mol. Plant Microbe Interact. 9:511-522(1996).  
CC -!- FUNCTION: ASSOCIATED WITH RESISTANCE AGAINST STEM RUST FUNGI.  
CC -!- SIMILARITY: Belongs to the thaumatin family.  
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-----  
EMBL; L39774; AAB09224.1; -  
HSSP; P33679; 1DU5.  
-----

R InterPro: IPR001938; Thaumatin.  
R Pfam: PF00314; Thaumatin; 1.  
R PRINTS; PR00347; THAUMATIN.  
R ProDom; PD001321; Thaumatin; 1.  
R SMART; SM00205; THN; 1.  
R PROSITE; PS00316; THAUMATIN; 1.  
W Plant defense; Pathogenesis-related protein; Fungicide;  
W Multigene family; Signal.  
T SIGNAL 1 21  
T CHAIN 22 169  
T POTENTIAL.  
T THAUMATIN-LIKE PATHOGENESIS-RELATED  
T PROTEIN 1.  
Q SEQUENCE 169 AA; 17353 MW; 7377CA770CC2B09D CRC64;  
Query Match 4.9%; Score 6; DB 1; Length 169;  
Best Local Similarity 100.0%; Pred. No. 88;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Y 38 LSCITLS 43  
b 90 LSCITLS 95  
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RESULT 51  
RST4\_AVEA  
ID RST4\_AVEA STANDARD; PRT; 169 AA.  
AC PS0696;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Thaumatin-like pathogenesis-related protein 2 precursor.  
GN RASTL-2.  
OS Avena sativa (Oat).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Aveneae; Avena.  
OC NCBI\_TaxID=4498;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Rodney;  
RX MEDLINE=96303536; PubMed=8755626;  
RA Lin K.C., Bushnell W.R., Szabo L.J., Smith A.G.;  
RT "Isolation and expression of a host response gene family encoding  
thumatin-like proteins in incompatible oat-stem rust fungus  
interactions.";  
RL Mol. Plant Microbe Interact. 9:511-522(1996).  
CC -!- FUNCTION: ASSOCIATED WITH RESISTANCE AGAINST STEM RUST FUNGI.  
CC -!- SIMILARITY: Belongs to the thaumatin family.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
EMBL; L39775; AB09225.1; -  
DR HSPSP; P33679; LDU5  
DR InterPro: IPR001938; Thaumatin.  
DR Pfam; PF00314; thaumatin; 1.  
DR PRINTS; PR00347; THAUMATIN.  
DR ProDom; PD001321; Thaumatin; 1.  
DR SMART; SM00205; THN; 1.  
DR PROSITE; PS00316; THAUMATIN; 1.  
KW Plant defense; Pathogenesis-related protein; Fungicide;  
KW Multigene family; Signal.  
FT SIGNAL 1 21  
FT CHAIN 22 169  
FT POTENTIAL.  
FT THAUMATIN-LIKE PATHOGENESIS-RELATED  
FT PROTEIN 1.  
SQ SEQUENCE 169 AA; 17403 MW; 0030CE363CCBE79 CRC64;  
Query Match 4.9%; Score 6; DB 1; Length 169;  
Best Local Similarity 100.0%; Pred. No. 88;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Y 38 LSCITLS 43  
b 90 LSCITLS 95  
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RESULT 53  
RST4\_AVEA  
ID RST4\_AVEA STANDARD; PRT; 169 AA.  
AC PS0696;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Thaumatin-like pathogenesis-related protein 4 precursor.

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 38 LSCITLS 43  
DB 90 LSCITLS 95  
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RESULT 52  
RST3\_AVEA  
ID RST3\_AVEA STANDARD; PRT; 169 AA.  
AC PS0697;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Thaumatin-like pathogenesis-related protein 3 precursor.  
GN RASTL-3.  
OS Avena sativa (Oat).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Aveneae; Avena.  
OC NCBI\_TaxID=4498;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Rodney;  
RX MEDLINE=96303536; PubMed=8755626;  
RA Lin K.C., Bushnell W.R., Szabo L.J., Smith A.G.;  
RT "Isolation and expression of a host response gene family encoding  
thumatin-like proteins in incompatible oat-stem rust fungus  
interactions.";  
RL Mol. Plant Microbe Interact. 9:511-522(1996).  
CC -!- FUNCTION: ASSOCIATED WITH RESISTANCE AGAINST STEM RUST FUNGI.  
CC -!- SIMILARITY: Belongs to the thaumatin family.  
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-----  
EMBL; L39776; AB09226.1; -  
DR HSPSP; P33679; LDU5  
DR InterPro: IPR001938; Thaumatin.  
DR Pfam; PF00314; thaumatin; 1.  
DR PRINTS; PR00347; THAUMATIN.  
DR ProDom; PD001321; Thaumatin; 1.  
DR SMART; SM00205; THN; 1.  
DR PROSITE; PS00316; THAUMATIN; 1.  
KW Plant defense; Pathogenesis-related protein; Fungicide;  
KW Multigene family; Signal.  
FT SIGNAL 1 21  
FT CHAIN 22 169  
FT POTENTIAL.  
FT THAUMATIN-LIKE PATHOGENESIS-RELATED  
FT PROTEIN 3.  
SQ SEQUENCE 169 AA; 17328 MW; 647CA7D5D54108AF CRC64;  
Query Match 4.9%; Score 6; DB 1; Length 169;  
Best Local Similarity 100.0%; Pred. No. 88;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 38 LSCITLS 43  
DB 90 LSCITLS 95  
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RESULT 53  
RST4\_AVEA  
ID RST4\_AVEA STANDARD; PRT; 169 AA.  
AC PS0696;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Thaumatin-like pathogenesis-related protein 4 precursor.





A Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,  
A Leathem S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,  
A Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;  
T "Genome sequence of *Yersinia pestis*, the causative agent of plague";  
L Nature 413:523-527(2001).  
N [2]  
P SEQUENCE FROM N.A.  
X STRAIN=KIMS / Biovar Mediaevalis;  
X MEDLINE=22137863; PubMed=12142430;  
C Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,  
A Peng N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,  
A Retherston J.D., Lindler L.B., Brubaker R.R., Plano G.V.,  
A Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,  
A Perry R.D.;  
A "Genome sequence of *Yersinia pestis* KIM";  
T J. Bacteriol. 184:4601-4611(2002).  
L [-] FUNCTION: Protease subunit of a proteasome-like degradation  
C complex (By similarity).  
C [-] SUBUNIT: Interacts with hslU (By similarity).  
C [-] SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
C [-] SIMILARITY: BELONGS TO PEPTIDASE FAMILY T1B. HSLV SUBFAMILY.  
C  
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C  
R EMBL; AJ414141; CAC8971.1; -;  
R EMBL; AE013628; AAM83887.1; -;  
R PIR; A10013; A10013.  
R MEROPS: T01.006; -;  
R HAMAP; MF\_00248; -; 1  
R InterPro; IPR001353; Protease\_protease.  
R Pfam; PF00227; protease; 1.  
R Hydrolase; Protease; Complete  
W INIT MET 0 BY SIMILARITY.  
T ACT SITE 1 1 BY SIMILARITY.  
T ACT SITE 1 1 BY SIMILARITY.  
Q SEQUENCE 173 AA; 18763 MW; 4F6DD964BDA75F2C CRC64;  
  
Query Match 4.9%; Score 6; DB 1; Length 173;  
Best Local Similarity 100.0%; Pred. No. 90;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Y 105 VQPEDD 110  
| | | | |  
b 113 VQPEDD 118  
  
RESULT 56  
NSC PHODV  
ID \_VNSC PHODV STANDARD; PRT; 174 AA.  
AC P35940;  
VT 01-JUN-1994 (Rel. 29, Created)  
YT 01-JUN-1994 (Rel. 29, Last sequence update)  
YT 01-OCT-1994 (Rel. 30, Last annotation update)  
DE Nonstructural protein C.  
EN P/V/C.  
DS Phocine distemper virus (PDV).  
DC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
DC Paramyxoviridae; Paramyxovirinae; Morbillivirus.  
DX NCBI\_TaxID=11240;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=U1ster/88;  
RC MEDLINE=92300361; PubMed=1535099;  
RA Curran M.D., Rima B.K.;  
RT "The genes encoding the phospho- and matrix proteins of phocine  
RT distemper virus";  
RL J. Gen. Virol. 73:1567-1591(1992).  
RN [2]

RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate DK88-4A;  
RX MEDLINE=92341068; PubMed=1634877;  
RA Blixenkron-Moeller M., Sharma B., Varsanyi T., Hu A., Norrby E.,  
RA Koevamees J.;  
RT "Sequence analysis of the genes encoding the nucleocapsid protein and  
RT phosphoprotein (P) of phocid distemper virus, and editing of the P  
RT gene transcript";  
RL J. Gen. Virol. 73:885-893(1992).  
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CC  
DR EMBL; D10371; BAA01204.1; -;  
DR EMBL; X75960; CAA53574.1; -;  
DR PIR; JQ1564;  
DR InterPro; IPR003875; Paramyxovir\_NSC.  
DR Pfam; PF02725; Paramyxo\_NS\_C; 1.  
RW Nonstructural protein.  
KW CONFLICT 26 26 A -> V (IN REF. 2).  
SQ SEQUENCE 174 AA; 20321 MW; A25FF482E94C3A43 CRC64;  
  
Query Match 4.9%; Score 6; DB 1; Length 174;  
Best Local Similarity 100.0%; Pred. No. 90;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 54 VSWYQQ 59  
| | | | |  
Db 121 VSWYQQ 126  
  
RESULT 57  
TLP\_ORYSA  
ID \_TLP\_ORYSA STANDARD; PRT; 177 AA.  
AC P31110;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Thaumatin-like protein precursor.  
OS Oryza sativa (Rice)  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Nohrin;  
RX MEDLINE=94143469; PubMed=8310049;  
RA Reimann C., Dudler R.;  
RT "cDNA cloning and sequence analysis of a pathogen-induced  
RT thaumatin-like protein from rice (*Oryza sativa*)";  
RL Plant Physiol. 101:1113-1114(1993).  
CC [-] SUBCELLULAR LOCATION: Secreted (Potential).  
CC [-] INDUCTION: By pathogen infection.  
CC [-] SIMILARITY: Belongs to the thaumatin family.  
CC  
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CC  
DR EMBL; X68197; CAA48278.1; -;  
DR PIR; S25551; S25551.  
DR HSSP; P33679; 1DU5.  
DR Gramene; P31110; -;

JR InterPro; IPR001938; Thaumatin.  
 JR Pfam; PF00314; Thaumatin; 1.  
 JR PRINTS; PF00347; THAUMATIN.  
 JR ProDom; PD001321; Thaumatin; 1.  
 JR SMART; SM00205; TEN; 1.  
 JR PROSITE; PS00316; THAUMATIN; 1.  
 KW Signal. 1 26 POTENTIAL.  
 KW SIGNAL. 27 177 THAUMATIN-LIKE PROTEIN.  
 FT CHAIN  
 3Q SEQUENCE 177 AA; 17992 MW; 7B9BC9A07AA9FF CRC64;

Query Match 4.9%; Score 6; DB 1; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 92;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 38 LSCTLS 43  
 DB 96 LSCTLS 101

## RESULT 58

CYCOC-BUCAP  
 ID CYCOC-BUCAP STANDARD; PRT; 189 AA.  
 AC Q8K955;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome O ubiquinol oxidase subunit III (EC 1.10.3.-).  
 GN CYC OC BUSG454.  
 OS Buchnera aphidicola (subsp. Schizaphis graminum).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Buchnera.  
 OX NCBI\_TaxID=98794;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22084549; PubMed=12089438;  
 RA Tamas I., Klason L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,  
 RA Wernegreen J.J., Sandstrom J.P., Moran N.A., Anderson S.G.E.;  
 RT "50 million years of genomic stasis in endosymbiotic bacteria."  
 RL Science 296:2376-2379 (2002).  
 CC -!- FUNCTION: Cytochrome O terminal oxidase complex is the component  
 CC of the aerobic respiratory chain that predominates when cells are  
 CC grown at high aeration (By similarity).  
 CC -!- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 3 family.  
 CC  
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 CC  
 CC EMBL; AB014121; AA67997.1; -  
 CC InterPro; IPR000298; CytC\_oxdse\_III.  
 CC Pfam; PF00510; COX3; 1.  
 CC ProDom; PD000382; CytC\_oxdse\_III; 1.  
 CC PROSITE; PS02533; COX3; 1.  
 CC Oxidoreductase; Electron transport; Transmembrane; Complete proteome.  
 FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 11 31 POTENTIAL.  
 FT DOMAIN 32 52 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 53 73 POTENTIAL.  
 FT DOMAIN 74 81 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 82 102 POTENTIAL.  
 FT DOMAIN 103 122 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 123 143 POTENTIAL.  
 FT DOMAIN 144 161 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 162 182 POTENTIAL.  
 FT DOMAIN 183 189 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 189 AA; 22162 MW; 1513BB6C59CF558 CRC64;  
 3Q SEQUENCE

Query Match 4.9%; Score 6; DB 1; Length 189;  
 Best Local Similarity 100.0%; Pred. No. 97;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 6 LSFLLM 11  
 DB 95 LSFLLM 100

## RESULT 59

APOM MOUSE  
 ID APOM MOUSE STANDARD; PRT; 190 AA.  
 AC Q9Z1R3;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Apolipoprotein M (Apo-M) (Apom) (NG20).  
 GN APOM.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Xu N., Dahlbaeck B.;  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129;  
 RA Rowen L., Qin S., Madan A., Abbasi N., James R., Dickhoff R.,  
 RA Shaffer T., Ratcliffe A., Loretz C., Laaky S., Hood L.;  
 RT "Sequence of the mouse major histocompatibility class III region."  
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Embryo;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojbori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
 RA Schirral L., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Kamiya M., Lee N.H.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mommaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690 (2001).  
 CC -!- FUNCTION: Probably involved in lipid transport.  
 CC -!- SUBCELLULAR LOCATION: Secreted (Potential).  
 CC -!- SIMILARITY: BELONGS TO THE LIPOCALIN FAMILY. Highly divergent.

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 -----

EMBL; AF207820; AAP23407.1; -  
 EMBL; AF109719; AAC82478.1; -

EMBL; AK004530; BAB23349.1; -  
MGD; MGI:1930124; Apom.  
Transport; Lipid transport; HDL; Signal; Lipocalin.  
SIGNAL 1 722 NOT CLEAVED (POTENTIAL).  
DISULFID 23 169 POTENTIAL.  
DISULFID 95 185 POTENTIAL.  
DISULFID 130 159 POTENTIAL.  
SEQUENCE 190 AA; 21273 MW; 3D5614DADF277C4 CRC64;  
Query Match 4.9%; Score 6; DB 1; Length 190;  
Best Local Similarity 100.0%; Pred. No. 97;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
61 AGSAPR 66  
75 AGSAPR 80  
RESULT 60  
POM RAT  
D AFOM RAT STANDARD; PRT; 190 AA.  
C FL463C; Q9QX19;  
I 01-AUG-1990 (Rel. 15, Created)  
T 16-OCT-2001 (Rel. 40, Last sequence update)  
E 28-FEB-2003 (Rel. 41, Last annotation update)  
A Apolipoprotein M precursor (Apo-M) (Apom) (protein Pxl).  
P AFOM  
S Rattus norvegicus (Rat).  
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
X NCBI\_TaxID=10116;  
N SEQUENCE FROM N.A.  
P STRAIN=Sprague-Dawley; TISSUE=Liver;  
A Xu N.; Dahlbaeck B.;  
L Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
N [1]  
P SEQUENCE OF 18-33.  
X MEDLINE=90122905; PubMed=2297521;  
A Blatter M.-C., James R.W., Borghini I., Martin B.M.,  
Hochstrasser A.-C., Pomatta D.;  
T "A novel high-density lipoprotein particle and associated protein in  
rat plasma";  
L Biochim. Biophys. Acta 1042:19-27(1990).  
C -1- FUNCTION: Probably involved in lipid transport.  
C -1- SUBCELLULAR LOCATION: Secreted. Associated with HDL.  
C -1- TISSUE SPECIFICITY: Plasma protein.  
C -1- SIMILARITY: BELONGS TO THE LIPOCALIN FAMILY. Highly divergent.  
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C  
R EMBL; AF207821; AAF23408.1; -  
W Transport; Lipid transport; HDL; Signal; Lipocalin.  
T SIGNAL 1 17  
T CHAIN 18 190 APOLIPOPROTEIN M.  
T DISULFID 23 169 POTENTIAL.  
T DISULFID 95 185 POTENTIAL.  
T DISULFID 130 159 POTENTIAL.  
T CONFLICT 30 30 M -> T (IN REF. 2).  
Q SEQUENCE 190 AA; 21512 MW; E507BD6C202CBBAF CRC64;  
Query Match 4.9%; Score 6; DB 1; Length 190;  
Best Local Similarity 100.0%; Pred. No. 97;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
61 AGSAPR 66  
75 AGSAPR 80

Db 75 AGSAPR 80  
RESULT 61  
I18B MOUSE  
ID I18B MOUSE STANDARD; PRT; 191 AA.  
AC Q9Z0M9; Q9CUH2; Q9Z0N0;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Interleukin-18 binding protein precursor (IL-18BP) (Interferon gamma  
inducing factor binding protein).  
GN IL18BP OR IGIFBP.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 27-31; 51-54; 92-137;  
RP 155-158 AND 162-167.  
RC STRAIN=CD-1; TISSUE=Serum;  
RX MEDLINE=99192308; PubMed=10094485;  
RA Aizawa Y., Akita K., Tanai M., Korigoe K., Mori T., Nishida Y.,  
Ushio S., Nakada Y., Tanimoto T., Ikegami H., Ikeda M., Kurimoto M.;  
RT "Cloning and expression of interleukin-18 binding protein.";  
RL FEBS Lett. 445:338-342(1999).  
RN [2]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE=99146382; PubMed=10023777;  
RA Novick D., Kim S.H., Pantuzzi G., Reznikov L.L., Dinarello C.A.,  
Rubinstein M.;  
RT "Interleukin-18 binding protein: a novel modulator of the Th1 cytokine  
response.";  
RL Immunity 10:127-136(1999).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Skin;  
RX MEDLINE=99263157; PubMed=10329540;  
RA Xiang Y., Moss B.;  
RT "Identification of human and mouse homologs of the MCS11-53L-54L  
family of secreted glycoproteins encoded by the Molluscum contagiosum  
poxvirus.";  
RL Virology 257:297-302(1999).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC STRAIN=C57BL/6J; TISSUE=Embryo, Small intestine, and Tongue;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamahaka I.,  
Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,  
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Gasavant T.,  
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pescio G., Quackenbush J.,  
Schrml L.M., Staub P., Suzuki R., Tomita M., Wagner L., Washio T.,  
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
Blake J., Boffelli D., Bojunga N., Carninci P., de Bernaldo M.F.,  
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
Gustincich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
Wyehaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,  
Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

```
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
A Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S.N., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
A Whiting M., Madan A., Young A.C., Shavchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
A Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalhus D.E.,
A Schnerich A., Schein J.E., Jones S.J.M., Marra M.A.,
T human and mouse cDNA sequences."
T "Generation and initial analysis of more than 15,000 full-length
L Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
L -!- FUNCTION: Binds to IL-18 and inhibits its activity. Functions as
C an inhibitor of the early Th1 cytokine response (By similarity).
C -!- SUBCELLULAR LOCATION: Secreted (Potential).
C -!- ALTERNATIVE PRODUCTS:
C Event=Alternative splicing; Named isoforms=2;
C Names=1;
C IsoId=Q9Z0M9-1; Sequences=Displayed;
C Names=2;
C IsoId=Q9Z0M9-2; Sequences=VSP 002517;
C -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
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C -----
C EMBL; AB019505; BAA76375.1; ALT_INIT.
C EMBL; AF110802; AAD17193.1; -.
C EMBL; AF110803; AAD17194.1; -.
C EMBL; AF122907; AAD41052.1; ALT_INIT.
C EMBL; AK009721; BAB26462.1; ALT_INIT.
C EMBL; AK003370; BAB22744.1; ALT_INIT.
C EMBL; AK008452; BAB25677.1; ALT_INIT.
C EMBL; AK009877; BAB26558.1; -.
C EMBL; BC018332; AAH18332.1; ALT_INIT.
C MGD; MG1:1333800; 1118bp.
C GO; GO:0042007; F:interleukin-18 binding activity; ISS.
C GO; GO:0006955; P:immune response; ISS.
C InterPro; IPR007110; Ig-like.
C InterPro; IPR003006; Ig_Mc.
C Pfam; PF00047; Ig; 1.
C PROSITE; PS00835; IG-LIKE; 1.
C Immunoglobulin domain; Glycoprotein; Signal; Alternative splicing.
C SIGNAL 1 26
C CHAIN 27 191 INTERLEUKIN-18 BINDING PROTEIN.
C DOMAIN 58 159 IG-LIKE C2-TYPE.
C DISULFID 79 143 BY SIMILARITY.
C CARBOHYD 72 72 N-LINKED (GLNAC. . .) (POTENTIAL).
C CARBOHYD 96 96 N-LINKED (GLNAC. . .) (POTENTIAL).
C CARBOHYD 118 118 N-LINKED (GLNAC. . .) (POTENTIAL).
C CARBOHYD 140 140 N-LINKED (GLNAC. . .) (POTENTIAL).
C VARSPLIC 163 191 DGLTADPPSQEITLSSHSFVSRGAGPVA -> VRLNKEGI
C QGWERYLQKGLAPFPQVPS (in isoform 2).
C /FTID=VSP 002517.
C SEQUENCE 191 AA; 21035 MW; B2F306A3051165EB CRC64;
Query Match 4.9%; Score 6; DB 1; Length 191;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 32 PQQVAQ 37
DB 148 PQQVAQ 153
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RESULT 62
VG66_BPMD2
ID VG66_BPMD2 STANDARD; PRT; 199 AA.
AC O64258;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Gene 66 protein (GP66).
GN 66.
OS Mycobacteriophage D29.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=28369;
RN [1]_TaxID=28369;
RP SEQUENCE FROM N.A.
RX MEDLINE=98300335; PubMed=9636706;
RA Ford M.E., Sarkis G.J., Belanger A.E., Hendrix R.W., Hatfull G.F.;
RT "Genome structure of mycobacteriophage D29: implications for phage
RT evolution."
RL J. Mol. Biol. 279:143-164 (1998).
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CC -----
CC EMBL; AF022214; AAC18507.1; -.
CC FIR; A72808; A72808.
CC InterPro; IPR004843; M-peptidase.
CC Pfam; PF00149; Metallophos; 1.
CC SEQUENCE 199 AA; 22878 MW; 63E20BFD2C5BCAD5 CRC64;
Query Match 4.9%; Score 6; DB 1; Length 199;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 AQLDAL 28
DB 59 AQLDAL 64
RESULT 63
URK_DEIRA
ID URK_DEIRA STANDARD; PRT; 210 AA.
AC Q9RXZ5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Uridine kinase (EC 2.7.1.48) (Uridine monophosphokinase) (Cytidine
DE monophosphokinase).
DE UNK OR DR0159.
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=RI / ATCC 13939 / DSM 20539 / NCIB 9279;
RA MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vanatavean J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1."
RL Science 286:1571-1577 (1999).
```

C -1- CATALYTIC ACTIVITY: ATP + uridine = ADP + UMP.  
C -1- CATALYTIC ACTIVITY: ATP + cytidine = ADP + CMP.  
C -1- PATHWAY: Pyrimidine Salvage pathway.  
C -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
C -1- SIMILARITY: BELONGS TO THE URIDINE KINASE FAMILY.  
C  
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C  
R EMBL; AE001878; AAP09747.1; -.  
R PIR; E75553; E75553.  
R TIGR; DR0159; -.  
R HAMAP; MF 00551; -; 1.  
R InterPro; IPR006082; PRK.  
R InterPro; IPR006083; PRK URK.  
R InterPro; IPR000764; Uridine\_kin.  
R Pfam; PF00485; PRK; 1.  
R PRINTS; PR00478; PHRBLKINASE.  
R PRINTS; PR00988; URIDINKINASE.  
R TIGRFAMs; TIGR00235; udk; 1.  
M Transferase; Kinase; ATP-binding; Complete proteome.  
T NP BIND 14 ATP (POTENTIAL).  
Q SEQUENCE 210 AA; 23660 MW; 1226B9CAD6805882 CRC64;  
  
Query Match 4.9%; Score 6; DB 1; Length 210;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Y 24 QLDALL 29  
b 75 QLDALL 80  
  
RESULT 64  
RPF SYN3 D TRPE SYN3 STANDARD; PRT; 218 AA.  
C P7435;  
T 01-NOV-1997 (Rel. 35, Created)  
T 01-NOV-1997 (Rel. 35, Last sequence update)  
T 28-FEB-2003 (Rel. 41, Last annotation update)  
E N-(5'-phosphoribosyl)anthranilate isomerase (EC 5.3.1.24) (PRAI).  
N TRPF OR SLL0356.  
S Synechocystis sp. (strain PCC 6803).  
X Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
X NCBI\_TaxID=1148;  
X [1]  
X SEQUENCE FROM N.A.  
X MEDLINE=97061201; PubMed=8905231;  
X Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,  
X Miyajima N., Hirosewa M., Sugita M., Sasamoto S., Kimura T.,  
X Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,  
X Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,  
X Yamada M., Yasuda M., Tabata S.;  
T "Sequence analysis of the genome of the unicellular cyanobacterium  
T Synechocystis sp. strain PCC6803. II. Sequence determination of the  
T entire genome and assignment of potential protein-coding regions.";  
L DNA Res. 3:109-136(1996).  
C -1- CATALYTIC ACTIVITY: N-(5-phospho-beta-D-ribose)-anthranilate = 1-  
C (2-carboxyphenylamino)-1-deoxy-D-ribose 5-phosphate.  
C -1- PATHWAY: Tryptophan biosynthesis; third step.  
C -1- SIMILARITY: BELONGS TO THE TRPF FAMILY.  
C  
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C  
R EMBL; D90915; BAA18536.1; -.  
R PIR; S76407; S76407.  
R HSSP; Q56320; LNSJ.  
R HAMAP; MF 00135; -; 1.  
R InterPro; IPR001240; PRAI.  
R Pfam; PF00697; PRAI; 1.  
KW Isomerase; Tryptophan biosynthesis; Complete proteome.  
SQ SEQUENCE 218 AA; 23881 MW; 37D6035030G55A4F CRC64;  
  
Query Match 4.9%; Score 6; DB 1; Length 218;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 23 AQLDAL 28  
DB 208 AQLDAL 213  
  
RESULT 65  
GLNA\_DUNSA STANDARD; PRT; 234 AA.  
ID GLNA\_DUNSA  
AC F11600;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase)  
DE (Fragment)  
OS Dunaliella salina.  
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
OC Dunaliellaceae; Dunaliella.  
OX NCBI\_TaxID=3046;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Long Z., Nelson N.;  
RL Submitted (MAY-1989) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate +  
CC L-glutamine.  
CC -1- SUBUNIT: Homooctamer.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
C  
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C or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
C  
R EMBL; X15280; CAA33353.1; -.  
R PIR; S04888; AJDEQ.  
R InterPro; IPR001691; GLN\_synth.  
R Pfam; PF00120; Gln-synt; 1.  
R PROSITE; PS00180; GLNA\_1; PARTIAL.  
R PROSITE; PS00181; GLNA\_ATP; 1.  
KW Ligase.  
FT NON TER 1  
SQ SEQUENCE 234 AA; 26224 MW; D5EB25319131DDF6 CRC64;  
  
Query Match 4.9%; Score 6; DB 1; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 113 YICSVG 118  
DB 38 YICSVG 43  
  
RESULT 66  
YMF\_ECOLI STANDARD; PRT; 234 AA.  
ID YMF\_ECOLI  
AC P75968;

CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).  
CC  
R EMBL; D90915; BAA18536.1; -.  
R PIR; S76407; S76407.  
R HSSP; Q56320; LNSJ.  
R HAMAP; MF 00135; -; 1.  
R InterPro; IPR001240; PRAI.  
R Pfam; PF00697; PRAI; 1.  
KW Isomerase; Tryptophan biosynthesis; Complete proteome.  
SQ SEQUENCE 218 AA; 23881 MW; 37D6035030G55A4F CRC64;  
  
Query Match 4.9%; Score 6; DB 1; Length 218;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 23 AQLDAL 28  
DB 208 AQLDAL 213  
  
RESULT 65  
GLNA\_DUNSA STANDARD; PRT; 234 AA.  
ID GLNA\_DUNSA  
AC F11600;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase)  
DE (Fragment)  
OS Dunaliella salina.  
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
OC Dunaliellaceae; Dunaliella.  
OX NCBI\_TaxID=3046;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Long Z., Nelson N.;  
RL Submitted (MAY-1989) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate +  
CC L-glutamine.  
CC -1- SUBUNIT: Homooctamer.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
C  
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C  
R EMBL; X15280; CAA33353.1; -.  
R PIR; S04888; AJDEQ.  
R InterPro; IPR001691; GLN\_synth.  
R Pfam; PF00120; Gln-synt; 1.  
R PROSITE; PS00180; GLNA\_1; PARTIAL.  
R PROSITE; PS00181; GLNA\_ATP; 1.  
KW Ligase.  
FT NON TER 1  
SQ SEQUENCE 234 AA; 26224 MW; D5EB25319131DDF6 CRC64;  
  
Query Match 4.9%; Score 6; DB 1; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 113 YICSVG 118  
DB 38 YICSVG 43  
  
RESULT 66  
YMF\_ECOLI STANDARD; PRT; 234 AA.  
ID YMF\_ECOLI  
AC P75968;

15-JUL-1998 (Rel. 36, Created)  
15-JUL-1998 (Rel. 36, Last sequence update)  
16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein ymfE.  
3N YMF E OR B1138.  
3S Escherichia coli.  
3C Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
3C Enterobacteriaceae; Escherichia.  
3X NCBI\_TaxID=562;  
3N [1]  
SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Ferna N.T., Burland V.,  
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
Mau B., Shao Y.,  
RA The complete genome sequence of Escherichia coli K-12.";  
RT Science 277:1453-1474(1997).  
RL -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC  
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CC  
CC EMBL; AF016223; AAC46106.1; -;  
DR HAMAP; MF 01014; -; 1.  
DR InterPro; IPR003009; FMN enzyme.  
DR InterPro; IPR006063; His4.  
DR InterPro; IPR006062; His biosynth.  
DR Pfam; PF00977; His biosynth; 1.  
DR TIGRFAMs; TIGR00007; TIGR00007; 1.  
KW Isomerase; Histidine biosynthesis.  
SQ SEQUENCE 234 AA; 27578 MW; BAA40C588D285DC2 CRC64;  
Query Match 4.9%; Score 6; DB 1; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 91 KDEAHN 96  
DB 120 KDEAHN 125  
RESULT 67  
HIS4\_RHOCA  
ID HIS4\_RHOCA STANDARD; PRT; 236 AA.  
AC Q30725;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]  
DE imidazole-4-carboxamide isomerase (EC 5.3.1.16)  
DE (Phosphoribosylformimino-5-aminomidazole carboxamide ribotide  
DE isomerase).  
GN HIS4  
OS Rhodobacter capsulatus (Rhodospseudomonas capsulata).  
CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;  
CC Rhodobacteraceae; Rhodobacter.  
OX NCBI\_TaxID=1061;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MT1131;  
RX MEDLINE=98132396; PubMed=9473054;  
RA Koch H.G., Huang O., Daldal F.;  
RT "Isolation and characterization of Rhodobacter capsulatus mutants  
RT affected in cytochrome cb3 oxidase activity".  
RL J. Bacteriol. 180:969-978(1998).  
CC -!- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-5-[(5-

phosphoribosylamino)methylideneamino]imidazole-4-carboxamide = 5-  
[(5-phospho-1-deoxyribulos-1-ylamino)methylideneamino]-1-(5-  
phosphoribosyl)imidazole-4-carboxamide.  
-!- PATHWAY: Histidine biosynthesis; fourth step.  
CC SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -!- SIMILARITY: BELONGS TO THE HIS4 / HISF FAMILY.  
CC  
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CC  
CC EMBL; AF016223; AAC46106.1; -;  
DR HAMAP; MF 01014; -; 1.  
DR InterPro; IPR003009; FMN enzyme.  
DR InterPro; IPR006063; His4.  
DR InterPro; IPR006062; His biosynth.  
DR Pfam; PF00977; His biosynth; 1.  
DR TIGRFAMs; TIGR00007; TIGR00007; 1.  
KW Isomerase; Histidine biosynthesis.  
SQ SEQUENCE 236 AA; 24298 MW; 122170D814E9B901 CRC64;  
Query Match 4.9%; Score 6; DB 1; Length 236;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 31 FPGQVA 36  
DB 120 FPGQVA 125  
RESULT 68  
SPEH\_STRPY  
ID SPEH\_STRPY STANDARD; PRT; 236 AA.  
AC Q9X5C8;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Exotoxin type H precursor (SPE H).  
GN SPEH OR SPY1008  
OS Streptococcus pyogenes.  
CC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
CC Streptococcus.  
OX NCBI\_TaxID=1314;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=M15;  
RX MEDLINE=99092428; PubMed=9874566;  
RA Proft T., McFatt S.L., Berkahn C.J., Fraser J.D.;  
RT "Identification and characterization of novel superantigens from  
RT Streptococcus pyogenes".  
RL J. Exp. Med. 189:189-102(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;  
RX MEDLINE=21192684; PubMed=11296296;  
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,  
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,  
Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,  
Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;  
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes".  
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).  
CC -!- SUBUNIT: Binds to major histocompatibility complex class II beta  
CC chain.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- DISEASE: Mitogenic for human peripheral blood lymphocytes.  
CC -!- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN  
CC FAMILY.  
CC  
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R EMBL; AF124500; AAK30989.1; -;  
R EMBL; AB006546; AAK33907.1; -;  
R PDB; 1ET9; 24-MAY-00.  
R PDB; 1EUA; 00.  
R InterPro; IPR006123; Staph/Strep toxin.  
R InterPro; IPR006126; Staph/Strep tox.  
R InterPro; IPR006173; Staph tox OB.  
R Pfam; PF02876; Staph\_Strip\_tox\_C; 1.  
R Pfam; PF01123; Staph\_Strip\_toxin; 1.  
R PROSITE; PS00277; STAPH\_STREP\_TOXIN\_1; FALSE\_NEG.  
R PROSITE; PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
W Toxin; Signal; Complete proteome; 3D-structure.  
T SIGNAL 1 32 POTENTIAL.  
T CHAIN 3 236 EXOTOXIN TYPE H.  
T Q SEQUENCE 236 AA; 27485 MW; 16352923907AD40D CRC64;

Query Match 4.9%; Score 6; DB 1; Length 236;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0;

Y 5 CLSFL 10 STANDARD; PRT; 237 AA.  
b 20 CLSFL 25

## RESULT 69

RL HUMAN  
D\_NRL\_HUMAN STANDARD; PRT; 237 AA.  
P54845;  
01-OCT-1996 (Rel. 34, Created)  
01-OCT-1996 (Rel. 34, Last sequence update)  
15-SEP-2003 (Rel. 42, Last annotation update)  
YE Neural retina-specific leucine zipper protein (NRL) (D14946E).  
NRL.  
DS Homo sapiens (Human).  
DC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
DC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
DX NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
IC TISSUE=Retina;  
IC MEDLINE=92108034; PubMed=1729696;  
JA Swaroop A., Xu J.Z., Pawar H., Jackson A.U., Skolnick C., Agarwal N.;  
"A conserved retina-specific gene encodes a basic motif/leucine  
zipper domain.";  
Proc. Natl. Acad. Sci. U.S.A. 89:266-270(1992).  
[2]  
SEQUENCE FROM N.A.  
RC TISSUE=Retina;  
JA Submittal (OCT-1993) to the EMBL/GenBank/DBJ databases.  
[3]  
SEQUENCE FROM N.A.  
XP MEDLINE=98008930; PubMed=9344655;  
XA Farjo O., Jackson A.U., Piek-Dahl S., Scott K., Kimberling W.J.,  
XA Sieving P.A., Richards J.E., Swaroop A.;  
"Human bzip transcription factor gene NRL: structure, genomic  
sequence, and fine linkage mapping at 14q11.2 and negative mutation  
analysis in patients with retinal degeneration.";  
Genomics 45:395-401(1997).  
[4]  
SEQUENCE FROM N.A.  
RP TISSUE=Eye;  
XA MEDLINE=22386257; PubMed=12477932;  
XA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
XA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diachenko L., Marusa K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Bosa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Roha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
"Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[5]  
VARIANT ADPR THR-50.  
MEDLINE=99206598; PubMed=1012380;  
RA Bessant D.A.R., Payne A.M., Mitton K.P., Wang Q.-L., Swain P.K.,  
RA Plant C., Bird A.C., Zack D.J., Swaroop A., Bhattacharya S.S.;  
"A mutation in NRL is associated with autosomal dominant retinitis  
pigmentosa.";  
Nat. Genet. 21:355-356(1999).  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- TISSUE SPECIFICITY: NEURAL RETINA.  
CC -!- DISEASE: Defects in NRL are a cause of autosomal dominant  
retinitis pigmentosa (ADRP) [MIM:162080].  
CC -!- SIMILARITY: Belongs to the bZIP family.  
CC -!- DATABASE: NAME-Mutations of the NRL gene;  
NOTE=Retina International's Scientific Newsletter;  
WWW="http://www.retina-international.com/sci-news/nrlmut.htm".  
-----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

EMBL; M95925; AAA96828.1; -;  
EMBL; M81840; AAA59948.1; -;  
EMBL; U95012; AAB82768.1; -;  
EMBL; BC012395; AAH12395.1; -;  
PIR; A41796; A41796.  
TRANSFAC; T01082;  
Gene; HGNC:18002; NRL.  
MIM; 162080; -;  
GO; GO:0005634; C:nucleus; TAS.  
GO; GO:0003677; F:DNA binding activity; TAS.  
GO; GO:0003704; F:specific RNA polymerase II transcription fa...; TAS.  
GO; GO:0007468; P:regulation of rhodopsin gene activity; TAS.  
GO; GO:0006366; P:transcription from Pol II promoter; TAS.  
GO; GO:0007601; P:vision; TAS.  
InterPro; IPR004827; TF\_bZIP.  
Pfam; PF03131; bZIP\_Maf; 1.  
SMART; SM00338; BRLZ; 1.  
PROSITE; PS0217; BZIP; 1.  
PROSITE; PS00036; BZIP\_BASIC; FALSE\_NEG.  
Transcription regulation; DNA-binding; Nuclear protein;  
Disease mutation; Retinitis pigmentosa; Vision.  
BASIC MOTIF.  
LEUCINE-ZIPPER.  
DOMAIN 159 185  
DOMAIN 187 208  
VARIANT 50 50  
S -> T (in ADRP; increased  
transactivation activity).  
/FTID=VAR\_009268.

SEQUENCE 237 AA; 25940 MW; CCABEDC1123614 CRC64;

Query Match 4.9%; Score 6; DB 1; Length 237;



```
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 23 AQLDAL 28
b 196 AQLDAL 201

RESULT 70
RL MOUSE
D_NRL_MOUSE STANDARD; PRT; 237 AA.
C P54846;
T 01-OCT-1996 (Rel. 34, Created)
T 01-OCT-1996 (Rel. 34, Last sequence update)
T 28-FEB-2003 (Rel. 41, Last annotation update)
E Neural retina-specific leucine zipper protein (NRL).
N NRL.
S Mus musculus (Mouse).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
X NCBI_TaxID=10090;
N [1]
P SEQUENCE FROM N.A.
C STRAIN=BALB/c; TISSUE=Retina;
X MEDLINE=94116986; PubMed=8288222;
A Farjo O., Jackson A.U., Xu J., Gryzenia M., Skolnick C.,
A Agarwal N., Swarcop A.;
N "Molecular characterization of the murine neural retina leucine
zipper gene, Nrl."
C Genomics 18:216-222(1993).
C -1- SUBCELLULAR LOCATION: Nuclear.
C -1- TISSUE SPECIFICITY: NEURAL RETINA.
C -1- SIMILARITY: Belongs to the bZIP family.
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
C EMBL; L14935; AAA16843.1; -
C PIR; A48912; A48912.
C TRANSFAC; T01438; -
C MGD; MGI:102567; Nrl.
C InterPro; IPR004827; TF bZIP.
C InterPro; IPR004826; TF Maf.
C Pfam; PF03131; bZIP Maf; 1.
C SMART; SM00338; BRLZ; 1.
C PROSITE; PS00217; bZIP.
C PROSITE; PS00036; bZIP_BASIC; FALSE_NEG.
C Transcription regulation; DNA-binding; Nuclear protein.
C DNA BIND 159 185
C DOMAIN 187 208 LEUCINE-ZIPPER.
C SEQUENCE 237 AA; 26083 MW; APLA2B372C95EC8 CRC64;

Query Match 4.9%; Score 6; DB 1; Length 237;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQLDAL 28
Db 196 AQLDAL 201

RESULT 71
UPK THEMA
ID UPK THEMA STANDARD; PRT; 237 AA.
AC Q9WZ25;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
```

```
DE Putative undecaprenol kinase (EC 2.7.1.66) (Bacitracin resistance
DE protein). BACA OR TM0893.
GN UPK OR BACA OR TM0893.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=23336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS8 / DSM 3109;
RX MEDLINE=93287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima."
RL Nature 399:323-329(1999).
CC -1- FUNCTION: Probably phosphorylates undecaprenol to undecaprenyl
phosphate. Confers resistance to bacitracin (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + undecaprenol = ADP + undecaprenyl
phosphate.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- MISCELLANEOUS: Bacitracin is thought to be involved in inhibition
of peptidoglycan synthesis by sequestering undecaprenyl
diphosphate reducing the pool of lipid carrier available.
CC -1- SIMILARITY: BELONGS TO THE UPK FAMILY.
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C EMBL; AE001754; AAD35974.1; -
C PIR; F72321; F72321.
C TIGR; TM0893; -
C HAMAP; MF_01006; -; 1.
C InterPro; IPR003824; BACA.
C Pfam; PF02673; BACA; 1.
C Transferrase; Kinase; Antibiotic resistance; Transmembrane;
C Complete proteome.
C TRANSMEM 36 55 POTENTIAL.
C TRANSMEM 67 84 POTENTIAL.
C TRANSMEM 99 118 POTENTIAL.
C TRANSMEM 125 147 POTENTIAL.
C TRANSMEM 167 186 POTENTIAL.
C TRANSMEM 191 209 POTENTIAL.
C TRANSMEM 219 236 POTENTIAL.
C SEQUENCE 237 AA; 26036 MW; 759239335C5PE10F CRC64;

Query Match 4.9%; Score 6; DB 1; Length 237;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 LDALLV 30
Db 129 LDALLV 134

RESULT 72
PSB6 MOUSE
ID PSB6 MOUSE STANDARD; PRT; 238 AA.
AC Q60692; Q60693;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Proteasome subunit beta type 6 precursor (EC 3.4.25.1) (Proteasome
delta chain) (Macropain delta chain) (Multicatalytic endopeptidase
complex delta chain) (Proteasome subunit Y).
```



N PSMB6 OR LMP19.  
S Mus musculus (Mouse).  
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
X NCBI\_TaxID=10090;  
[1]  
N SEQUENCE FROM N.A.  
C STRAIN=DBA/2J; TISSUE=Liver;  
C MEDLINE=95317820; PubMed=7797265;  
A Woodward E.C., Monaco J.J.;  
T "Characterization and mapping of the gene encoding mouse proteasome  
L subunit DELTA (Imp19).";  
L Immunogenetics 42:128-34 (1995).  
C -1- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX  
C WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH ARG,  
C PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT NEUTRAL OR  
C SLIGHTLY BASIC pH. THE PROTEASOME HAS AN ATP-DEPENDENT PROTEOLYTIC  
C ACTIVITY. MAY CATALYZE BASAL PROCESSING OF INTRACELLULAR ANTIGENS.  
C -1- CATALYTIC ACTIVITY: Cleavage at peptide bonds with very broad  
C specificity.  
C -1- PATHWAY: Involved in an ATP/ubiquitin-dependent non-lysosomal  
C proteolytic pathway.  
C -1- SUBUNIT: The proteasome is composed of at least 15 non identical  
C subunits which form a highly ordered ring-shaped structure. This  
C subunit can be displaced by the equivalent immune-specific subunit  
C PSMB9.  
C -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.  
C -1- SIMILARITY: Belongs to peptidase family T1B.  
C  
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C  
C EMBL: U13393; AAA75375.1; ALT INIT.  
C EMBL: U13394; AAA75376.1; ALT\_INIT.  
C HSPD; P38624; IRP.  
C MEROPS: T01.010; -.  
C MGD; MGI:104880; PsmB6.  
C InterPro: IPR000243; Proteasome\_B.  
C InterPro: IPR001353; Protease.  
C Pfam: PF00227; proteasome\_1.  
C PRINTS: PR00141; PROTEASOME.  
C PROSITE: PS00854; PROTEASOME\_B; 1.  
C Proteasome; Hydrolase; Protease; Zymogen.  
C PROPEP 1 33 BY SIMILARITY.  
C CHAIN 34 238 A -> T.  
C VARIANT 38 38 A -> T.  
C VARIANT 89 89 A -> T.  
C SEQUENCE 238 AA; 25425 MW; 7AEFC23BEE4145A6 CRC64;

Query Match 4.9%; Score 6; DB 1; Length 238;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y' 60 RAGSAP 65

Db 9 RAGSAP 14

RESULT 73

HIS4 BRUME  
ID HIS4 BRUME STANDARD; PRT; 243 AA.  
AC Q8VE36;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase (EC 5.3.1.16)  
DE (Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide

DE isomerase).  
GN HIS4 OR BMEI2042.  
OS Brucella melitensis.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Brucellaceae; Brucella.  
OX NCBI\_TaxID=29459;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=16M / ATCC 23456 / Biotype 1;  
RC MEDLINE=20020109; PubMed=11756688;  
RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mijer C., Los T.,  
RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,  
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltzman E.,  
RA Selkov E., Elser P.H., Hagius S., O'Callaghan D., Letesson J.-J.,  
RA Haselkorn R., Kyprides N., Overbeek R.;  
RT "The genome sequence of the facultative intracellular pathogen  
RT Brucella melitensis.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).  
CC -1- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-5-[(5-  
CC phosphoribosylamino)methylideneamino]imidazole-4-carboxamide = 5-  
CC [(5-phospho-1-deoxyribulose-1-ylamino)methylideneamino]-1-(5-  
CC phosphoribosyl)imidazole-4-carboxamide.  
CC -1- PATHWAY: Histidine biosynthesis; fourth step.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).  
CC -1- SIMILARITY: BELONGS TO THE HIS4 / HISF FAMILY.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
C EMBL: AE009637; AAL53223.1; -.  
DR F1R; AD3507; AD3507.  
DR HAMAP; MF\_01014; -. 1.  
DR InterPro: IPR003009; FMN enzyme.  
DR InterPro: IPR006063; His4.  
DR InterPro: IPR006062; His biosynth.  
DR Pfam: PF00977; His biosynth; 1.  
DR TIGRFAMs: TIGR00007; TIGR00007; 1.  
DR isomerase; Histidine biosynthesis; Complete proteome.  
KW SEQUENCE 243 AA; 25589 MW; 1B264AC48A4D199A CRC64;  
SQ  
Query Match 4.9%; Score 6; DB 1; Length 243;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 31 FPGQVA 36  
Db 120 FPGQVA 125  
RESULT 74  
HIS4 BRUSU  
ID HIS4 BRUSU STANDARD; PRT; 243 AA.  
AC Q8FY08;  
DT 15-SEP-2003 (Rel. 42, Created)  
DT 15-SEP-2003 (Rel. 42, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase (EC 5.3.1.16)  
DE (Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide  
DE isomerase).  
GN HIS4 OR BR2084.  
OS Brucella suis.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Brucellaceae; Brucella.  
OX NCBI\_TaxID=29461;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=1330 / Biovar 1;  
RC

```

IX MEDLINE=22247741; PubMed=12771122;
IA Paulsen I.T., Seshadri R., Nelson K.E., Eissen J.A., Heidelberg J.F.,
IA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
IA Daugherty S.C., Deboy R.T., Durkin A.S., Kolony J.F., Madupu R.,
IA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
IA Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
IA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;
IA "The Brucella suis genome reveals fundamental similarities between
IA animal and plant pathogens and symbionts."
IA Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153 (2002).
IC -1- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-5-[(5-
IC phosphoribosylamino)methylideneamino]imidazole-4-carboxamide = 5-
IC [(5-phospho-1-deoxyribulos-1-ylamino)methylideneamino]-1-(5-
IC phosphoribosyl)imidazole-4-carboxamide.
IC -1- PATHWAY: Histidine biosynthesis; fourth step.
IC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
IC -1- SIMILARITY: BELONGS TO THE HISA / HISF FAMILY.
IC
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IC
IC -----
IC EMBL; AE014495; AAK30974.1; -.
IC TIGR; BR2084; -.
IC HAMAP; MF_01014; -.
IC InterPro; IPR003009; FMN enzyme.
IC InterPro; IPR006063; His4.
IC InterPro; IPR006062; His biosynth.
IC Pfam; PF00977; His biosynth; 1.
IC TIGRFAMs; TIGR00007; TIGR00007; 1.
IC Isomerase; Histidine biosynthesis; Complete proteome.
IC SEQUENCE 243 AA; 25601 MW; 2C34672A986CC478 CRC64;
IC
IC Query Match 4.9%; Score 6; DB 1; Length 243;
IC Best Local Similarity 100.0%; Pred. No. 1.2e+02;
IC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
IC
IC QY 31 PFGQVA 36
IC Db 120 PFGQVA 125
IC
IC RESULT 75
IC HIS4_AGR75 STANDARD; PRT; 247 AA.
IC
IC AC P58790;
IC DT 28-FEB-2003 (Rel. 41, Created)
IC DT 28-FEB-2003 (Rel. 41, Last sequence update)
IC DT 28-FEB-2003 (Rel. 41, Last annotation update)
IC DE 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]
IC imidazole-4-carboxamide isomerase (EC 5.3.1.16)
IC DE (Phosphoribosylformimino-5-aminomidazole carboxamide ribotide
IC isomerase).
IC DE HISA OR ATU0040 OR AGR_C63.
IC GN Agrobacterium tumefaciens (strain C58 / ATCC 33970).
IC OS Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
IC OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
IC OX NCBI_TaxID=176299;
IC [1]
IC
IC SEQUENCE FROM N.A.
IC MEDLINE=21608550; PubMed=11743193;
IC RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
IC RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
IC RA Chen Y., Paulsen I.T., Eissen J.A., Karp P.D., Bovee D. Sr.,
IC RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
IC RA Kutayavin T., Levy R., Li M.-J., McLlland E., Palmieri A.,
IC RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,
IC RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
IC Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

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RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RA "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58."
RL Science 294:2317-2323 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmlet K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wellam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Planagan C., Crowell C., Gursun J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RA "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RL Science 294:2323-2328 (2001).
CC -1- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-5-[(5-
CC phosphoribosylamino)methylideneamino]imidazole-4-carboxamide = 5-
CC [(5-phospho-1-deoxyribulos-1-ylamino)methylideneamino]-1-(5-
CC phosphoribosyl)imidazole-4-carboxamide.
CC -1- PATHWAY: Histidine biosynthesis; fourth step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE HISA / HISF FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AE008978; AAL41071.1; -.
CC EMBL; AE007946; AAK85864.1; -.
CC PIR; A12581; A12581.
CC PIR; G97363; G97363.
CC HAMAP; MF_01014; -.
CC InterPro; IPR003009; FMN enzyme.
CC InterPro; IPR006063; His4.
CC InterPro; IPR006062; His biosynth.
CC Pfam; PF00977; His biosynth; 1.
CC TIGRFAMs; TIGR00007; TIGR00007; 1.
CC Isomerase; Histidine biosynthesis; Complete proteome.
CC SEQUENCE 247 AA; 26027 MW; 9DA6142FEC740104 CRC64;
CC
CC Query Match 4.9%; Score 6; DB 1; Length 247;
CC Best Local Similarity 100.0%; Pred. No. 1.2e+02;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 31 PFGQVA 36
CC Db 120 PFGQVA 125
CC

```

Search completed: February 9, 2004, 12:58:00  
Job time : 30 secs

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# M protein - protein search, using sw model

un on: February 9, 2004, 12:49:57 ; Search time 52 Seconds  
(without alignments)  
610.394 Million cell updates/sec

file: US-09-981-876-200

effect score: 123

sequence: 1 MACRCLSLMGLTFLSVSQT.....PVQPEDDADYCSVGXGFSF 123

coring table: OLIGO

Gapop 60.0 , Gapext 60.0

searched: 830525 seqs, 258052604 residues

word size : 0

total number of hits satisfying chosen parameters: 830525

minimum DB seq length: 0

maximum DB seq length: 2000000000

post-processing: Listing first 100 summaries

database :

SPTREMBL 23.\*

1: sp.archaea.\*

2: sp.bacteria.\*

3: sp.fungi.\*

4: sp.human.\*

5: sp.invertebrate.\*

6: sp.mhc.\*

7: sp.mammal.\*

8: sp.organelle.\*

9: sp.phage.\*

10: sp.plant.\*

11: sp.rodent.\*

12: sp.virus.\*

13: sp.vertibrate.\*

14: sp.unclassified.\*

15: sp.rvrius.\*

16: sp.bacteriap.\*

17: sp.archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	8.9	123	11	Q61243 mus musculus
2	8	6.5	104	17	Q97W39 sulfolobus
3	8	6.5	195	4	Q8WV17 homo sapien
4	8	6.5	266	4	Q9H611 homo sapien
5	8	6.5	272	11	Q8B172 mus musculus
6	8	6.5	491	5	Q20058 caenorhabdi
7	8	6.5	650	11	Q8B123 mus musculus
8	7	5.7	93	2	Q9X7B6 mycobacteri
9	7	5.7	109	6	Q9N0W5 cryptocolagus
10	7	5.7	112	8	Q9XNK0 mytilus sp.
11	7	5.7	135	4	Q9H524 hmo sapien
12	7	5.7	145	17	Q9HN94 halobacteri
13	7	5.7	150	16	Q8FS88 corynebacte
14	7	5.7	243	16	Q93J21 streptomyc
15	7	5.7	252	5	P90688 branchisto
16	7	5.7	252	16	Q8BHP0 xanthomonas

17	7	5.7	256	16	Q8DS61
18	7	5.7	258	16	Q8YPV1
19	7	5.7	265	16	Q9VYV6
20	7	5.7	265	16	Q8NXX3
21	7	5.7	270	2	Q9X5Q2
22	7	5.7	272	16	Q9RUS9
23	7	5.7	289	16	Q8PST9
24	7	5.7	298	11	Q8K3T7
25	7	5.7	307	16	Q8E6E3
26	7	5.7	307	16	Q8R0S8
27	7	5.7	313	16	Q8FSW1
28	7	5.7	317	16	Q8NUS9
29	7	5.7	321	16	Q98LJ3
30	7	5.7	335	11	Q8BZ35
31	7	5.7	357	16	Q8PMT5
32	7	5.7	371	16	Q9CEM2
33	7	5.7	375	16	Q8UHK2
34	7	5.7	401	16	Q8X7D8
35	7	5.7	401	16	Q8FHT5
36	7	5.7	404	2	Q8RSK7
37	7	5.7	407	11	Q8BPZ8
38	7	5.7	415	16	Q8PLC9
39	7	5.7	456	2	Q9R6T0
40	7	5.7	457	16	Q8XSS9
41	7	5.7	462	16	Q9RYH5
42	7	5.7	464	16	Q8ZFP3
43	7	5.7	468	5	Q8G5Z8
44	7	5.7	468	5	Q9V175
45	7	5.7	468	5	Q8MQM1
46	7	5.7	484	17	Q9HQW0
47	7	5.7	518	16	Q8ZP05
48	7	5.7	519	16	Q8Z674
49	7	5.7	526	16	Q8ZNO8
50	7	5.7	526	16	Q8Z5G3
51	7	5.7	526	16	Q8XQ29
52	7	5.7	528	16	Q8ZF26
53	7	5.7	537	16	Q8D075
54	7	5.7	549	16	Q8X7L8
55	7	5.7	549	16	Q8FG11
56	7	5.7	553	5	Q9U203
57	7	5.7	558	10	Q9SNV7
58	7	5.7	614	5	P91720
59	7	5.7	659	5	Q9U202
60	7	5.7	689	5	Q8WPL5
61	7	5.7	701	16	Q8G4I2
62	7	5.7	828	12	Q993H5
63	7	5.7	1443	5	Q8WTB2
64	7	5.7	1512	2	Q93HF2
65	7	5.7	1765	5	Q9VS30
66	7	5.7	1770	5	Q9VS29
67	7	5.7	2852	2	Q8A21
68	7	5.7	4051	5	Q8Z04
69	6	4.9	21	4	Q9NRI7
70	6	4.9	43	6	Q8A453
71	6	4.9	56	5	Q9U447
72	6	4.9	56	12	Q96829
73	6	4.9	61	17	Q8TJT4
74	6	4.9	61	17	Q8PZ97
75	6	4.9	64	10	Q8LRE7
76	6	4.9	72	10	Q5FR81
77	6	4.9	76	2	Q9J326
78	6	4.9	80	4	Q8N4H1
79	6	4.9	80	16	Q9RZA2
80	6	4.9	81	16	Q91322
81	6	4.9	87	10	Q9ZRM9
82	6	4.9	88	16	Q84E0
83	6	4.9	95	16	Q92ZC4
84	6	4.9	99	2	Q8FG2
85	6	4.9	99	16	Q8SLW3
86	6	4.9	101	4	Q81ZD8
87	6	4.9	103	16	O06257
88	6	4.9	105	2	Q9AMS9
89	6	4.9	107	4	Q9NSD6



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101 TISPVQPE 108
149 TISPVQPE 156

RESULT 4
ID Q20058 PRELIMINARY; PRT; 266 AA.
AC Q20058;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE F35G12.12 protein.
DE F35G12.12
GN F35G12.12
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Chui C.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. PubMed=9851916;
RX MEDLINE=99069613;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; 246242; CAA86334.2; -.
DR WormPep; F35G12.12; CE31499.
SQ SEQUENCE 491 AA; 55833 MW; 89F86FD9C656883E CRC64;

Query Match 6.5%; Score 8; DB 5; Length 491;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 VLAQLDAL 28
DB 208 VLAQLDAL 215

RESULT 7
ID Q8BIZ3 PRELIMINARY; PRT; 650 AA.
AC Q8BIZ3;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE DNA helicase homolog homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK049153; BAC33702.1; -.
SQ SEQUENCE 650 AA; 70941 MW; 0330ABA54006DDE4 CRC64;

Query Match 6.5%; Score 8; DB 11; Length 650;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 TISPVQPE 108
DB 162 TISPVQPE 169

RESULT 8
ID Q9X7B6 PRELIMINARY; PRT; 93 AA.
AC Q9X7B6;

101 TISPVQPE 108
149 TISPVQPE 156

RESULT 5
ID Q8BIZ3 PRELIMINARY; PRT; 272 AA.
AC Q8BIZ3;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE DNA helicase homolog homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK028460; BAC25963.1; -.
SQ SEQUENCE 272 AA; 29562 MW; 7A1A044ACCEB29C2 CRC64;

Query Match 6.5%; Score 8; DB 11; Length 272;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 TISPVQPE 108
DB 162 TISPVQPE 169

RESULT 6
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QY 53 GVSYYQQ 59
DB 32 GVSYYQQ 38

RESULT 10
Q9XNKO PRELIMINARY; PRT; 112 AA.
ID Q9XNKO
AC Q9XNKO;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Cytochrome c oxidase subunit III (EC 1.9.3.1) (Cytochrome c oxidase
DE polypeptide III) (Fragment).
GN COIII.
OS Mytilus sp.
OG Mitochondrion.
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
ON NCBI_TaxID=61855;
OX [1]
RP SEQUENCE FROM N.A.
RA Kim I., Min B.-Y., Yoon M.-H., Yoo M.-S., Kim D.-H.;
RT "Unusual mitochondrial DNA polymorphism of the blue mussel (Mytilus
RT edulis) species complex on the southern coast of Korea.";
RL Korean J. Biol. Sci. 3:79-87(1999).
CC -I- FUNCTION; SUBUNITS I, II AND III FORM THE FUNCTIONAL CORE OF THE
CC -I- ENZYME COMPLEX (BY SIMILARITY).
CC -I- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICYTOCHROME
CC C + 2 H(2)O.
CC -I- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 3 FAMILY.
CC EMBL; AF127466; RAD43264.1; -.
DR InterPro; IPR000298; CytC_oxdase_III.
DR Pfam; PF00510; COX3; 1.
DR ProDom; PD000382; CytC_oxdase_III; 1.
DR PROSITE; PS00253; COX3; 1.
DR OXIGOREDUCTASE; Transmembrane; Mitochondrion.
KW NON_TER 1
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12930 MW; 143696990AAC473E2 CRC64;

Query Match 5.7%; Score 7; DB 8; Length 112;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 7 SFLMGMT 13
DB 9 SFLMGMT 15

RESULT 11
Q9H5Z4 PRELIMINARY; PRT; 135 AA.
ID Q9H5Z4
AC Q9H5Z4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ22755.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
OX [1]
RP SEQUENCE FROM N.A.
RA Tissue=ileal mucosa;
RA Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
RA Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
RA Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y.,
RA Obyavskii M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,
RA Isogai T., Sugano S.;
RA "NDO human cDNA sequencing project.";
RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RE EMBL; AK026408; BAB15473.1; -.
DR EMBL;

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R HSP; P01607; 1REI.  
R InterPro; IPR003006; IG\_MHC.  
R InterPro; IPR003596; IG\_V.  
R Pfam; PF00047; IG; 1.  
R SMART; SM00406; IG; 1.  
W Hypothetical protein.  
Q SEQUENCE 135 AA; 14780 MW; 652492DE930P401 CRC64;  
  
Query Match 5.7%; Score 7; DB 4; Length 135;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Y 65 PRVLYX 71  
b 24 PRVLYX 30  
  
RESULT 12  
9HN94 PRELIMINARY; PRT; 145 AA.  
C Q9HN94;  
D 01-MAR-2001 (T-EMBLrel. 16, Created)  
T 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)  
T 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)  
E Cytochrome c oxidase subunit II.  
N COX2 OR VNG2195G.  
S Halobacterium sp. (strain NRC-1).  
C Archaea; Euryarchaeota; Halobacteria; Halobacteriales;  
C Halobacteriaceae; Halobacterium.  
X NCBI\_TaxID=64091;  
N [1]  
F SEQUENCE FROM N.A.  
P MEDLINE=20504483; PubMed=11016950;  
X NG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,  
A Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,  
A Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,  
A Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,  
A Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,  
A Isenbarger T.A., Peck R.F., Pohlischroder M., Spudich J.L., Jung K.-H.,  
A Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,  
A Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;  
T "Genome sequence of Halobacterium species NRC-1.";  
L Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).  
C -1- COPACTOR: COPPER A AND HEME GROUP (BY SIMILARITY).  
C -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
C -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 2 FAMILY.  
R EMBL; AE005106; AAG20327.1; -.  
R HSP; P98052; 1EHK.  
R InterPro; IPR001505; Copper\_CuA.  
R InterPro; IPR002429; Cyt\_c\_ox\_2.  
R Pfam; PF00116; COX2; 1.  
R Prodom; PD000131; Copper\_CuA; 1.  
R PROSITE; PS00078; COX2; 1.  
W Copper; Oxidoreductase; Complete proteome.  
Q SEQUENCE 145 AA; 15591 MW; 3D67301DB92E887C CRC64;

Query Match 5.7%; Score 7; DB 17; Length 145;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Y 32 PGQVAQL 38  
b 86 PGQVAQL 92  
  
RESULT 13  
8FSS8 PRELIMINARY; PRT; 150 AA.  
C Q8FSS8;  
D 01-MAR-2003 (T-EMBLrel. 23, Created)  
Y 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)  
Y 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)  
E Hypothetical protein.

GN CE0304.  
OS Corynebacterium efficiens.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.  
OX NCBI\_TaxID=152794;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;  
RA Kawabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,  
RA Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,  
RA Usuda Y., Sugimoto S.;  
RT "The entire genomic sequence of Corynebacterium efficiens YS-314.";  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
RL EMBL; AP005215; BAC17114.1; -.  
DR Hypothetical protein; Complete proteome.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 150 AA; 16043 MW; 800D0BC94769F9FE CRC64;  
  
Query Match 5.7%; Score 7; DB 16; Length 150;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 60 RAGSAPR 66  
Db 82 RAGSAPR 88  
  
RESULT 14  
93J21 PRELIMINARY; PRT; 243 AA.  
ID Q93J21  
AC Q93J21;  
DT 01-DEC-2001 (T-EMBLrel. 19, Created)  
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)  
DE Putative GntR-family transcriptional regulator.  
GN SCO3986 OR SCBAC25E3.23.  
OS Streptomyces coelicolor.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RA Collins M., Harris D.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RC MEDLINE=97000351; PubMed=8843436;  
RA Redenbach M., Kieser H.M., Denapite D., Eichner A., Cullum J.,  
RA Kinashi H., Hopwood D.A.;  
RT "A set of ordered cosmids and a detailed genetic and physical map for  
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";  
RL Mol. Microbiol. 21:77-96(1996).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2) / M145;  
RX MEDLINE=21996410; PubMed=12000953;  
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,  
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,  
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,  
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,  
RA Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,  
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,  
RP Hopwood D.A.;  
RT "Complete genome sequence of the model actinomycete Streptomyces  
coelicolor A3(2).";

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RD Nature 417:141-147(2002).
CC -!- SIMILARITY: BELONGS TO THE GNTR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
CC -!- SIMILARITY: BELONGS TO THE DEOR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
DR EMBL; AL939118; CAC44710.1; -.
DR InterPro; IPR000524; HTH_GNTR.
DR Pfam; PF00392; gntr; 1.
DR PRINTS; PR00035; HTHGNTR.
DR SMART; SM00345; HTH GNTR; 1.
DR PROSITE; PS00043; HTH GNTR FAMILY; 1.
KW DNA-binding; Transcription-regulation; Complete proteome.
SQ SEQUENCE 243 AA; 26537 MW; 731CDB7A9CF8ED3 CRC64;

Query Match 5.7%; Score 7; DB 16; Length 243;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ALLVFPG 33
DB 217 ALLVFPG 223

RESULT 15
P90688 PRELIMINARY; PRT; 252 AA.
AC P90688;
CT 01-MAY-1997 (TRENBLrel. 03, Created)
CT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
CT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Engrailed protein.
EN AMPHIEN.
CS Branchiostoma floridae (Florida lancelet) (Amphioxus).
CC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
CC Branchiostoma.
CX NCBI_TaxID=7739;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97307778; PubMed=9165120;
RA Holland L.Z., Kene M., Williams N.A., Holland N.D.;
RT "sequence and embryonic expression of the amphioxus engrailed gene
RT (Amphixn): the metameric pattern of transcription resembles that of
RT its segment-polarity homolog in Drosophila."
RL Development 124:1723-1732(1997).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; U82487; AAB40144.1; -.
DR HSP; P02836; 3HDD.
DR InterPro; IPR000747; Engrailed.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_lambrepreser.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00026; ENGRAILED.
DR PRINTS; PR00031; HTHREPRESSR.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00033; ENGRAILED; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS00071; HOMEBOX 2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 252 AA; 27817 MW; D3A52A9DB4BA39F CRC64;

Query Match 5.7%; Score 7; DB 5; Length 252;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 SPVQPED 109
DB 21 SPVQPED 27

RESULT 16
Q9PFP0 PRELIMINARY; PRT; 252 AA.
AC Q9PFP0;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Trehalose-6-phosphate phosphatase.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
CX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.F., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tanura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Secubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AE011966; AAM38053.1; -.
DR InterPro; IPR006379; HAD_SF_IIB.
DR InterPro; IPR003337; Trehalose_Pase.
DR Pfam; PF02358; Trehalose_Pase_1.
DR TIGRFAMs; TIGR01484; HAD-SF-IIB; 1.
DR TIGRFAMs; TIGR00685; T6P; 1.
KW Complete proteome.
SQ SEQUENCE 252 AA; 27029 MW; C50CF23E1CA2C1D9 CRC64;

Query Match 5.7%; Score 7; DB 16; Length 252;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 LAQLDAL 28
DB 67 LAQLDAL 73

RESULT 17
Q9DS61 PRELIMINARY; PRT; 256 AA.
AC Q9DS61;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Putative pyrroline carboxylate reductase (EC 1.5.1.2).
GN PROC OR SMU.1974.
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
CX NCBI_TaxID=1309;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=UA159 / ATCC 700610 / Serotype C;
RX MEDLINE=22295063; PubMed=12397186;
RA Ajdic D., McShan W.M., McLaughlin R.E., Savić G., Chang J.,
RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
RA Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferretti J.J.;
RT "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
RT pathogen."

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L Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).
R EMBL: A3015020; AAN59579.1; -.
W Oxidoreductase; Complete proteome.
Q SEQUENCE 256 AA; 27101 MW; 0BAA131398EB60AF CRC64;

Query Match 5.7%; Score 7; DB 16; Length 256;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 17 VSQTVLA 23
| | | | |
b 194 VSQTVLA 200

RESULT 18
8:EPV1 PRELIMINARY; PRT; 258 AA.
C Q8YPV1;
T 01-MAR-2002 (TrEMBLrel. 20, Created)
T 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
T 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
E Hypothetical protein A114089.
N ALL4089.
S Anabaena sp. (strain PCC 7120).
C Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
X NCBI_TaxID=103690;
N [1]
P SEQUENCE FROM N.A.
X MEDLINE=21595285; PubMed=11759840;
A Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
A Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
A Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
A Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
A Yasuda M., Tabata S.;
T "Complete genomic sequence of the filamentous nitrogen-fixing
T cyanobacterium Anabaena sp. strain PCC 7120.";
L DNA Res. 8:205-213 (2001).
R EMBL: AP003595; BAB75788.1; -.
W Hypothetical protein; Complete proteome.
Q SEQUENCE 258 AA; 29638 MW; 741FBC39089ECA49 CRC64;

Query Match 5.7%; Score 7; DB 16; Length 258;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 19 QTVLAQL 25
| | | | |
b 92 QTVLAQL 98

RESULT 19
D Q99VV6 PRELIMINARY; PRT; 265 AA.
C Q99VV6;
T 01-JUN-2001 (TrEMBLrel. 17, Created)
T 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
T 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
E SA0620 protein (Secretory antigen Ssa homologue).
N SAV0665 OR SA0620.
S Staphylococcus aureus (strain Mu50 / ATCC 700699), and
S Staphylococcus aureus (strain N315).
C Bacteria; Firmicutes; Bacillales; Staphylococcus.
X NCBI_TaxID=158878, 158879;
N [1]
P SEQUENCE FROM N.A.
C SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
X MEDLINE=21311952; PubMed=11418146;
A Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
A Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
A Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
A Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
A Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
A Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RL aureus.";
RL Lancet 357:1225-1240 (2001).
DR EMBL: AP003360; BAB56827.1; -.
DR EMBL: AP003131; BAB41853.1; -.
DR InterPro: IPR002482; LysM.
DR Pfam: PF01476; LysM; 2.
DR SMART: SM00257; LysM; 2.
KW Complete proteome.
SQ SEQUENCE 265 AA; 28187 MW; 16A8159D0F3C0285 CRC64;

Query Match 5.7%; Score 7; DB 16; Length 265;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 LVFPQGV 35
| | | | |
DB 61 LVFPQGV 67

RESULT 20
Q8NKR3 PRELIMINARY; PRT; 265 AA.
ID Q8NKR3
AC Q8NKR3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE MW0627 protein.
GN MW0627.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Twana N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Tanimoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827 (2002).
DR EMBL: AP004824; BAB94492.1; -.
DR InterPro: IPR002482; LysM.
DR Pfam: PF01476; LysM; 2.
KW Complete proteome.
SQ SEQUENCE 265 AA; 28173 MW; 0958118E183F1696 CRC64;

Query Match 5.7%; Score 7; DB 16; Length 265;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 LVFPQGV 35
| | | | |
DB 61 LVFPQGV 67

RESULT 21
Q9X5Q2 PRELIMINARY; PRT; 270 AA.
ID Q9X5Q2
AC Q9X5Q2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Milt.
GN Milt.
OS Streptomyces lavendulae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1914;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL 2564;
```

```
IX MEDLINE=99201491; PubMed=10099135;
XA Mao Y., Varoglu M., Sherman D.H.;
XT "Molecular characterization and analysis of the biosynthetic gene
cluster for the antitumor antibiotic mitomycin C from Streptomyces
lavendulae NRRL 2564."
UL Chem. Biol. 6:251-263(1999).
UR EMBL: AF127374; AAD28452.1; -.
RR InterPro; IPR000205; NAD binding.
RR InterPro; IPR006155; Shikimate_DH.
RR InterPro; IPR000594; Thif_domain.
RR Pfam; PF01488; Shikimate_DH; 1.
RQ SEQUENCE 270 AA; 28130 MW; F6537EB0949C77FE CRC64;

Query Match 5.7%; Score 7; DB 2; Length 270;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ZY 23 AQLDALL 29
ZB 168 AQLDALL 174

RESULT 22
ZYRUS9 PRELIMINARY; PRT; 272 AA.
ID Q9RUS9;
AC STRAIN=RI;
RT "Genome sequence of the radioresistant bacterium Deinococcus
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Doddson R.J., Hart D.H., Gwin M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
Fraser C.N.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
radiodurans R1."
RL Science 286:1571-1577(1999).
DR EMBL; AE001977; AAP10873.1; -.
DR TIGR; DR1303; -.
DR InterPro; IPR000515; BPD_transp.
DR Pfam; PF00528; BPD_transp; 1.
DR PROSITE; PS00402; BPD_TRANSF_INN_MEMBER; 1.
KW Complete proteome.
SQ SEQUENCE 272 AA; 30264 MW; 0DA0CF07D6BA6A3F CRC64;

Query Match 5.7%; Score 7; DB 16; Length 272;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ZY 6 LSFLIMG 12
ZB 244 LSFLIMG 250

RESULT 23
ZYR5T9 PRELIMINARY; PRT; 289 AA.
ID Q8P5T9;
AC Q8P5T9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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DE Transcriptional regulator.
GN XCC246.
GS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
CX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Paria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AE012442; AAM42516.1; -.
DR InterPro; IPR000847; HTH_LysR.
DR InterPro; IPR005119; LysR_subst.
DR Pfam; PF00426; HTH_1; 1.
DR Pfam; PF03466; LysR_substrate; 1.
DR PRINTS; PR00039; HTHLYSR.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
KW Complete proteome.
SQ SEQUENCE 289 AA; 31936 MW; 3B0D47F87512F912 CRC64;

Query Match 5.7%; Score 7; DB 16; Length 289;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 LAQLDAL 28
DB 131 LAQLDAL 137

RESULT 24
ID Q8K2T7 PRELIMINARY; PRT; 298 AA.
AC Q8K2T7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Similar to hypothetical protein FLJ13614.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029845; AAB29845.1; -.
KW Hypothetical protein.
SQ SEQUENCE 298 AA; 33669 MW; 34CD1CE3AD80B7FB CRC64;

Query Match 5.7%; Score 7; DB 11; Length 298;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 PEDDADY 113
DB 107 PEDDADY 113
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Db      286 PEDDADY 292

RESULT 25
Q8E6E3
ID Q8E6E3 PRELIMINARY; PRT; 307 AA.
AC Q8E6E3
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein.
EN GBS0629.

OS Streptococcus agalactiae (serotype III).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216495;
RN [1]
RC STRAIN=NM316 / Serotype III;
RX MEDLINE=2224508; PubMed=12354221;
RA Glaser P., Rusniox C., Buchrieser C., Chevallier P., Frangeul L.,
RA Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
RA Kunst F.;
RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
RT invasive neonatal disease.";
RL Mol. Microbiol. 45:1499-1513(2002).
DR EMBL; AL766846; CAD46273.1; -.
DR SAGaList; gbs0629; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 307 AA; 33928 MW; 5D359E74AFD40C16 CRC64;

Query Match 5.7%; Score 7; DB 16; Length 307;
Best Local Similarity 100.0%; Pred. No. 77; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

2Y 18 SQTVLAQ 24
Db 22 SQTVLAQ 28

RESULT 26
Q8E0S8
ID Q8E0S8 PRELIMINARY; PRT; 307 AA.
AC Q8E0S8;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Cell wall surface anchor family protein.
EN SAG0646.

OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216466;
RN [1]
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=2222988; PubMed=12200547;
RA Tettelin H., Masiognani V., Cieslewicz M.J., Eisen J.A., Peterson S.,
RA Wessels L.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radu D., Fedorova N.B., Scarian D., Khouri H., Mulligan S.,
RA Carthy H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,
RA Rinaldo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
DR EMBL; AE014220; AAM99538.1; -.
DR TIGR; SAG0646; -.
KW Complete proteome.
SQ SEQUENCE 307 AA; 33928 MW; 5D359E74AFD40C16 CRC64;

Query Match 5.7%; Score 7; DB 16; Length 307;
Best Local Similarity 100.0%; Pred. No. 77; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

2Y 18 SQTVLAQ 24
Db 22 SQTVLAQ 28

RESULT 27
Q8FSW1
ID Q8FSW1 PRELIMINARY; PRT; 313 AA.
AC Q8FSW1;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Putative thioredoxin reductase.
EN CE2933.

OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RA Kawarabayashi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
RA Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
RA Usuda Y., Sugimoto S.;
RT "The entire genomic sequence of Corynebacterium efficiens YS-314.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005224; BAC19743.1; -.
KW Complete proteome.
SQ SEQUENCE 313 AA; 34025 MW; 602AF9C5A5FC961F CRC64;

Query Match 5.7%; Score 7; DB 16; Length 313;
Best Local Similarity 100.0%; Pred. No. 78; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

2Y 62 GSAPRYL 68
Db 116 GSAPRYL 122

RESULT 28
Q8NL59
ID Q8NL59 PRELIMINARY; PRT; 317 AA.
AC Q8NL59;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Thioredoxin reductase (EC 1.6.4.5).
EN CGL3090.

OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005283; BAC00484.1; -.
DR InterPro; IPR000759; Adrndx_reductase.
DR InterPro; IPR001327; PAD_pyridox.
DR InterPro; IPR001013; Pyridine_redux.
DR InterPro; IPR003042; Rng_mnnoxigenase.
DR InterPro; IPR005982; Thioredox_reduct.
DR Pfam; PF00070; Pyr_redux; 1.
DR PRINTS; PR00419; ADXRTASE.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00469; PNDRTASEII.

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DR PRINTS; PRO0420; RNMGNOXGNASE.
DR TIGRFAMs; TIGR01292; TRX_reduct; 1.
DR PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
DR OXICOREDUCTASE; Complete proteome.
KW OXICOREDUCTASE 317 AA; 34255 MW; DB290007549BB457 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 16; Length 317;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 GSAPRYL 68
DB 120 GSAPRYL 126

RESULT 29
Q98LI3 PRELIMINARY; PRT; 321 AA.
AC Q98LI3
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical protein mill1010.
GN MLI1010.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RL DNA Res 7:331-338(2000).
DR EMBL; AP002996; BAB48480.1; --
DR InterPro; IPR002220; DHDPS.
DR Pfam; PF00701; DHDPS; 1.
DR PRINTS; PRO0146; DHPICNSTHASE.
DR ProDom; PD001859; DHDPS; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 321 AA; 34990 MW; 1FA700B822B8CF95 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 16; Length 321;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 DALLVFP 32
DB 107 DALLVFP 113

RESULT 30
Q8BZ35 PRELIMINARY; PRT; 335 AA.
AC Q8BZ35
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical aminoacyl-transfer RNA synthetases class-II containing
DE protein.
OS Xus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6J; TISSUE=Vagina;

RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium.
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK036810; BAC29587.1; --
KW Hypothetical protein.
SQ SEQUENCE 335 AA; 36950 MW; 3D4875D4FF548219 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 11; Length 335;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 OLDALLV 30
DB 305 OLDALLV 311

RESULT 31
Q8PMY5 PRELIMINARY; PRT; 357 AA.
AC Q8PMY5
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE 2-nitropropane dioxygenase.
GN XAC1290.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=2202145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Cicarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Paria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";
RL Nature 417:459-463(2002).
DR EMBL; AE011759; AAM36161.1; --
DR InterPro; IPR004136; 2nprop dioxygen.
DR InterPro; IPR003009; FMN_enzyme.
DR Pfam; PF03060; NPD; 1.
KW Dioxygenase; Complete proteome.
SQ SEQUENCE 357 AA; 36732 MW; 7437EB83901C84C0 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 16; Length 357;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AOLDALL 29
DB 118 AOLDALL 124

RESULT 32
Q9CEM2 PRELIMINARY; PRT; 371 AA.
ID Q9CEM2

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Q9CEM2; 2001 (TrEMBLrel. 17, Created)  
 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 Permease.  
 N YSIB OR L11815.  
 S Lactococcus lactis (subsp. lactis) (Streptococcus lactis).  
 C Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.  
 X NCBI\_TaxID=1360;  
 [1]  
 P SEQUENCE FROM N.A.  
 C STRAIN=IL1403;  
 X MEDLINE=21235186; PubMed=11337471;  
 A Bolotin A., Wincker P., Manger S., Jaillon O., Malarme K.,  
 A Weissenbach J., Ehrlich S.D., Sorokin A.,  
 T "the complete genome sequence of the lactic acid bacterium Lactococcus  
 T lactis ssp. lactis IL1403."  
 L Genome Res. 11:731-753(2001).  
 R EMBL; AE006411; AAK05913.1; -.  
 R InterPro: IPR002549; UPF0118.  
 R Pfam: PF01594; UPF0118; 1.  
 R Complete proteome.  
 W SEQUENCE 371 AA; 41524 MW; 4CF474A1FDA1289A CRC64;  
 Q

Query Match 5.7%; Score 7; DB 16; Length 371;  
 Best Local Similarity 100.0%; Pred. No. 90;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 25 LDALLVF 31  
 b 229 LDALLVF 235

RESULT 33  
 8UHK2 PRELIMINARY; PRT; 375 AA.  
 C 8UHK2  
 D 8UHK2  
 T 01-JUN-2002 (TrEMBLrel. 21, Created)  
 T 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 T 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 Y HISS OR ATU0678 OR AGR C 1214.  
 N Agrobacterium tumefaciens (strain C58 / ATCC 33970).  
 S Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 X Rhizobiaceae; Rhizobium.  
 X NCBI\_TaxID=176299;  
 [1]  
 N SEQUENCE FROM N.A.  
 X MEDLINE=21608550; PubMed=11743193;  
 A Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,  
 A Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,  
 A Chen Y., Paulsen I.T., Eilen J.A., Karp P.D., Sovee D. Sr.,  
 A Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,  
 A Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,  
 A Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,  
 A Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,  
 A Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,  
 A Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,  
 A Nester E.W.;  
 T "The genome of the natural genetic engineer Agrobacterium tumefaciens  
 T C58."  
 T Science 294:2317-2323(2001).  
 [2]  
 X SEQUENCE FROM N.A.  
 X MEDLINE=21608551; PubMed=11743194;  
 A Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Mullin L.,  
 A Grollio B., Goldman B.S., Cao Y., Askenazi M., Hailing C., Mullin L.,  
 A Houmieu K., Gordon J., Vaudin M., Tarchouk O., Epp A., Liu F.,  
 A Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,  
 A Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,  
 A Cielo C., Slater S.  
 T "Genome sequence of the plant pathogen and biotechnology agent  
 T Agrobacterium tumefaciens C58."

RL Science 294:2323-2328(2001).  
 DR EMBL; AE009036; AAL41694.1; -.  
 DR EMBL; AE008002; AAK86487.1; -.  
 KW Aminocyl-trNA synthetase; Complete proteome.  
 SQ SEQUENCE 375 AA; 40755 MW; B1FABE4ECAD6C6AD CRC64;  
 Query Match 5.7%; Score 7; DB 16; Length 375;  
 Best Local Similarity 100.0%; Pred. No. 91;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQDALL 29  
 Db 173 AQDALL 179

RESULT 34  
 Q8X7D8 PRELIMINARY; PRT; 401 AA.  
 AC Q8X7D8  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Putative oxidoreductase.  
 GN YC1W OR Z2513 OR ECS1860.  
 OS Escherichia coli O157:H7.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=83334;  
 RN [1]  
 N SEQUENCE FROM N.A.  
 R STRAIN=O157:H7 / EDL933 / ATCC 700927;  
 RX MEDLINE=21074935; PubMed=11208551;  
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,  
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
 RA Gotsfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
 RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamocousis K.,  
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
 RA Welch R.A., Blattner F.R.;  
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."  
 RL Nature 409:529-533(2001).  
 [2]  
 N SEQUENCE FROM N.A.  
 R STRAIN=O157:H7 / RIMD 0509952;  
 RX MEDLINE=21156231; PubMed=11258796;  
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,  
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;  
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli  
 RT O157:H7 and genomic comparison with a laboratory strain K-12."  
 RL DNA Res. 8:111-22(2001).  
 DR EMBL; AE005378; AAG56525.1; -.  
 DR EMBL; AP002556; BAB3283.1; -.  
 KW Complete proteome.  
 SQ SEQUENCE 401 AA; 45189 MW; DA83621180F25577 CRC64;

Query Match 5.7%; Score 7; DB 16; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 97;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 PDRFSA 90  
 Db 356 PDRFSA 362

RESULT 35  
 Q8FHT5 PRELIMINARY; PRT; 401 AA.  
 ID Q8FHT5  
 AC Q8FHT5  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein yciW.

```
3N YCIW OR C1758.
3S Escherichia coli O6.
3C Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
3C Enterobacteriaceae; Escherichia.
3X NCBI_TaxID=217992;
3N [1]_
3P SEQUENCE FROM N.A.
3C STRAIN=O6:HI / CFT073 / ATCC 700928;
3X MEDLINE=22386234; PubMed=12471157;
3A Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
3A Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
3A Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
3A Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
3R "Extensive mosaic structure revealed by the complete genome sequence
3T of uropathogenic Escherichia coli."
3T Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
3L EMBL; AE016760; AAN80224.1; -
3K Hypothetical protein; Complete proteome.
3Q SEQUENCE 401 AA; 45077 MW; 9F36B59BEC6FF470 CRC64;

Query Match 5.7%; Score 7; DB 16; Length 401;
Best Local Similarity 100.0%; Pred. No. 97; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 84 PDRFSAA 90
DB 356 PDRFSAA 362

RESULT 36
Q8RSK7 PRELIMINARY; PRT; 404 AA.
AC Q8RSK7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 42.6 kDa protein.
OS uncultured bacterium.
OG Plasmid pB4.
OC Bacteria; environmental samples.
OX NCBI_TaxID=77133;
3N [1]_
3P SEQUENCE FROM N.A.
3A Tauch A.;
3R "The IncP beta plasmid pB4 encodes a tripartite antibiotic efflux
3T system of the RND-MFP-OEP type conferring erythromycin and
3T roxithromycin resistance in Pseudomonas sp. B13."
3R Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
3L EMBL; A7431260; CAD24357.1; -
3R InterPro: IPR003439; ABC transporter.
3R PROSITE: PS00211; ABC_TRANSPORTER; 1.
3K Hypothetical protein; Plasmid.
3Q SEQUENCE 404 AA; 42586 MW; ECAE469A421602A6 CRC64;

Query Match 5.7%; Score 7; DB 2; Length 404;
Best Local Similarity 100.0%; Pred. No. 97; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 22 LAQLDAL 28
DB 172 LAQLDAL 178

RESULT 37
Q8BPZ8 PRELIMINARY; PRT; 407 AA.
AC Q8BPZ8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

5C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
5X NCBI_TaxID=10090;
5N [1]_
5P SEQUENCE FROM N.A.
5C MEDLINE=22354683; PubMed=12466851;
5X STRAIN=C57BL/6J; TISSUE=Eye;
5A The PANTOM Consortium.
5R "Analysis of the mouse transcriptome based on functional annotation of
5T 60,770 full-length cDNAs."
5L Nature 420:563-573(2002).
5R EMBL; AK051816; BAC34780.1; -
5K Hypothetical protein.
5Q SEQUENCE 407 AA; 46039 MW; FB8B05A197A2BC64 CRC64;

Query Match 5.7%; Score 7; DB 11; Length 407;
Best Local Similarity 100.0%; Pred. No. 98; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 107 PEDDADY 113
DB 395 PEDDADY 401

RESULT 38
Q8PLC9 PRELIMINARY; PRT; 415 AA.
ID Q8PLC9;
AC Q8PLC9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Inner membrane protein.
GN XAC1873.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
3N [1]_
3P SEQUENCE FROM N.A.
3C STRAIN=306 / ATCC 13902 / XV 101;
3X MEDLINE=22022145; PubMed=12024217;
3A da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
3A Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
3A Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
3A Ciarrelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
3A Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,
3A Formighieri E.F., Franco M.C., Greggio C.C., Lemos E.G.M., Lemos M.V.F.,
3A Katsuyama A.M., Kishi L.T., Leite R.P., Martine-Rossi N.M.,
3A Locali E.C., Machado M.A., Madeira A.M.B.N., Miyaki C.Y., Moon D.H.,
3A Martins E.C., Meidanis J., Menck C.F.M., Oliveira M.C., Oliveira V.R.,
3A Moreira L.M., Novo M.T.M., Okura V.K., Silveira M.C., de Souza R.F.,
3A Pereira H.A.F., Rossi A., Sena J.A.D., Silva C., Tezera R.I.D.,
3A Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezera R.I.D.,
3A Setubal J.C., Kitajima J.P.;
3R "Comparison of the genomes of two Xanthomonas pathogens with differing
3T host specificities."
3L Nature 417:459-463(2002).
3R EMBL; AE011820; AAM36735.1; -
3K Complete proteome.
3Q SEQUENCE 415 AA; 47385 MW; B527492E96CE6811 CRC64;

Query Match 5.7%; Score 7; DB 16; Length 415;
Best Local Similarity 100.0%; Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 23 AQLDALL 29
DB 284 AQLDALL 290

RESULT 39
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9R6T0
D QSR6T0 PRELIMINARY; PRT; 456 AA.
C QSR6T0
T 01-MAY-2000 (TReMBLrel. 13, Created)
Y 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
N 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
Ccs1.
N Ccs1.
S Synechococcus sp. (strain PCC 6301) (Anacystis nidulans).
C Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
N NCBI_TaxID=1139;
P SEQUENCE FROM N.A.
C STRAIN=PCC 6301;
X MEDLINE=91271233; PubMed=1905010;
A Tsinoiremas N.F., Castets A.M., Harrison M.A., Allen J.F.,
A Tandeau de Marsac N.;
T "Photosynthetic electron transport controls nitrogen assimilation in
T cyanobacteria by means of posttranslational modification of the glbB
T gene product.";
U Proc. Natl. Acad. Sci. U.S.A. 88:4565-4569(1991).
N (2)
P SEQUENCE FROM N.A.
C STRAIN=PCC 6301;
A Inoue K., Bryant D.A.;
T "Genes required for c-type cytochrome biogenesis.";
L Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
R EMBL; AF079137; AAP04332.1; -.
Q SEQUENCE 456 AA; 50460 MW; 80087557590A22E2 CRC64;

Query Match 5.7%; Score 7; DB 2; Length 456;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 21 VLAQLDA 27
| | | | |
b 439 VLAQLDA 445

RESULT 40
D QXSS9 PRELIMINARY; PRT; 457 AA.
C QXSS9;
T 01-MAR-2002 (TReMBLrel. 20, Created)
Y 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
N 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
E Hypothetical transmembrane protein RSP0388.
N RSP0388 OR RS00816.
S Ralstonia solanacearum (Pseudomonas solanacearum).
X Plasmid megaplasmid.
C Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
R Ralstoniaceae; Ralstonia.
N NCBI_TaxID=305;
P SEQUENCE FROM N.A.
C STRAIN=GM11000;
X MEDLINE=21681879; PubMed=11823852;
A Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
A Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
A Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Denange N.,
A Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
A Siguer P., Thebault P., Whalen M., Wincker P., Levy M.,
A Weissenbach J., Boucher C.A.;
T "Genome sequence of the plant pathogen Ralstonia solanacearum.";
N Nature 415:497-502(2002).
R EMBL; AL646078; CAD17539.1; -.
D InterPro; IPR003006; IG_MHC.
R PROSITE; PS00290; IG_MHC; 1.
Q Plasmid; Hypothetical protein; Complete proteome.
Q SEQUENCE 457 AA; 51786 MW; 4155F8078DBBD25E CRC64;

Query Match 5.7%; Score 7; DB 16; Length 457;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 LAQLDAL 28
| | | | |
Db 374 LAQLDAL 380

RESULT 41
QSRVH5 PRELIMINARY; PRT; 462 AA.
C QSRVH5;
T 01-MAY-2000 (TReMBLrel. 13, Created)
Y 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
N 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE Kynureninase, putative.
GN D5A0338.
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
N NCBI_TaxID=1299;
P SEQUENCE FROM N.A.
C STRAIN=R1;
X MEDLINE=20036896; PubMed=10567266;
A White O., Eise J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
A Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
A Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
A Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
A Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
A Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
A Fraser C.M.;
T "Genome sequence of the radioresistant bacterium Deinococcus
T radiodurans R1.";
R Science 286:1571-1577(1999).
DR EMBL; AE001863; AAF12444.1; -.
DR TIGR; DRA0338; -.
KW Complete proteome.
SQ SEQUENCE 462 AA; 49548 MW; E6C5EB37B04P431F CRC64;

Query Match 5.7%; Score 7; DB 16; Length 482;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 LAQLDAL 28
| | | | |
Db 62 LAQLDAL 68

RESULT 42
QSZFF3 PRELIMINARY; PRT; 464 AA.
C QSZFF3;
T 01-MAR-2002 (TReMBLrel. 20, Created)
Y 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
N 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Putative membrane protein (putative transport protein).
GN YPO1759 OR Y2549.
OS Versinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Versinia.
N NCBI_TaxID=632;
P SEQUENCE FROM N.A.
C STRAIN=CO-92 / Biovar Orientalis;
X MEDLINE=21470413; PubMed=11586360;
A Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
A Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
A Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
A Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
A Feilwell T., Hamlin N., Holroyd S., Jagers K., Kariyasev A.V.,
A Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
A Sammonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
T "Genome sequence of Versinia pestis, the causative agent of plague.";
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1L Nature 413:523-527(2001).
1N [2]
1P SEQUENCE FROM N.A.
1Q STRAIN=KIM5 / Biovar Mediaevalis;
1R MEDLINE=42137863; PubMed=12142430;
1S Deng W., Burland V., Flunkett G., III, Boutin A., Mayhew G.F., Liss P.,
1T Peria N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
1U Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
1V Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
1W Perry R.D.;
1X "Genome sequence of Yersinia pestis KIM.";
1Y J. Bacteriol. 194:4601-4611(2002).
1Z EMBL; AJ414150; CAC90578.1; -.
2R EMBL; AE013857; AAM86104.1; -.
2S InterPro; IPR000644; CBS domain.
2T InterPro; IPR005170; CorC HlyC.
2U InterPro; IPR005496; TerC.
2V Pfam; PF00571; CBS; 2.
2W Pfam; PF03471; CorC HlyC; 1.
2X Pfam; PF03741; TerC; 1.
2Y "Hypothetical protein; Complete proteome.
2Z SEQUENCE 464 AA; 51095 MW; CEC95AC2411112416 CRC64;
3Q
Query Match 5.7%; Score 7; DB 16; Length 464;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2Y 5 CLSFLM 11
2B 139 CLSFLM 145
RESULT 43
296528 PRELIMINARY; PRT; 468 AA.
AC C98528
AC C98528;
AC 01-MAY-1999 (TReMBLrel. 10, Created)
AC 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
AC 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
AC Synapse-enriched clathrin adaptor protein LAP.
AC LAP OR BCDA:GM10787 OR C92520.
AC Drosophila melanogaster (Fruit fly).
AC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
AC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
AC Ephydroidea; Drosophilidae; Drosophila.
AC NCBI TaxID=7227;
AC [1]
AC SEQUENCE FROM N.A.
AC MEDLINE=93098207; PubMed=9883738;
AC Zhang B., Koh Y.H., Beckstead R.B., Budnik V., Ganetzky B.,
AC Bellen H.J.;
AC "Synaptic vesicle size and number are regulated by a clathrin adaptor
AC protein required for endocytosis.";
AC Neuron 21:1465-1475(1998).
AC EMBL; AF075247; AAD08669.1; -.
AC FlyBase; FBgn0026210; lap.
AC InterPro; IPR001026; ENTH.
AC Pfam; PF01417; ENTH; 1.
AC SMART; SM00273; ENTH; 1.
AC SEQUENCE 468 AA; 49807 MW; F78D60A559E4CB00 CRC64;
3Q
Query Match 5.7%; Score 7; DB 5; Length 468;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 AQLDALL 29
DB 187 AQLDALL 193
RESULT 44
Q9VI75 PRELIMINARY; PRT; 468 AA.
ID Q9VI75

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AC Q9VI75;
AC 01-MAY-2000 (TReMBLrel. 13, Created)
AC 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
AC 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
AC LAP protein.
AC LAP OR BCDA:GM10787 OR C92520.
AC Drosophila melanogaster (Fruit fly).
AC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
AC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
AC Ephydroidea; Drosophilidae; Drosophila.
AC NCBI TaxID=7227;
AC [1]
AC SEQUENCE FROM N.A.
AC STRAIN=BERKELEY;
AC MEDLINE=20196006; PubMed=10731132;
AC Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
AC Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
AC George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
AC Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
AC Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
AC Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
AC April J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
AC Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
AC Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
AC Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
AC Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
AC Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
AC de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
AC Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
AC Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
AC Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
AC Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
AC Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
AC Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
AC Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
AC Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
AC Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
AC Liu X., Mattel B., McIntosh T.C., McLeod W.B., McPherson D.,
AC Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
AC Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.B.,
AC Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
AC Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
AC Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
AC Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
AC Spier E., Spradling A.C., Turner R., Stappleton M., Strong R., Sun E.,
AC Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
AC Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
AC Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
AC Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
AC "The genome sequence of Drosophila melanogaster.";
AC Science 287:2185-2195(2000).
AC EMBL; AE003672; AAF54050.1; -.
AC FlyBase; FBgn0026210; lap.
AC InterPro; IPR001026; ENTH.
AC Pfam; PF01417; ENTH; 1.
AC SMART; SM00273; ENTH; 1.
AC SEQUENCE 468 AA; 49867 MW; 4B3011615AF007A0 CRC64;
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QY 23 AQLDALL 29
DB 187 AQLDALL 193
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Q9VI75 PRELIMINARY; PRT; 468 AA.
ID Q9VI75
AC Q9VI75

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01-OCT-2002 (Tremblrel. 22, Created)  
01-OCT-2002 (Tremblrel. 22, Last sequence update)  
01-MAR-2003 (Tremblrel. 23, Last annotation update)  
RH473959.  
LAP OR BCDNA:GM10787 OR CG2520.  
Drosophila melanogaster (Fruit fly).  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
[1]  
SEQUENCE FROM N.A.  
STRAIN=Berkely;  
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
Champe M., Chavez C., Dorsett V., Drensek D., Farfan D., Frise E.,  
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,  
Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,  
Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
Celnik S.,  
Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
EMBL; AY128498; AAM75091.1; -  
FlyBase; FBgn0026210; lap.  
InterPro; IPR001026; ENTH.  
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SMART; SMO0273; ENTH; 1.  
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23 AQLDALL 29  
187 AQLDALL 193  
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ID Q9HQM0  
AC Q9HQM0  
DT 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
Vnc0983C.  
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Halobacterium sp. (strain NRC-1).  
Archaea; Euryarchaeota; Halobacteriia; Halobacteriales;  
Halobacteriaceae; Halobacterium.  
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MEDLINE=20504483; PubMed=11016950;  
NG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,  
Shukla H.D., Laaky S.R., Baliga N.S., Thorsson V., Sbrogna J.,  
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,  
Leithausen B., Keller K., Cruz R., Danson M.J., Hough D.W.,  
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,  
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,  
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,  
Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;  
"Genome sequence of Halobacterium species NRC-1";  
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).  
EMBL; AE005034; AAG19401.1; -  
InterPro; IPR000205; NAD binding.  
InterPro; IPR001667; Psesterase.  
InterPro; IPR003148; TrkA\_N.  
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Pfam; PF02254; TrkA; 1.  
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QY 15 LSVSQTV 21  
DB 287 LSVSQTV 293  
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ID Q8ZP05  
AC Q8ZP05  
DT 01-MAR-2002 (Tremblrel. 20, Created)  
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)  
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
DE Putative inner membrane protein.  
GN YOAB OR STM1828.  
OS Salmonella typhimurium.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Salmonella.  
NCBI\_TaxID=602;  
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STRAIN=LT2 / SGSC1412 / ATCC 700720;  
MEDLINE=21534948; PubMed=11677609;  
McClalland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
Waterston R., Wilson R.K.;  
"Complete genome sequence of Salmonella enterica serovar Typhimurium  
LT2";  
Nature 413:852-856(2001).  
EMBL; AE008781; AAL20743.1; -  
InterPro; IPR000644; CBS domain.  
InterPro; IPR005170; CorC\_HlyC.  
InterPro; IPR005496; TerC.  
Pfam; PF00571; CBS; 2.  
Pfam; PF03471; CorC\_HlyC; 1.  
Pfam; PF03741; TerC; 1.  
SMART; SMO0116; CBS; 2.  
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QY 5 CLSFLM 11  
DB 189 CLSFLM 195  
RESULT 48  
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ID Q8Z674  
AC Q8Z674  
DT 01-MAR-2002 (Tremblrel. 20, Created)  
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)  
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
DE Putative membrane protein.  
GN STY1958.  
OS Salmonella typhi.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Salmonella.  
NCBI\_TaxID=601;  
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SEQUENCE FROM N.A.  
STRAIN=CT18;  
MEDLINE=21534947; PubMed=11677608;  
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,  
Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,  
Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,  
Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,

Q8Z5G3 Q8Z5G3 PRELIMINARY; PRT; 526 AA.  
AC Q8Z5G3;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Putative membrane protein.  
GN YEGH OR STY2332.  
OS Salmonella typhi.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Salmonella.  
OX NCBI\_TaxID=602;  
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RC STRAIN=CT18;  
RX MEDLINE=215334947; PubMed=11677608;  
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham P., Brooks K., Chillingworth T., Connor P., Cronin A., Davis P., Davies R.M., Doad I., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;  
RT "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";  
RL Nature 413:848-852(2001).  
DR EMBL; AL627273; CAD02482.1;  
DR InterPro; IPR000644; CBS domain.  
DR InterPro; IPR005170; CorC\_HlyC.  
DR InterPro; IPR005496; Terc.  
DR Pfam; PF00571; CBS; 2.  
DR Pfam; PF03471; CorC\_HlyC; 1.  
DR Pfam; PF03741; Terc; 1.  
DR SMART; SM00116; CBS; 2.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 526 AA; 59003 MW; 8FD4A24177C33F5 CRC64;  
  
Query Match 5.7%; Score 7; DB 16; Length 526;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 CLSFLM 11  
Db 189 CLSFLM 195  
  
RESULT 51  
Q8XQP9 Q8XQP9 PRELIMINARY; PRT; 526 AA.  
AC Q8XQP9;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Probable transmembrane protein.  
GN RSP1172 OR RS05062.  
OS Ralstonia solanacearum (Pseudomonas solanacearum).  
OG Plasmid megaplasmid.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Ralstoniaceae; Ralstonia.  
OX NCBI\_TaxID=305;  
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RP SEQUENCE FROM N.A.  
RC STRAIN=GM11000;  
RX MEDLINE=21681879; PubMed=11823852;  
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billaut A., Brotter P., Camus J.C., Cattolico L., Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Denange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Signier P., Thebault P., Whalen M., Wincker P., Levy M., Weissbach J., Boucher C.A.;  
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";  
RL Nature 415:497-502(2002).

JA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;  
RT "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";  
RL Nature 413:848-852(2001).  
DR EMBL; AL627272; CAD05511.1;  
DR InterPro; IPR000644; CBS domain.  
DR InterPro; IPR005170; CorC\_HlyC.  
DR InterPro; IPR005496; Terc.  
DR Pfam; PF00571; CBS; 2.  
DR Pfam; PF03471; CorC\_HlyC; 1.  
DR Pfam; PF03741; Terc; 1.  
DR SMART; SM00116; CBS; 2.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 519 AA; 56523 MW; 68918E845E3087 CRC64;  
  
Query Match 5.7%; Score 7; DB 16; Length 519;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 CLSFLM 11  
Db 189 CLSFLM 195  
  
RESULT 49  
Q8ZQN8 Q8ZQN8 PRELIMINARY; PRT; 526 AA.  
AC Q8ZQN8;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Putative inner membrane protein.  
GN YEGH OR STW2119.  
OS Salmonella typhimurium.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Salmonella.  
OX NCBI\_TaxID=602;  
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RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Bante M., Du F., Hon S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;  
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium LT2.";  
RL Nature 413:852-856(2001).  
DR EMBL; AE008794; AAL21023.1;  
DR InterPro; IPR000644; CBS domain.  
DR InterPro; IPR005170; CorC\_HlyC.  
DR InterPro; IPR005496; Terc.  
DR Pfam; PF00571; CBS; 2.  
DR Pfam; PF03471; CorC\_HlyC; 1.  
DR Pfam; PF03741; Terc; 1.  
DR SMART; SM00116; CBS; 2.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 526 AA; 58973 MW; 3BD4B0E40DA6F3EF CRC64;  
  
Query Match 5.7%; Score 7; DB 16; Length 526;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 CLSFLM 11  
Db 189 CLSFLM 195  
  
RESULT 50

R EMBL; AL646083; CAD19323.1; -;  
R InterPro; IPR000644; CBS domain.  
R InterPro; IPR005170; CorC HlyC.  
R InterPro; IPR005496; Terc.  
R Pfam; PF00571; CBS; 2.  
R Pfam; PF03471; CorC HlyC; 1.  
R Pfam; PF03741; Terc; 1.  
W Plasmid; Complete proteome.  
Q SEQUENCE 526 AA; 57719 MW; 4B0D7B20F5661A22 CRC64;  
  
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
y 5 CLSFLIM 11  
b 189 CLSFLIM 195  
  
RESULT 52  
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AC Q8ZF26; 2002 (Tremblrel. 20, Created)  
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)  
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
DE Putative membrane protein.  
NM YPO1527.  
NS Versinia pestis.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Yersinia.  
OX NCBI\_TaxID=632;  
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SEQUENCE FROM N.A.  
STRAIN=CO-92 / Biovar Orientalis;  
MEDLINE=21470413; PubMed=11586350;  
A Parkhill J., Wren B.W., Thomson N.R., Tibball R.W., Holden M.T.G.,  
A Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,  
A Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,  
A Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,  
A Fellwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,  
A Leather S., Mouton P.C.F., Quail M., Rutherford K.,  
A Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;  
IT "Genome sequence of Yersinia pestis, the causative agent of plague."  
IL Nature 413:523-527(2001).  
R EMBL; AJ414148; CAC90350.1; -;  
R InterPro; IPR000644; CBS domain.  
R InterPro; IPR005170; CorC HlyC.  
R InterPro; IPR005496; Terc.  
R Pfam; PF00571; CBS; 2.  
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R Pfam; PF03741; Terc; 1.  
R SMART; SM00116; CBS; 2.  
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
y 5 CLSFLIM 11  
b 189 CLSFLIM 195  
  
RESULT 53  
8D075 Q8D075 PRELIMINARY; PRT; 537 AA.  
AC Q8D075;  
DT 01-MAR-2003 (Tremblrel. 23, Created)  
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
DE Putative membrane protein.

GN Y2643.  
OS Versinia pestis.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Yersinia.  
OX NCBI\_TaxID=632;  
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SEQUENCE FROM N.A.  
STRAIN=KIMS / Biovar Mediaevalis;  
MEDLINE=22137863; PubMed=12142430;  
A Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,  
A Ferns N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,  
A Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,  
A Straley S.C., McDonough K.A., Nilles M.D., Matson J.S., Blattner F.R.,  
A Perry R.D.;  
RT "Genome sequence of Yersinia pestis KIM."  
RL J. bacteriol. 184:4601-4611(2002).  
DR EMBL; AE013866; RAM96196.1; -;  
Q SEQUENCE 537 AA; 60323 MW; F787C0D811CF81EC CRC64;  
  
Query Match 5.7%; Score 7; DB 16; Length 537;  
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y 5 CLSFLIM 11  
b 189 CLSFLIM 195  
  
RESULT 54  
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AC Q8X7L8; 2002 (Tremblrel. 20, Created)  
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)  
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
DE Putative transport protein.  
GN VSGH OR Z3229 OR ECS2868.  
OS Escherichia coli O157:H7.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=83334;  
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SEQUENCE FROM N.A.  
STRAIN=O157:H7 / EDL933 / ATCC 700927;  
R MEDLINE=21074935; PubMed=11206551;  
A Perna N.T., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
A Rose D.J., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
A Grofbeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamowski K.,  
A Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
A Welch R.A., Blattner F.R.;  
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."  
RL Nature 409:529-533(2001).  
[2]  
SEQUENCE FROM N.A.  
STRAIN=O157:H7 / RIMD 0509952;  
R MEDLINE=21156231; PubMed=11258796;  
A Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
A Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
A Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,  
A Kihara S., Shiba T., Hattori M., Shinagawa H.,  
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12."  
RL DNA Res. 8:11-22(2001).  
DR EMBL; AE005432; AAG57123.1; -;  
DR EMBL; AP002560; BAB36291.1; -;  
DR InterPro; IPR000644; CBS domain.  
DR InterPro; IPR005170; CorC HlyC.  
DR InterPro; IPR005496; Terc.  
DR Pfam; PF00571; CBS; 2.  
DR Pfam; PF03471; CorC HlyC; 1.  
DR Pfam; PF03741; Terc; 1.  
DR SMART; SM00116; CBS; 2.

W Complete proteome.  
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 5 CLSFLM 11  
b 211 CLSFLM 217  
PRT; 549 AA.

RESULT 55  
ID Q9U203 PRELIMINARY;  
AC Q9U203  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Hypothetical protein yegh.  
GN YEGH OR C2590.  
OS Escherichia coli O6.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=217992;  
RN [1]  
RP SEQUENCE FROM N.A.  
SC STRAIN=O6:HI / CFT073 / ATCC 700928;  
TX MEDLINE=22388234; PubMed=12471157;  
XA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,  
YA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,  
ZA Mayhew G.P., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,  
XA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;  
RT "Extensive mosaic structure revealed by the complete genome sequence  
of uropathogenic Escherichia coli."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).  
DR EMBL; AE016763; AA81046.1; -  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 549 AA; 62057 MW; C4CCL18FCA60FD6B5 CRC64;

Query Match 5.7%; Score 7; DB 16; Length 549;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 5 CLSFLM 11  
b 211 CLSFLM 217  
PRT; 553 AA.

RESULT 56  
ID Q9U203 PRELIMINARY;  
AC Q9U203  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Y57G11C.9a protein.  
GN Y57G11C.9 OR Y57G11C.9A.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
SC McMurray A.A.;  
TX Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
XA [2]  
YA SEQUENCE 99069613; PubMed=9851916;  
RN [2]  
RP MEDLINE=99069613; PubMed=9851916;  
RA none;  
RT "Genome sequence of the nematode C.elegans: A platform for  
investigating biology."  
RA Science 282:2012-2018 (1998).

DR EMBL; Z99281; CAB54457.1; -  
DR WormPep; Y57G11C.9a; CE24476.  
DR InterPro; IPR000504; RNA\_rec\_mot.  
DR Pfam; PF00076; rim; 1.  
DR SMART; SM00360; RRM; 1.  
DR PROSITE; PS0102; RRM; 1.  
SQ SEQUENCE 553 AA; 63571 MW; A7F22D32D8B9C36 CRC64;

Query Match 5.7%; Score 7; DB 5; Length 553;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 QLDALLV 30  
DB 545 QLDALLV 551  
PRT; 558 AA.

RESULT 57  
ID Q9SNV7 PRELIMINARY;  
AC Q9SNV7  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE Pe0 katanin.  
OS Chlamydomonas reinhardtii.  
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
OC Chlamydomonadaceae; Chlamydomonas.  
OX NCBI\_TaxID=3055;  
RN [1]  
RP SEQUENCE FROM N.A.  
SC MEDLINE=99329821; PubMed=10401578;  
XA Lohret T.A., Zhao L., Quarby L.M.;  
YA "Cloning of Chlamydomonas pe0 katanin and localization to the site of  
RT outer doublet severing during deflagellation."  
RL Cell Motil. Cytoskeleton 43:221-231 (1999).  
DR EMBL; AF205377; AAF12877.1; -  
DR InterPro; IPR003593; AAA\_Atpase.  
DR InterPro; IPR003593; AAA\_Atpase\_cent.  
DR Pfam; PF00004; AAA; 1.  
DR SMART; SM00382; AAA; 1.  
DR PROSITE; PS00674; AAA; 1.  
KW ATP-binding.  
SQ SEQUENCE 558 AA; 60144 MW; 7A9DCCT787C028AB CRC64;

Query Match 5.7%; Score 7; DB 10; Length 558;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 RAGSAPR 66  
DB 182 RAGSAPR 198  
PRT; 614 AA.

RESULT 58  
ID P91720 PRELIMINARY;  
AC P91720  
DT 01-MAY-1997 (TREMBlrel. 03, Created)  
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Decapentaplegic protein.  
GN DPP.  
OS Drosophila virilis (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7244;  
RN [1]  
RP SEQUENCE FROM N.A.  
SC MEDLINE=9725212; PubMed=9071585;  
XA Newfield S.J., Padgett R.W., Findley S.D., Richter B.G., Sanicola M.,

LA de Cuevas M., Gelbart W.M.;  
ST "Molecular evolution at the decapentaplegic locus in Drosophila."  
IL Genetics 145:297-303(1997).  
XC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

RR EMBL; U63855; AAC47555.1; --  
RR HSP; P12643; 3BMP.  
RR FlyBase; FBgn0013109; Dvir\dpp.  
RR InterPro; IPR002405; Inhibin\_alpha.  
RR InterPro; IPR001839; TGFb.  
RR InterPro; IPR001111; TGFb\_N.  
RR Pfam; PF00019; TGF-beta; 1.  
RR Pfam; PF00688; TGFp\_propeptide; 1.  
RR PRINTS; PR00669; INHIBINA.  
RR ProDom; PD000357; TGFb; 1.  
RR SMART; SM00204; TGFb; 1.  
RR PROSITE; PS00250; TGF\_BETA\_1; 1.  
IQ SEQUENCE 614 AA; 63055 MW; DQF20A4093403DCP CRC64;

Query Match 5.7%; Score 7; DB 5; Length 614;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 15 LSVSQTIV 21  
|||  
b 360 LSVSQTIV 366

RESULT 59  
9U202 PRELIMINARY; PRT; 659 AA.  
ID Q9U202  
AC Q9U202;  
DT 01-MAR-2000 (TrEMBLrel. 13, Created)  
DT 01-MAR-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2000 (TrEMBLrel. 23, Last annotation update)  
DE Y57G11C.3b protein.  
EN Y57G11C.9 OR Y57G11C.9B.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoides;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
[1]  
LA SEQUENCE FROM N.A.  
LA McMurray A.A.;  
IL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
IN [2]  
IN SEQUENCE FROM N.A.  
IN MEDLINE=99069613; PubMed=9851916;  
IP SEQUENCE FROM N.A.  
IX none;  
IT "Genome sequence of the nematode C.elegans: A platform for  
IT investigating biology."  
IL Science 282:2012-2018(1998).  
IL EMBL; Z99281; CAB54458.1; --  
RR WormPep; Y57G11C.9b; CE24477.  
RR InterPro; IPR000504; RNA\_rec\_mot.  
RR Pfam; PF00076; rim; 1.  
RR SMART; SM00360; RRM; 1.  
RR PROSITE; PS50102; RRM; 1.  
IQ SEQUENCE 659 AA; 74740 MW; 8FC6694B17D98989 CRC64;

Query Match 5.7%; Score 7; DB 5; Length 659;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 24 QLDALLY 30  
|||  
b 651 QLDALLY 657

RESULT 60  
9BWPL5 PRELIMINARY; PRT; 689 AA.  
ID Q8WPL5  
AC Q8WPL5;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Similar to wasp protein (Fragment).  
GN BAC001.19.  
OS Oikopleura dioica.  
OC Eukaryota; Metazoa; Chordata; Urochordata; Appendicularia;  
OC Oikopleuridae; Oikopleura.  
OX NCBI\_TaxID=34765;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA seo H.C., Kube M., Edvardson R.B., Jensen M.F., Beck A., Spriet E.,  
RA Gorsky G., Thompson E.M., Lehrach H., Reinhardt R., Chourrout D.;  
RT "The marine chordate Oikopleura dioica has a miniature genome."  
RL Science 0:0-0(2001).  
DR EMBL; AF374376; AAL56445.1; --  
FT NON\_TER 1  
SQ SEQUENCE 689 AA; 76360 MW; D4ECE941408B404P CRC64;

Query Match 5.7%; Score 7; DB 5; Length 689;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 LTISPQV 106  
|||  
Db 318 LTISPQV 324

RESULT 61  
Q8G412 PRELIMINARY; PRT; 701 AA.  
ID Q8G412  
AC Q8G412;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical protein with similarity to z5950 product of Escherichia  
DE coli O157:H7.  
GN BL1400.  
OS Bifidobacterium longum.  
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;  
OC Bifidobacteriaceae; Bifidobacterium.  
OX NCBI\_TaxID=216816;  
[1]  
LA SEQUENCE FROM N.A.  
LA STRAIN=NCC 2705;  
RX MEDLINE=22294977; PubMed=12381787;  
RA Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,  
RA Pessi G., Zwaalen M.-C., Desiere F., Bork P., Delley M.,  
RA Pidmore R.D., Arigoni F.;  
RT "The genome sequence of Bifidobacterium longum reflects its adaptation  
RT to the human gastrointestinal tract."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).  
DR EMBL; AB014770; AAN25199.1; --  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 701 AA; 79712 MW; 2927BB3B4D002446 CRC64;

Query Match 5.7%; Score 7; DB 16; Length 701;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 QLDALLY 30  
|||  
Db 100 QLDALLY 106

RESULT 62  
Q993H5 PRELIMINARY; PRT; 828 AA.  
ID Q993H5  
AC Q993H5;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)  
DE ORF35.  
OS Callitriche herpesvirus 3.



DR Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
DR Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
DR Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,  
DR Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
DR Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
DR Borkova D., Borchan M.R., Buck J., Brokstein P., Brottier P.,  
DR Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
DR Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
DR de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
DR Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
DR Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
DR Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
DR Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
DR Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
DR Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
DR Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
DR Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
DR Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
DR Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
DR Merkulov G., Milshina N.V., Mobarly C., Morris J., Moshrefi A.,  
DR Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
DR Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
DR Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
DR Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
DR Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
DR Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
DR Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
DR Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,  
DR Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
DR Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
DR Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
DR Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
DR "The genome sequence of *Drosophila melanogaster*.";  
DR Sequence 287:2185-2195(2000).  
DR [2]  
DR SEQUENCE FROM N.A.  
DR Celinker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,  
DR Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,  
DR Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,  
DR Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
DR Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,  
DR Periera S., Frise E., Galle R.F., Garg N.S., George R.A.,  
DR Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,  
DR Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,  
DR McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,  
DR Pacleb J., Paragov V., Park S., Patel S., Pfeiffer B.,  
DR Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
DR Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,  
DR Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
DR "Sequencing of *Drosophila melanogaster* genome.";  
DR Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR [3]  
DR SEQUENCE FROM N.A.  
DR Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
DR Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,  
DR Tupy J.L., Bergman C., Berman B., Carlson J.W., Celinker S.E.,  
DR Clamp M., Drysdale R., Emmert D., Frise E., Gray A., Harris N.,  
DR Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,  
DR Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,  
DR Ashburner M., Gelbart W.M., Rubin G.M., Murgall C.J., Lewis S.E.;  
DR "Annotation of *Drosophila melanogaster* genome.";  
DR Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR [4]  
DR SEQUENCE FROM N.A.  
DR Adams M.D., Celinker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;  
DR Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR [5]  
DR SEQUENCE FROM N.A.  
DR FlyBase;  
DR Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE003560; AAF50600.2;  
DR FlyBase; FBGN0052387; CG32387.  
DR InterPro; IPR003962; FNIII\_subd.

DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG\_C2.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF00041; fn3; 6.  
DR Pfam; PF00047; ig; 7.  
DR PRINTS; PRO0014; FNTYPEIII.  
DR SMART; SM00060; FN3; 6.  
DR SMART; SM00409; IG; 9.  
DR SMART; SM00408; IGC2; 9.  
DR PROSITE; PS00835; IG LIKE; 9.  
DR Immunoglobulin domain; Repeat.  
DR SQ SEQUENCE 1765 AA; 193274 MW; 81A6A498A903E905 CRC64;  
  
Query Match 5.7%; Score 7; DB 5; Length 1765;  
Best Local Similarity 100.0%; Pred.No. 3.5e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 100 LTISPQV 106  
DB 540 LTISPQV 546  
|||||  
|||  
  
RESULT 66  
Q9VS29 PRELIMINARY; PRT; 1770 AA.  
ID Q9VS29  
AC Q9VS29  
DT 01-MAY-2000 (TrEMBLrel\_13, Created)  
DT 01-OCT-2002 (TrEMBLrel\_22, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel\_23, Last annotation update)  
DE CG32387 protein.  
GN CG32387 OR CG8618 OR CG8619 OR CG14828.  
OS *Drosophila melanogaster* (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkeley;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Borchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarly C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

3A Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
 3A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 3A Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 3A Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 3A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 3A "The genome sequence of *Drosophila melanogaster*.";  
 3L Science 287:2185-2195(2000).  
 3N [2]  
 3P SEQUENCE FROM N.A.  
 3A Ceiniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,  
 3A Evans C.B., Gocayne J.D., Anantides P.G., Brandon R.C., Rogers Y.,  
 3A Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,  
 3A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
 3A Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,  
 3A Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,  
 3A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,  
 3A Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,  
 3A McIntosh T.C., Noy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,  
 3A Pacios J., Paragas V., Park S., Patel S., Pfeiffer B.,  
 3A Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
 3A Stapleton M., Strong R., Svirskaas R., Tector C., Tyler J.,  
 3A Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
 3A "Sequencing of *Drosophila melanogaster* genome.";  
 3L Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 3N [3]  
 3P SEQUENCE FROM N.A.  
 3A Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
 3A Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,  
 3A Tupy J.L., Bergman B., Beran B., Carlson J.W., Ceiniker S.E.,  
 3A Clamp M., Drysdale R., Emmert D., Frise B., de Grey A., Harris N.,  
 3A Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,  
 3A Searle S.M.J., Smith E., Shu S., Smutnick F., Whitfield E.,  
 3A Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
 3A "Annotation of *Drosophila melanogaster* genome.";  
 3L Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 3N [4]  
 3P SEQUENCE FROM N.A.  
 3A Adams M.D., Ceiniker S.E., Gibbs R.A., Rubin G.M., Venter J.C.;  
 3A Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 3N [5]  
 3P SEQUENCE FROM N.A.  
 3A FlyBase;  
 3L Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 3A EMBL; AB025342; -;  
 3A FlyBase; FBN0052387; CG32387.  
 3A InterPro; IPR003962; FNI11\_subd.  
 3A InterPro; IPR003961; FNI11.  
 3A InterPro; IPR003599; Ig.  
 3A InterPro; IPR007110; Ig-like.  
 3A InterPro; IPR003598; Ig\_e2.  
 3A InterPro; IPR003006; Ig\_MHC.  
 3A Pfam; PF00041; fn3; 6.  
 3A Pfam; PF00047; fn3; 8.  
 3A PRINTS; PR00014; FNTYPE111.  
 3A SMART; SM00060; FN3; 6.  
 3A SMART; SM00409; IG; 9.  
 3A SMART; SM00408; IGC2; 9.  
 3A PROSITE; PS00835; IG LIKE; 9.  
 3A Immunoglobulin domain; Repeat.  
 3A SEQUENCE 1770 AA; 193905 MW; 6C1D43D05CC98A7A CRC64;  
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 Query Match 5.7%; Score 7; DB 5; Length 1770;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 100 LTISPVQ 106  
 DB 540 LTISPVQ 546  
 RESULT 67  
 Q9RA21 PRELIMINARY; PRT; 2652 AA.  
 ID Q9RA21  
 AC Q96204 PRELIMINARY; PRT; 4091 AA.  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
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 CC -1- FUNCTION: THIS PROTEIN IS THE CARRIER OF THE GROWING FATTY ACID CHAIN IN FATTY ACID BIOSYNTHESIS (BY SIMILARITY).  
 EMBL; AB025342; BAA89382.1; -;  
 HSSP; P25715; 1MLA.  
 DR InterPro; IPR003231; Acyl carrier.  
 DR InterPro; IPR001227; Acyltransferase.  
 DR InterPro; IPR000794; Ketoacyl-synth.  
 DR InterPro; IPR006163; Fp\_bind.  
 DR Pfam; PF00699; Acyl\_transf; 1.  
 DR Pfam; PF00109; ketoacyl-synth; 1.  
 DR Pfam; PF02801; ketoacyl-synth C; 1.  
 DR Pfam; PF00550; pp-binding; 1.  
 DR TIGRfams; TIGR00517; acyl carrier; 5.  
 DR PROSITE; PS50075; ACP DOMAIN; 5.  
 DR Fatty acid biosynthesis; Phosphopantetheine.  
 KW Fatty acid biosynthesis; Phosphopantetheine.  
 SQ SEQUENCE 2652 AA; 283894 MW; 0C97B2A781F9099 CRC64;  
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 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
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 DE PF00555C.  
 GN PF00555C.  
 OS Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.  
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 RA Koonin E.V., Shalton S., Mason T., Yu K., Fujii C., Pederson J.,  
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 GN PF00555C.  
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 QY 16 SVSQTVL 22  
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 AC Q9RA21  
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 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Genes, similar to eicosapentaenoic acid synthase gene cluster (Acyl carrier protein) (ACP).  
 DE eicosapentaenoic acid-producing bacterium *Vibrio marinus* strain MP-1.";  
 DE Biosynthol. Lett. 21:939-945(1999).  
 CC -1- FUNCTION: THIS PROTEIN IS THE CARRIER OF THE GROWING FATTY ACID CHAIN IN FATTY ACID BIOSYNTHESIS (BY SIMILARITY).  
 EMBL; AB025342; BAA89382.1; -;  
 HSSP; P25715; 1MLA.  
 DR InterPro; IPR003231; Acyl carrier.  
 DR InterPro; IPR001227; Acyltransferase.  
 DR InterPro; IPR000794; Ketoacyl-synth.  
 DR InterPro; IPR006163; Fp\_bind.  
 DR Pfam; PF00699; Acyl\_transf; 1.  
 DR Pfam; PF00109; ketoacyl-synth; 1.  
 DR Pfam; PF02801; ketoacyl-synth C; 1.  
 DR Pfam; PF00550; pp-binding; 1.  
 DR TIGRfams; TIGR0051



A Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,  
A Carlson J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,  
A Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,  
A Chan M.-S., Nene V., Shalim S.J., Suh B., Peterson J., Anguoli S.,  
A Pertea M., Allen J., Selengut J., Hatt D., Mather M.W., Vaidya A.B.,  
A Martin D.M.A., Fairclark A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,  
A McFadden G.I., Cummings I.M., Subramanian G.M., Mungall C.,  
A Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,  
A Fraser C.M., Barrall B.,  
T "Genome sequence of the human malaria parasite Plasmodium  
T falciparum";  
L Nature 419:498-511(2002).  
R ENBL; AB001402; AAC71900.1; -.  
W Hypothetical protein.  
Q SEQUENCE 4091 AA; 494204 MW; 9E90BF6123BB976A CRC64;

Query Match 5.7%; Score 7; DB 5; Length 4091;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
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Y 4 RCLSFL 10  
b 990 RCLSFL 996

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ID Q9NR17 PRELIMINARY; PRT; 21 AA.  
AC Q9NR17  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DE Pancreatic polypeptide-2.  
GN PPY2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
RA Herzog H., Couzens M., Liu M.;  
RA "Peptide YY-2 (PPY2) and pancreatic polypeptide-2 (PPY2): Species  
RA specific evolution of novel members of the neuropeptide Y gene  
RA family";  
RA Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
RA ENBL; AF222903; AAF73875.1; -.  
RA Genew; HGNC:9328; PPY2.  
SQ SEQUENCE 21 AA; 2179 MW; 2F23E50FF18BFF7D CRC64;

Query Match 4.9%; Score 6; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 84;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Y 2 ACRLS 7  
b 4 ACRLS 9

RESULT 70  
ID Q28453 PRELIMINARY; PRT; 43 AA.  
AC Q28453;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Alpha A-crystallin (Fragment).  
OS Leontopithecus rosalia (Golden lion tamarin).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;  
OC Leontopithecus.  
NCBI\_TaxID=30588;  
[1]  
SEQUENCE FROM N.A.

RX MEDLINE=96139023; PubMed=8587135;  
RA Jaworski C.J.;  
RT "A reassessment of mammalian alpha A-crystallin sequences using DNA  
RT sequencing: implications for anthropoid affinities of tarsier.";  
RL J. Mol. Evol. 41:901-908(1995).  
DR EMBL; U24067; AAA97569.1; -.  
DR InterPro; IPR001436; Crystallin\_alpha.  
DR InterPro; IPR002068; Hsp20.  
DR Pfam; PF00011; HSP20; 1.  
DR PRINTS; PR00299; ACRYSTALLIN.  
FT NON\_TER 1 43  
FT NON\_TER 43 43  
SQ SEQUENCE 43 AA; 4444 MW; 6AC18572EBBCCF5F CRC64;

Query Match 4.9%; Score 6; DB 6; Length 43;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Y 38 LSCTLS 43  
b 9 LSCTLS 14

RESULT 71  
ID Q9U447 PRELIMINARY; PRT; 56 AA.  
AC Q9U447  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE Culmination specific protein 45D.  
GN 45D.  
OS Dictyostelium discoideum (Slime mold).  
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostellium.  
NCBI\_TaxID=44689;  
[1]  
SEQUENCE FROM N.A.  
RA Loughran G.F., Pinter K., Gross J.D.;  
RA "Culmination specific mRNA";  
RA Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
RA ENBL; AF203735; AAF20921.1; -.  
SQ SEQUENCE 56 AA; 6411 MW; BBFED54797DB37A0 CRC64;

Query Match 4.9%; Score 6; DB 5; Length 56;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Y 38 LSCTLS 43  
b 34 LSCTLS 39

RESULT 72  
ID Q96829 PRELIMINARY; PRT; 56 AA.  
AC Q96829  
DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Polyprotein (Fragment).  
OS Hepatitis A virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
OC Hepatovirus.  
NCBI\_TaxID=12092;  
[1]  
SEQUENCE FROM N.A.  
RA STRAIN=406909;  
RA MEDLINE=97247817; PubMed=9093940;  
RA Taylor M.B.;  
RA "Molecular epidemiology of South African strains of hepatitis A virus;  
RA 1982-1996";  
RL J. Med. Virol. 51:273-279(1997).



GenCore version 5.1.6  
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DM protein - protein search, using sw model

run on: February 9, 2004, 12:48:32 ; Search time 47 Seconds  
(without alignments)

415.391 Million cell updates/sec

Title: US-09-981-876-200

Perfect score: 123

Sequence: 1 MACRCISFLMTGLSVSQT.....PVPEDDADYCVSVGYGFSP 123

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

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Post-processing: Listing first 100 summaries

Database: A\_Geneseq\_19Jun03.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	123	100.0	123	19	AAW75123
2	123	100.0	123	21	AAW24061
3	123	100.0	123	21	AAW66655
4	123	100.0	123	22	AAU12372
5	123	100.0	123	22	AAW51778
6	123	100.0	123	24	ABU56770
7	123	100.0	123	24	ABU57046
8	123	100.0	123	24	ABU59851
9	123	100.0	123	24	ABU59071

10	123	100.0	123	24	ABU59218	Human secreted/tra
11	123	100.0	123	24	ABU59367	Novel human secret
12	123	100.0	123	24	ABU60502	Human secreted/tra
13	123	100.0	123	24	ABU57993	Human PRO polypept
14	123	100.0	123	24	ABU58924	Human secreted/tr
15	123	100.0	123	24	ABU13884	Human PRO619 polyp
16	123	100.0	123	24	ABU10839	Human PRO polypept
17	119	96.7	141	22	AAW39690	Human polypeptide
18	107	87.0	113	22	AAW41476	Human polypeptide
19	9	7.3	258	23	ABP45354	Human BlyS binding
20	8	6.5	235	22	AAW38953	Human polypeptide
21	8	6.5	246	23	AAW20273	Human lung specifi
22	8	6.5	526	23	ABG66690	Human novel polype
23	8	6.5	588	23	ABG66689	Human novel polype
24	8	6.5	689	22	AAE01020	Human pif-1 type h
25	8	6.5	1249	22	ABG21666	Novel human diagno
26	7	5.7	14	24	ABP76447	Peptidomimetic ant
27	7	5.7	14	24	ABP76448	Peptidomimetic ant
28	7	5.7	103	16	AAW80091	Human derived ligh
29	7	5.7	103	20	AAW95489	Human T lymphocyte
30	7	5.7	104	13	AAW26962	Human T lymphocyte
31	7	5.7	104	15	AAW54313	Anti-HIV gp120 imm
32	7	5.7	104	17	AAW01271	VL region of HIV n
33	7	5.7	104	21	AAW95123	Anti-gp120 antibod
34	7	5.7	104	21	AAW98232	Anti-gp120 antibod
35	7	5.7	105	22	ABG22849	Novel human diagno
36	7	5.7	109	15	AAW50217	HSV glycoprotein F
37	7	5.7	109	22	AAW98230	Rabbit anti-A33 an
38	7	5.7	109	22	AAW98231	Rabbit anti-A33 an
39	7	5.7	109	22	AAW98232	Rabbit anti-A33 an
40	7	5.7	109	22	AAW98233	Humanised anti-A33
41	7	5.7	109	22	AAW98234	Humanised anti-A33
42	7	5.7	109	22	AAW98235	Humanised anti-A33
43	7	5.7	109	22	AAW98236	Humanised anti-A33
44	7	5.7	109	22	AAW98237	Humanised anti-A33
45	7	5.7	109	22	AAW98238	Humanised anti-A33
46	7	5.7	109	22	AAW98239	Humanised anti-A33
47	7	5.7	109	22	AAW75149	Rabbit anti A33 an
48	7	5.7	109	22	AAW75150	Rabbit anti A33 an
49	7	5.7	109	22	AAW75151	Humanised rabbit a
50	7	5.7	109	22	AAW75152	Human anti A33 ant
51	7	5.7	109	22	AAW75153	Human anti A33 ant
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53	7	5.7	109	22	AAW75155	Human anti A33 ant
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55	7	5.7	109	22	AAW75157	Human anti A33 ant
56	7	5.7	109	22	AAW75158	Human anti A33 ant
57	7	5.7	111	15	AAW54277	Anti-HIV gp41 immu
58	7	5.7	111	16	AAW69089	Anti-HIV gp41 immu
59	7	5.7	111	17	AAW01322	VL of Fab, GL 41
60	7	5.7	111	18	AAW08738	Human anti-HIV Fab
61	7	5.7	111	21	AAW95172	Anti-gp41 light ch
62	7	5.7	111	21	AAW98281	Anti-gp41 light ch
63	7	5.7	120	23	ABG64978	Human albumin fusi
64	7	5.7	120	23	ABG64980	Human albumin fusi
65	7	5.7	120	23	AAE21465	Human gene 14 enco
66	7	5.7	120	23	AAE21495	Human gene 14 enco
67	7	5.7	121	22	AAU17887	Novel human respir
68	7	5.7	122	22	ABG18228	Novel human diagno
69	7	5.7	161	22	ABG12887	Novel human diagno
70	7	5.7	182	22	ABG19759	Novel human diagno
71	7	5.7	211	22	ABW11775	Human 14274 recept
72	7	5.7	214	18	AAW45517	NANUC-2 light chai
73	7	5.7	214	18	AAW07615	Ulcerative colitis
74	7	5.7	214	19	AAW64571	Human UC PANCA mon
75	7	5.7	214	20	AAW34039	NANUC-2 antibody 1
76	7	5.7	214	21	AAW57337	UC PANCA MAB NANUC
77	7	5.7	223	22	ABG18298	Novel human diagno
78	7	5.7	223	21	AAW15547	Human immune syste
79	7	5.7	235	23	ABP45852	Human BlyS binding
80	7	5.7	243	23	ABP45852	Novel human diagno
81	7	5.7	244	22	ABG19289	Novel human diagno
82	7	5.7	245	23	ABP45885	Human BlyS binding
			251	23	ABP45490	Human BlyS binding

83 7 5.7 257 23 ABP45241 Human Blys binding  
84 7 5.7 259 23 ABP45266 Human Blys binding  
85 7 5.7 255 24 ABJ18943 Pathogen specific  
86 7 5.7 270 21 ABG32538 S. lavendulae Mit  
87 7 5.7 277 22 ABG19760 Novel human diagno  
88 7 5.7 307 23 ABP27372 Streptococcus poly  
89 7 5.7 307 23 AAU77622 S. agalactiae extr  
90 7 5.7 317 22 AAG93163 C glutamicum prote  
91 7 5.7 322 21 AAG39031 Arabidopsis thalia  
92 7 5.7 371 23 AB555164 Lactococcus lactis  
93 7 5.7 413 22 AEG09223 Novel human diagno  
94 7 5.7 419 24 ABF79333 N. gonorrhoeae ami  
95 7 5.7 419 24 ABP80542 N. gonorrhoeae ami  
96 7 5.7 468 22 ABB59169 Drosophila melanog  
97 7 5.7 597 22 AEG06708 Novel human diagno  
98 7 5.7 597 22 AEG26819 Novel human diagno  
99 7 5.7 848 22 AEG25748 Novel human diagno  
100 7 5.7 934 16 AAR76063 Human MSH2 protein

ALIGNMENTS

RESULT 1  
ID AAW75123 standard; Protein; 123 AA.  
AC AAW75123;  
XT 25-MAR-2003 (updated)  
XT 28-JAN-1999 (first entry)  
DE Human secreted protein encoded by gene 67 clone HRGDF73.

Human; secreted protein; fusion protein; gene therapy; protein therapy;  
diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
developmental abnormality; foetal deficiency; blood; allergy; renal;  
immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
osteoporosis; arthritis; cecitis; lung; thyroiditis; thyroid; digestion;  
endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

XX Homo sapiens.  
XX WO9839446-A2.  
XX 11-SEP-1998.

XX 06-MAR-1998; 98WO-US04482.

XX 07-MAR-1997; 97US-0038621.  
XX 07-MAR-1997; 97US-0040161.  
XX 07-MAR-1997; 97US-0040162.  
XX 07-MAR-1997; 97US-0040163.  
XX 07-MAR-1997; 97US-0040333.  
XX 07-MAR-1997; 97US-0040334.  
XX 07-MAR-1997; 97US-0040336.  
XX 07-MAR-1997; 97US-0040628.  
XX 11-APR-1997; 97US-0043311.  
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XX 11-APR-1997; 97US-0043672.

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PR 23-MAY-1997; 97US-0047618.  
PR 23-MAY-1997; 97US-0047632.  
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PR 06-JUN-1997; 97US-0048964.  
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PR 22-AUG-1997; 97US-0056630.  
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PR 22-AUG-1997; 97US-0056884.  
PR 22-AUG-1997; 97US-0056886.  
PR 22-AUG-1997; 97US-0056887.  
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PR 22-AUG-1997; 97US-0056889.  
PR 22-AUG-1997; 97US-0056892.  
PR 22-AUG-1997; 97US-0056893.  
PR 22-AUG-1997; 97US-0056894.  
PR 22-AUG-1997; 97US-0056903.  
PR 22-AUG-1997; 97US-0056908.  
PR 22-AUG-1997; 97US-0056909.  
PR 22-AUG-1997; 97US-0056910.  
PR 22-AUG-1997; 97US-0056911.  
PR 05-SEP-1997; 97US-0057650.  
PR 05-SEP-1997; 97US-0057761.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX PA

X I Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC, Bednarik DP;  
 X II Endress CA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;  
 X III Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;  
 X IV Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;  
 X V WPI; 1998-609887/51.  
 X VI N-PSDB; AAV34220.  
 X VII New isolated human genes and the secreted polypeptides they encode  
 X VIII - useful for diagnosis and treatment of e.g. cancers, neurological  
 X IX disorders, immune diseases, inflammation or blood disorders  
 X X Claim 1; Page 320-321; 447pp; English.

X This sequence represents a secreted human protein encoded by the gene  
 X clone detailed in the descriptor line.  
 X The gene can be used to generate fusion proteins by linking to the gene  
 X to a human immunoglobulin Fc portion (e.g. AAV34145) for increasing the  
 X stability of the fused protein as compared to the human protein only.  
 X The invention relates to 70 novel genes and their fragments (nucleic  
 X acid sequences: AAV34154-V34276; amino acid sequences AAV75057-W75179)  
 X which are useful for preventing, treating or ameliorating medical  
 X conditions e.g. by protein or gene therapy. Also, pathological  
 X conditions can be diagnosed by determining the amount of the new  
 X polypeptides in a sample or by determining the presence of mutations in  
 X the new polynucleotides. Specific uses are described for each of the 70  
 X polynucleotides, based on which tissues they are most highly expressed in  
 X (see AAV34154 for described uses).  
 X (Updated on 25-MAR-2003 to correct PF field.)  
 X (Updated on 25-MAR-2003 to correct PI field.)

X Sequence 123 AA;

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Y 1 MACRCLSFLMGTFLSVTSQTLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQQR 60  
 b 1 MACRCLSFLMGTFLSVTSQTLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQQR 60  
 Y 61 AGSAPRYLLYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVPQEDDADYYCYSVG 120  
 b 61 AGSAPRYLLYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVPQEDDADYYCYSVG 120  
 Y 121 FSP 123  
 b 121 FSP 123

RESULT 2  
 VAB24061  
 ID AAB24061 standard; Protein; 123 AA.  
 CX AAB24061;  
 CX 29-JAN-2001 (first entry)  
 CX Human PRO619 protein sequence SEQ ID NO:16.  
 CX Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;  
 CX Proliferation; tumorigenesis; identification; cancer; cytostatic;  
 CX neutropic; neuroprotective; antiinflammatory; immunosuppressive;  
 CX immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;  
 CX neuronal disorder; glioma disorder; astrocytoma disorder; angiogenic;  
 CX hypothalamic disorder; glandular disorder; macrophagal disorder;  
 CX epithelial disorder; stromal disorder; blastocoele disorder;  
 CX inflammatory disorder; immunologic disorder.  
 CX Homo sapiens.  
 CX WO2000053755-A2.

XX 14-SEP-2000.  
 PD 06-JAN-2000; 2000WO-US00376.  
 PF 08-MAR-1999; 99WO-US05028.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 07-JUL-1999; 99US-0143048.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 05-JAN-2000; 2000WO-US00219.  
 XX (GETH ) GENENTECH INC.  
 PA Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;  
 PI Watanabe CK, Wood WI;  
 XX WPI; 2000-572270/53.  
 XX N-PSDB; AAC58371.  
 XX Thirty PRO polynucleotides encoding PRO polypeptides, useful in the  
 XX treatment, diagnosis and prevention of cancer -  
 XX Claim 61; Fig 10; 286pp; English.

XX The present invention describes an isolated antibody that binds to  
 XX one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,  
 XX PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,  
 XX PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,  
 XX PRO1187, PRO1281, PRO239, PRO334, PRO337, PRO370, PRO2094, PRO  
 XX PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell  
 XX growth. The PRO polypeptides and nucleotides are useful in the  
 XX treatment, diagnosis and prevention of cancer. The antibodies and other  
 XX anti-tumour compounds may be used to treat various conditions, including  
 XX those characterised by overexpression and/or activation of the amplified  
 XX PRO genes. Exemplary conditions or disorders to be treated with such  
 XX antibodies and other compounds include benign or malignant tumours  
 XX (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,  
 XX colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic  
 XX carcinomas, sarcomas, glioblastomas, and various head and neck tumours),  
 XX leukaemias and lymphoid malignancies, other disorders such as neuronal,  
 XX glial, astrocytic, hypothalamic and other glandular, macrophagal,  
 XX epithelial, stromal and blastocoele disorders, and inflammatory,  
 XX angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR  
 XX primers and hybridisation probes used in the isolation of the human PRO  
 XX sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human  
 XX PRO polynucleotide and protein sequences given in the exemplification of  
 XX the present invention.

Sequence 123 AA;  
 Query Match 100.0%; Score 123; DB 21; Length 123;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-117;  
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MACRCLSFLMGTFLSVTSQTLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQQR 60  
 Db 1 MACRCLSFLMGTFLSVTSQTLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQQR 60  
 Qy 61 AGSAPRYLLYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVPQEDDADYYCYSVG 120  
 Db 61 AGSAPRYLLYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVPQEDDADYYCYSVG 120  
 Qy 121 FSP 123  
 Db 121 FSP 123

RESULT 3  
 AAY66655  
 ID AAY66655 standard; protein; 123 AA.

XX AC AAY66655;  
XX DT 05-APR-2000 (first entry)  
XX DE Membrane-bound protein PRO619.  
XX KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
XX KW Pharmaceutical; receptor immunoadhesin; gene mapping.  
XX CS Homo sapiens.  
XX PN WO9963088-A2.  
XX PD 09-DEC-1999.  
XX PF 02-JUN-1999; 99WO-US12252.  
XX 02-JUN-1998; 98US-0087607.  
XX 02-JUN-1998; 98US-0087609.  
XX 02-JUN-1998; 98US-0087759.  
XX 03-JUN-1998; 98US-0087827.  
XX 04-JUN-1998; 98US-0088021.  
XX 04-JUN-1998; 98US-0088025.  
XX 04-JUN-1998; 98US-0088028.  
XX 04-JUN-1998; 98US-0088029.  
XX 04-JUN-1998; 98US-0088030.  
XX 04-JUN-1998; 98US-0088033.  
XX 04-JUN-1998; 98US-0088326.  
XX 05-JUN-1998; 98US-0088167.  
XX 05-JUN-1998; 98US-0088202.  
XX 05-JUN-1998; 98US-0088212.  
XX 05-JUN-1998; 98US-0088217.  
XX 09-JUN-1998; 98US-0088655.  
XX 10-JUN-1998; 98US-0088722.  
XX 10-JUN-1998; 98US-0088730.  
XX 10-JUN-1998; 98US-0088734.  
XX 10-JUN-1998; 98US-0088738.  
XX 10-JUN-1998; 98US-0088740.  
XX 10-JUN-1998; 98US-0088741.  
XX 10-JUN-1998; 98US-0088742.  
XX 10-JUN-1998; 98US-0088810.  
XX 10-JUN-1998; 98US-0088811.  
XX 10-JUN-1998; 98US-0088824.  
XX 10-JUN-1998; 98US-0088825.  
XX 10-JUN-1998; 98US-0088826.  
XX 11-JUN-1998; 98US-0088858.  
XX 11-JUN-1998; 98US-0088861.  
XX 11-JUN-1998; 98US-0088863.  
XX 11-JUN-1998; 98US-0088876.  
XX 12-JUN-1998; 98US-0089090.  
XX 12-JUN-1998; 98US-0089105.  
XX 16-JUN-1998; 98US-0089440.  
XX 16-JUN-1998; 98US-0089512.  
XX 16-JUN-1998; 98US-0089514.  
XX 17-JUN-1998; 98US-0089532.  
XX 17-JUN-1998; 98US-0089538.  
XX 17-JUN-1998; 98US-0089598.  
XX 17-JUN-1998; 98US-0089599.  
XX 17-JUN-1998; 98US-0089600.  
XX 17-JUN-1998; 98US-0089653.  
XX 18-JUN-1998; 98US-0089801.  
XX 18-JUN-1998; 98US-0089907.  
XX 18-JUN-1998; 98US-0089908.  
XX 19-JUN-1998; 98US-0089947.  
XX 19-JUN-1998; 98US-0089948.  
XX 22-JUN-1998; 98US-0090246.  
XX 22-JUN-1998; 98US-0090252.  
XX 22-JUN-1998; 98US-0090254.  
XX 23-JUN-1998; 98US-0090349.  
XX 23-JUN-1998; 98US-0090355.  
XX 24-JUN-1998; 98US-0090429.  
PR 24-JUN-1998; 98US-0090431.  
PR 24-JUN-1998; 98US-0090435.  
PR 24-JUN-1998; 98US-0090444.  
PR 24-JUN-1998; 98US-0090445.  
PR 24-JUN-1998; 98US-0090472.  
PR 24-JUN-1998; 98US-0090472.  
PR 24-JUN-1998; 98US-0090535.  
PR 24-JUN-1998; 98US-0090538.  
PR 24-JUN-1998; 98US-0090540.  
PR 25-JUN-1998; 98US-0090557.  
PR 25-JUN-1998; 98US-0090576.  
PR 25-JUN-1998; 98US-0090678.  
PR 25-JUN-1998; 98US-0090688.  
PR 25-JUN-1998; 98US-0090690.  
PR 25-JUN-1998; 98US-0090691.  
PR 25-JUN-1998; 98US-0090694.  
PR 25-JUN-1998; 98US-0090695.  
PR 25-JUN-1998; 98US-0090696.  
PR 26-JUN-1998; 98US-0090862.  
PR 26-JUN-1998; 98US-0090863.  
PR 01-JUL-1998; 98US-0091358.  
PR 01-JUL-1998; 98US-0091360.  
PR 01-JUL-1998; 98US-0091360.  
PR 02-JUL-1998; 98US-0091478.  
PR 02-JUL-1998; 98US-0091486.  
PR 02-JUL-1998; 98US-0091519.  
PR 02-JUL-1998; 98US-0091826.  
PR 02-JUL-1998; 98US-0091828.  
PR 02-JUL-1998; 98US-0091833.  
PR 02-JUL-1998; 98US-0091846.  
PR 02-JUL-1998; 98US-0091673.  
PR 07-JUL-1998; 98US-0091978.  
PR 07-JUL-1998; 98US-0091982.  
PR 09-JUL-1998; 98US-0092182.  
PR 10-JUL-1998; 98US-0092472.  
PR 20-JUL-1998; 98US-0093339.  
PR 30-JUL-1998; 98US-0094651.  
PR 04-AUG-1998; 98US-0095282.  
PR 04-AUG-1998; 98US-0095285.  
PR 04-AUG-1998; 98US-0095301.  
PR 04-AUG-1998; 98US-0095302.  
PR 04-AUG-1998; 98US-0095318.  
PR 04-AUG-1998; 98US-0095321.  
PR 04-AUG-1998; 98US-0095325.  
PR 10-AUG-1998; 98US-0095916.  
PR 10-AUG-1998; 98US-0095929.  
PR 10-AUG-1998; 98US-0096012.  
PR 11-AUG-1998; 98US-0096143.  
PR 11-AUG-1998; 98US-0096146.  
PR 12-AUG-1998; 98US-0096329.  
PR 17-AUG-1998; 98US-0096757.  
PR 17-AUG-1998; 98US-0096766.  
PR 17-AUG-1998; 98US-0096773.  
PR 17-AUG-1998; 98US-0096791.  
PR 17-AUG-1998; 98US-0096867.  
PR 17-AUG-1998; 98US-0096881.  
PR 17-AUG-1998; 98US-0096894.  
PR 17-AUG-1998; 98US-0096895.  
PR 17-AUG-1998; 98US-0096897.  
PR 18-AUG-1998; 98US-0096949.  
PR 18-AUG-1998; 98US-0096950.  
PR 18-AUG-1998; 98US-0096959.  
PR 18-AUG-1998; 98US-0096960.  
PR 18-AUG-1998; 98US-0097022.  
PR 18-AUG-1998; 98US-0097141.  
PR 20-AUG-1998; 98US-0097218.  
PR 24-AUG-1998; 98US-0097661.  
PR 24-AUG-1998; 98US-0097951.  
PR 26-AUG-1998; 98US-0097952.  
PR 26-AUG-1998; 98US-0097954.  
PR 26-AUG-1998; 98US-0097955.  
PR 26-AUG-1998; 98US-0097971.

26-AUG-1998; 98US-0097974.  
 26-AUG-1998; 98US-0097978.  
 26-AUG-1998; 98US-0097979.  
 26-AUG-1998; 98US-0097986.  
 26-AUG-1998; 98US-0098014.  
 31-AUG-1998; 98US-0098525.  
 16-SEP-1998; 98US-0100634.  
 12-JAN-1999; 99US-0115565.  
 (GETH ) GENENTECH INC.  
 Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
 Wood WI, Yuan J;  
 WPI; 2000-072883/06.  
 N-PSDB; AAZ64983.  
 Membrane-bound proteins and related nucleotide sequences  
 claim 12; Fig 68; 822pp; English.  
 The invention provides membrane-bound PRO polypeptides and  
 polynucleotides encoding them. The PRO sequences of the invention were  
 identified based on extracellular domain homology screening. The PRO  
 sequences have homology with proteins including LDL receptors, TIE  
 ligands and various enzymes. The membrane-bound proteins and receptor  
 molecules are useful as pharmaceutical and diagnostic agents. Receptor  
 immunoadhesins, for instance, can be used as therapeutic agents to block  
 receptor-ligand interactions. The membrane-bound proteins can also be  
 employed for screening of potential peptide or small molecule inhibitors  
 of the relevant receptor/ligand interaction. The PRO encoding sequences  
 are useful as hybridization probes, in chromosome and gene mapping and in  
 the generation of antisense RNA and DNA. PRO nucleic acid sequences  
 will also be useful for the preparation of PRO polypeptides, especially  
 by recombinant techniques.  
 Sequence 123 AA;  
 Query Match 100.0%; Score 123; DB 21; Length 123;  
 Best Local Similarity 100.0%; Pred. NO. 4.8e-117;  
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 MACRCLSFLLMGTFLSVSQTFLAQLDALLVFPQQAQLSCTLSPOHVTIRDYGVSMYQQR 60  
 1 MACRCLSFLLMGTFLSVSQTFLAQLDALLVFPQQAQLSCTLSPOHVTIRDYGVSMYQQR 60  
 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDAHNACVLTISPQPEDDADYCSVG 120  
 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDAHNACVLTISPQPEDDADYCSVG 120  
 121 FSP 123  
 121 FSP 123  
 RESULT 4  
 AAU12372  
 ID AAU12372 standard; Protein; 123 AA.  
 AAU12372;  
 24-OCT-2001 (first entry)  
 Human PRO619 polypeptide sequence.  
 Human secretory and transmembrane; PRO; mammalian; cancer; lung;  
 breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;  
 cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;  
 adipocyte; A-peptide; factor VIIA; gene therapy.  
 Homo sapiens.  
 WO200140466-A2.

XX 07-JUN-2001.  
 XX 01-DEC-2000; 2000WO-US32678.  
 XX 01-DEC-1999; 99WO-US28301.  
 XX 02-DEC-1999; 99WO-US28634.  
 XX 02-DEC-1999; 99WO-US28551.  
 XX 02-DEC-1999; 99WO-US28564.  
 XX 02-DEC-1999; 99WO-US28565.  
 XX 09-DEC-1999; 99US-0170262.  
 XX 16-DEC-1999; 99WO-US30095.  
 XX 20-DEC-1999; 99WO-US30911.  
 XX 20-DEC-1999; 99WO-US30999.  
 XX 30-DEC-1999; 99WO-US31243.  
 XX 06-JAN-2000; 2000WO-US00277.  
 XX 06-JAN-2000; 2000WO-US00376.  
 XX 11-FEB-2000; 2000WO-US03565.  
 XX 18-FEB-2000; 2000WO-US04341.  
 XX 18-FEB-2000; 2000WO-US04342.  
 XX 22-FEB-2000; 2000WO-US04414.  
 XX 24-FEB-2000; 2000WO-US04914.  
 XX 24-FEB-2000; 2000WO-US05004.  
 XX 01-MAR-2000; 2000WO-US05601.  
 XX 20-MAR-2000; 2000WO-US07377.  
 XX 21-MAR-2000; 2000WO-US07532.  
 XX 30-MAR-2000; 2000WO-US08439.  
 XX 17-MAY-2000; 2000WO-US13705.  
 XX 22-MAY-2000; 2000WO-US14042.  
 XX 30-MAY-2000; 2000WO-US14941.  
 XX 02-JUN-2000; 2000WO-US15264.  
 XX 10-NOV-2000; 2000WO-US30873.  
 XX (GETH ) GENENTECH INC.  
 Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
 Gerritsen ME, Goddard A, Godowski FJ, Gurney AL, Sherwood S;  
 Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 WPI; 2001-408281/43.  
 N-PSDB; AAS21444.  
 Isolated, secretory and transmembrane PRO polypeptide used to detect  
 other PRO polypeptides, link bioactive molecules to cells expressing  
 PRO polypeptides, and detect the presence of mammalian tumours e.g.  
 lung, breast, prostate, cervical  
 Claim 12; Fig 402; 813pp; English.  
 AAU12172-AAU12446 represent novel human secretory and transmembrane  
 PRO polypeptides. The PRO polypeptides are useful to detect other  
 PRO polypeptides, to link bioactive molecules to cells expressing  
 PRO polypeptides, to modulate biological activities of cells expressing  
 PRO polypeptides, and to detect the presence of mammalian lung, colon,  
 breast, prostate, rectal, cervical or liver tumours by comparing PRO  
 polypeptide expression in a cell sample to that in a control sample.  
 Some of the 275 sequences are also useful to stimulate the release of  
 tumour necrosis factor-alpha (TNF-alpha) from human blood, the  
 proliferation or differentiation of chondrocytes, the proliferation or  
 gene expression in pericyte cells, the release of proteoglycans from  
 cartilage, the proliferation of inner ear utricular supporting cells or  
 of T-lymphocytes, the release of a cytokine from peripheral blood  
 monocytes (PBMCs), or the proliferation of endothelial cells. Some of  
 the PRO polypeptides may modulate glucose or free fatty acid uptake by  
 skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide  
 to factor VIIA. The PRO polypeptides can be used in assays to identify  
 molecules involved in binding interactions. The polynucleotides encoding  
 PRO polypeptides can be used to generate probes, antisense RNA/DNA,  
 transgenic or knock out animals and can be used in gene therapy.  
 Sequence 123 AA;  
 Query Match 100.0%; Score 123; DB 22; Length 123;

Best Local Similarity 100.0%; Pred. No. 4.8e-117; Mismatches 0; Indels 0; Gaps 0;  
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Y 1 MACRCLSFLLMGTFLLSVQTLAQLDALLVFFGQVAQLSCTLSPOHVTIRDYGVSWYQOR 60  
 D 1 MACRCLSFLLMGTFLLSVQTLAQLDALLVFFGQVAQLSCTLSPOHVTIRDYGVSWYQOR 60  
 Y 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISPVQPEDDADYYCSGVG 120  
 D 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISPVQPEDDADYYCSGVG 120  
 Y 121 FSP 123  
 D 121 FSP 123  
 RESULT 5  
 AAB65178  
 ID AAB65178 standard; Protein; 123 AA.  
 AC AAB65178;  
 X 02-APR-2001 (first entry)  
 X Human PRO619 (UNQ355) protein sequence SEQ ID NO:117.  
 X Human; secreted and transmembrane protein; PRO; cytotostatic;  
 X cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
 X diagnostic assay.  
 X Homo sapiens.  
 X WO2000073454-A1.  
 X 07-DEC-2000.  
 X 30-MAR-2000; 2000WO-US08439.  
 X 02-JUN-1999; 99WO-US12252.  
 X 23-JUN-1999; 99US-0141037.  
 X 07-JUL-1999; 99US-0143048.  
 X 20-JUL-1999; 99US-0144758.  
 X 26-JUL-1999; 99US-0145698.  
 X 28-JUL-1999; 99US-0146222.  
 X 17-AUG-1999; 99US-0149396.  
 X 15-SEP-1999; 99WO-US10190.  
 X 15-SEP-1999; 99WO-US21547.  
 X 08-OCT-1999; 99US-0158663.  
 X 30-NOV-1999; 99WO-US28313.  
 X 01-DEC-1999; 99WO-US28301.  
 X 16-DEC-1999; 99WO-US30095.  
 X 20-DEC-1999; 99WO-US30911.  
 X 05-JAN-2000; 2000WO-US00219.  
 X 06-JAN-2000; 2000WO-US00376.  
 X 11-FEB-2000; 2000WO-US03565.  
 X 18-FEB-2000; 2000WO-US04341.  
 X 22-FEB-2000; 2000WO-US04414.  
 X 24-FEB-2000; 2000WO-US04914.  
 X 24-FEB-2000; 2000WO-US05004.  
 X 02-MAR-2000; 2000WO-US05841.  
 X 15-MAR-2000; 2000WO-US06884.  
 X 20-MAR-2000; 2000WO-US07377.  
 X (GETH ) GENENTECH INC.  
 X Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 X Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
 X Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
 X Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams FM, Wood WI;  
 X Zhang Z;  
 X WPI; 2001-032160/04.  
 X N-PSDB; AAF44129.

XX PRO polynucleotides used to produce polypeptides used to target  
 PT bioactive molecules such as toxins, radiolabels or antibodies, to  
 PT specific cells, to cause targeted cell death -  
 X Claim 12; Fig 68; 935pp; English.  
 XX The present invention describes human secreted and transmembrane PRO  
 CC proteins. The PRO proteins have cytotostatic activity. The PRO proteins  
 CC can be used for targeted delivery of bioactive molecules, such as  
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
 CC sequences, and their fragments, can be used as hybridisation probes, in  
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA  
 CC and DNA. They may also be used to produce transgenic animals which are  
 CC used to develop and screen therapeutically useful reagents. The PRO  
 CC nucleotide and protein sequence can be used for tissue typing and in  
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
 CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.  
 X Sequence 123 AA;  
 SQ Query Match 100.0%; Score 123; DB 22; Length 123;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-117;  
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Q 1 MACRCLSFLLMGTFLLSVQTLAQLDALLVFFGQVAQLSCTLSPOHVTIRDYGVSWYQOR 60  
 D 1 MACRCLSFLLMGTFLLSVQTLAQLDALLVFFGQVAQLSCTLSPOHVTIRDYGVSWYQOR 60  
 Q 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISPVQPEDDADYYCSGVG 120  
 D 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISPVQPEDDADYYCSGVG 120  
 Q 121 FSP 123  
 D 121 FSP 123  
 RESULT 6  
 AAB66770  
 ID AAB66770 standard; Protein; 123 AA.  
 AC AAB66770;  
 X 23-MAY-2003 (first entry)  
 X Human PRO polypeptide #201.  
 X Human; PRO polypeptide; secreted and transmembrane protein;  
 X tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;  
 X differentiation; chondrocyte; tumour; genetic disorder;  
 X cytotostatic.  
 X Homo sapiens.  
 X US2003036180-A1.  
 X 20-FEB-2003.  
 X 09-MAY-2002; 2002US-0143114.  
 X 31-MAR-1997; 97WO-US05230.  
 X 12-JUN-1998; 98WO-US12456.  
 X 14-JUL-1998; 98WO-US14552.  
 X 28-AUG-1998; 98WO-US17888.  
 X 10-SEP-1998; 98WO-US18824.  
 X 14-SEP-1998; 98WO-US19093.  
 X 14-SEP-1998; 98WO-US19094.  
 X 14-SEP-1998; 98WO-US19177.  
 X 16-SEP-1998; 98WO-US19330.



1	MACRCLFLLMGTFLSVSQTVLAQLDALLVFPQVQAQLSCTLSPQHVITIRDYGSWYQOR	60	QY
1	MACRCLFLLMGTFLSVSQTVLAQLDALLVFPQVQAQLSCTLSPQHVITIRDYGSWYQOR	60	Db
61	AGSAPRVLIIYRSEEDHRRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYGSVGX	120	QY
61	AGSAPRVLIIYRSEEDHRRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYGSVGX	120	Db
121	FSP	123	QY
121	FSP	123	Db

Qy	121	FSP	123
Db	121	FSP	123

RESULT 7  
BU67046  
D ABU67046 standard; Protein; 123 AA.  
X C  
X C ABU67046;  
X T  
X T 27-MAY-2003 (first entry)  
X X  
X X Human secreted/transmembrane, PRO, protein SEQ ID 402.  
E X  
X X Human; secreted protein; transmembrane protein; PRO;  
W W inflammatory disease; organ failure; atherosclerosis; cardiac injury;  
W W infertility; birth defects; premature aging; AIDS; biosensor;  
W W acquired immunodeficiency syndrome; cancer; diabetic complication;  
W W bioreactor; tumour.  
X X  
X X Homo sapiens.  
X X  
X X US2003032155-A1.  
X X  
X X 13-FEB-2003.  
X X  
X X 03-MAY-2002; 2002US-0137865.  
X X  
X X 31-MAR-1997; 97WO-US05230.  
X X 12-JUN-1998; 98WO-US12456.  
X X 14-JUL-1998; 98WO-US14552.  
X X 28-AUG-1998; 98WO-US17888.  
X X 10-SEP-1998; 98WO-US18924.  
X X 14-SEP-1998; 98WO-US19093.  
X X 14-SEP-1998; 98WO-US19094.  
X X 14-SEP-1998; 98WO-US19177.  
X X 16-SEP-1998; 98WO-US19330.  
X X 17-SEP-1998; 98WO-US19437.  
X X 07-OCT-1998; 98WO-US21141.  
X X 29-OCT-1998; 98WO-US22991.  
X X 29-OCT-1998; 98WO-US22992.  
X X 20-NOV-1998; 98WO-US24855.  
X X 01-DEC-1998; 98WO-US25108.  
X X 05-JAN-1999; 99WO-US00106.  
X X 08-MAR-1999; 99WO-US05028.  
X X 10-MAR-1999; 99WO-US05190.  
X X 20-APR-1999; 99WO-US08615.  
X X 14-MAY-1999; 99WO-US10733.  
X X 02-JUN-1999; 99WO-US12252.  
X X 01-SEP-1999; 99WO-US20111.  
X X 08-SEP-1999; 99WO-US20594.  
X X 13-SEP-1999; 99WO-US20944.  
X X 15-SEP-1999; 99WO-US21090.  
X X 15-SEP-1999; 99WO-US21547.  
X X 05-OCT-1999; 99WO-US23089.  
X X 29-NOV-1999; 99WO-US28214.  
X X 30-NOV-1999; 99WO-US28313.  
X X 30-NOV-1999; 99WO-US28409.  
X X 01-DEC-1999; 99WO-US28301.  
X X 01-DEC-1999; 99WO-US28634.  
X X 02-DEC-1999; 99WO-US28551.  
X X 02-DEC-1999; 99WO-US28564.  
X X 02-DEC-1999; 99WO-US28565.  
X X 16-DEC-1999; 99WO-US30095.  
X X 20-DEC-1999; 99WO-US30911.  
X X 20-DEC-1999; 99WO-US30999.  
X X 22-DEC-1999; 99WO-US30720.  
X X 30-DEC-1999; 99WO-US31243.  
X X 30-DEC-1999; 99WO-US31274.  
X X 05-JAN-2000; 2000WO-US00219.  
X X 06-JAN-2000; 2000WO-US00277.  
X X 06-JAN-2000; 2000WO-US00376.  
X X 11-FEB-2000; 2000WO-US03565.  
X X 18-FEB-2000; 2000WO-US04341.  
X X 18-FEB-2000; 2000WO-US04342.  
X X 22-FEB-2000; 2000WO-US04414.  
X X 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 01-MAR-2000; 2000WO-US05601.  
PR 02-MAR-2000; 2000WO-US05746.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
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PR 24-AUG-2000; 2000WO-US23328.  
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PR 20-DEC-2000; 2000WO-US34956.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US06666.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 22-JUN-2001; 2001WO-US20116.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 20-DEC-2000; 2000US-0747259.  
PR 28-FEB-2001; 2001US-0796498.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0805689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854208.  
PR 18-MAY-2001; 2001US-0860216.  
PR 23-MAY-2001; 2001US-0866028.  
PR 23-MAY-2001; 2001US-0865034.  
PR 01-JUN-2001; 2001US-0872035.  
PR 05-JUN-2001; 2001US-0874503.  
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PR 16-AUG-2001; 2001US-0931636.  
PR 19-DEC-2001; 2001US-0028072.  
PA (GETH ) GENENTECH INC.  
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
XX Gerritsen ME, Goddard A, Godowski RJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
XX WPI; 2003-331925/31.  
XX N-PSDB; ACA04224.  
XX New secreted and transmembrane nucleic acids and polypeptides,  
PT designated as PRO, useful for treating inflammation, organ failure,  
PT atherosclerosis, cardiac injury, infertility, birth defects, premature  
PT aging, AIDS, or cancer  
XX Claim 12; Fig 402; 659pp; English.  
XX The invention relates to an isolated nucleic acid comprising, or which is  
CC at least 80% identical to, or the full-length coding sequence of, any of  
CC the 25 nucleotide sequences, encoding the corresponding PRO polypeptide  
CC (one of 275 secreted or transmembrane proteins). The nucleic acid  
CC further comprises the full-length coding sequence of the DNA deposited  
CC under American Type Culture Collection (ATCC) accession number in a list

C given in the specification. Also included are vectors and host  
C cells for producing PRO proteins, PRO fusion proteins, anti-PRO  
C antibodies, PRO extracellular domains and mature sequences, methods  
C of detecting PRO proteins, methods for stimulating the release of  
C TNF-alpha (tumour necrosis factor alpha) from human blood,  
C and the proliferation of differentiation of chondrocyte cells, the  
C proliferation of, or gene expression in pericyte cells, the release or  
C proteoglycans from cartilage, proliferation of inner ear utricular  
C supporting cells, the proliferation of T-lymphocyte cells, the release  
C of a cytokine from peripheral blood mononuclear cells (PBMC), or the  
C proliferation of endothelial cells, a method for modulating the uptake  
C of glucose or free fatty acid (FFA) by skeletal muscle cells,  
C a method for inhibiting the binding of A-peptide to factor VIIa,  
C or the differentiation of adipocyte cells, a method for detecting the  
C presence of a tumour in a mammal and an oligonucleotide probe derived  
C from any of the nucleotide sequences cited above. The nucleic acids and  
C polypeptides are useful for treating inflammatory diseases, organ  
C failure, atherosclerosis, cardiac injury, infertility, birth defects,  
C premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or  
C diabetic complications. The nucleic acids are useful as hybridisation  
C probes, in chromosome and gene mapping, and in generating antisense RNA  
C or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,  
C biosensors or bioreactors. Both are useful in tissue typing.  
C The present sequence represents a PRO protein of the invention.

Q Sequence 123 AA;

Query Match 100.0%; Score 123; DB 24; Length 123;  
Best Local Similarity 100.0%; Pred. No. 4.8e-117;  
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Y 1 MACRCLSFLILMGTFLLSVSTVLAQLDALLVFPQVQLSCTLSPOHVTIRYGVSWYQQR 60  
b 1 MACRCLSFLILMGTFLLSVSTVLAQLDALLVFPQVQLSCTLSPOHVTIRYGVSWYQQR 60  
  
Y 61 AGSAPRYLLYRSEEDHHPADIPRFSAAKDAHNACVLTISPVPEDDADYTCVGVYG 120  
b 61 AGSAPRYLLYRSEEDHHPADIPRFSAAKDAHNACVLTISPVPEDDADYTCVGVYG 120

Y 121 FSP 123

b 121 FSP 123

RESULT 8

BU59851

D ABU59851 standard; Protein; 123 AA.

X ABU59851;

X 13-MAY-2003 (first entry)

X Novel secreted and transmembrane protein PRO619.

X Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
X cardiac insufficiency disorder; cancer; tumour; immune response;  
X adrenal cortical capillary endothelial growth; c-fos induction;  
X vascular endothelial growth factor inhibition; VEGF inhibition;  
X endothelial cell growth inhibitor; T-lymphocytes stimulation;  
X retinal neurons cell survival; rod photoreceptor cell survival;  
X retinal disorder; retinitis pigmentosa; kidney disorder;  
X mammalian kidney mesangial cell proliferation; Berger disease;  
X dermatitis; hepatiformis; Crohn's disease; chondrocyte proliferation;  
X chondrocyte redifferentiation; sports injury; arthritis.

X Homo sapiens.

X US2003017563-A1.

X 23-JAN-2003.

X 07-MAY-2002; 2002US-0140808.

PR 31-MAR-1997; 97WO-US05230.  
PR 12-JUN-1998; 98WO-US12456.  
PR 14-JUL-1998; 98WO-US14552.  
PR 26-AUG-1998; 98WO-US17888.  
PR 10-SEP-1998; 98WO-US18824.  
PR 14-SEP-1998; 98WO-US19093.  
PR 14-SEP-1998; 98WO-US19094.  
PR 16-SEP-1998; 98WO-US19177.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 29-OCT-1998; 98WO-US22991.  
PR 29-OCT-1998; 98WO-US22992.  
PR 29-OCT-1998; 98WO-US24855.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 98WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 10-MAR-1999; 99WO-US05190.  
PR 20-APR-1999; 99WO-US08615.  
PR 14-MAY-1999; 99WO-US10733.  
PR 02-JUN-1999; 99WO-US12252.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 13-SEP-1999; 99WO-US20944.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 23-NOV-1999; 99WO-US28214.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 02-DEC-1999; 99WO-US28551.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 20-DEC-1999; 99WO-US30999.  
PR 22-DEC-1999; 99WO-US30720.  
PR 30-DEC-1999; 99WO-US31243.  
PR 30-DEC-1999; 99WO-US31274.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00277.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 01-MAR-2000; 2000WO-US05601.  
PR 02-MAR-2000; 2000WO-US05746.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US06866.  
PR 25-MAY-2001; 2001WO-US17092.



R 20-MAR-2000; 2000WC-US07377.  
R 30-MAR-2000; 2000WC-US08439.  
R 15-MAY-2000; 2000WC-US13358.  
R 17-MAY-2000; 2000WC-US13705.  
R 22-MAY-2000; 2000WC-US14042.  
R 30-MAY-2000; 2000WC-US14941.  
R 02-JUN-2000; 2000WC-US15264.  
R 28-JUL-2000; 2000WC-US20710.  
R 11-AUG-2000; 2000WC-US22031.  
R 23-AUG-2000; 2000WC-US23522.  
R 24-AUG-2000; 2000WC-US23328.  
R 08-NOV-2000; 2000WC-US30952.  
R 01-DEC-2000; 2000WC-US32678.  
R 28-FEB-2001; 2001WC-US06520.  
R 01-JUN-2001; 2001WC-US17800.  
R 20-JUN-2001; 2001WC-US19692.  
R 29-JUN-2001; 2001WC-US21066.  
R 09-JUL-2001; 2001WC-US21735.  
R 16-JUN-1997; 97US-049787P.  
R 17-OCT-1997; 97US-062250P.  
R 12-NOV-1997; 97US-065186P.  
R 13-NOV-1997; 97US-065311P.  
R 24-NOV-1997; 97US-066770P.  
R 25-FEB-1998; 98US-075945P.  
R 20-MAR-1998; 98US-078910P.  
R 28-APR-1998; 98US-083322P.  
R 07-MAY-1998; 98US-084600P.  
R 28-MAY-1998; 98US-087106P.  
R 02-JUN-1998; 98US-087607P.  
R 02-JUN-1998; 98US-087809P.  
R 02-JUN-1998; 98US-087859P.  
R 03-JUN-1998; 98US-088272P.  
R 04-JUN-1998; 98US-088221P.  
R 04-JUN-1998; 98US-088025P.  
R 04-JUN-1998; 98US-088026P.  
R 04-JUN-1998; 98US-088028P.  
R 04-JUN-1998; 98US-088029P.  
R 04-JUN-1998; 98US-088030P.  
R 04-JUN-1998; 98US-088033P.  
R 04-JUN-1998; 98US-088326P.  
R 05-JUN-1998; 98US-088167P.  
R 05-JUN-1998; 98US-088202P.  
R 05-JUN-1998; 98US-088212P.  
R 05-JUN-1998; 98US-088217P.  
R 09-JUN-1998; 98US-088655P.  
R 10-JUN-1998; 98US-088734P.  
R 10-JUN-1998; 98US-088738P.  
R 10-JUN-1998; 98US-088742P.  
R 10-JUN-1998; 98US-088810P.  
R 10-JUN-1998; 98US-088824P.  
R 10-JUN-1998; 98US-088826P.  
R 11-JUN-1998; 98US-088858P.  
R 11-JUN-1998; 98US-088861P.  
R 11-JUN-1998; 98US-088876P.  
R 12-JUN-1998; 98US-089105P.  
R 16-JUN-1998; 98US-089440P.  
R 16-JUN-1998; 98US-089512P.  
R 16-JUN-1998; 98US-089514P.  
R 17-JUN-1998; 98US-089532P.  
R 17-JUN-1998; 98US-089538P.  
R 17-JUN-1998; 98US-089598P.  
R 17-JUN-1998; 98US-089599P.  
R 17-JUN-1998; 98US-089600P.  
R 17-JUN-1998; 98US-089653P.  
R 18-JUN-1998; 98US-089801P.  
R 18-JUN-1998; 98US-089807P.  
R 18-JUN-1998; 98US-089908P.  
R 28-AUG-2001; 2001US-0941992.

(GETH ) GENENTECH INC.

I Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
I Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;

PI Grimaldi JC, Gurney AL, Kljavin LJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
DR WPI; 2003-247083/24.  
DR N-PSDB; ABX80196.  
XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
PT are therapeutically useful for enhancing immune response and in cancer  
PT treatments -  
XX Claim 12; Fig 68; 648pp; English.  
XX The invention describes an isolated human PRO polypeptide. The PRO  
CC polypeptides are useful in detecting PRO polypeptides in a sample, in  
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
CC in modulating at least one biological activity of a cell expressing a PRO  
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,  
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
CC useful for treating conditions or disorders where angiogenesis would be  
CC beneficial, e.g. wound healing and antagonist of this polypeptide are  
CC useful for treating cancerous tumours. PRO812 inhibits vascular  
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial  
CC cells and is thus useful for inhibiting endothelial cell growth in  
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,  
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
CC stimulated T-lymphocytes and are therapeutically useful for enhancing  
CC immune response. PRO828, PRO826, PRO1068 or PRO132 enhance survival of  
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
CC rod photoreceptor cells) and therefore are useful for treating retinal  
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813  
CC and PRO11066 induce proliferation of mammalian kidney mesangial cells,  
CC and therefore are useful for treating kidney disorders associated with  
CC decreased mesangial cell function such as Berger disease or other  
CC nephropathies associated with dermatitis, herpetiformis or Crohn's  
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
CC proliferation and/or redifferentiation of chondrocytes in culture and  
CC are thus useful for treating sports injuries, and arthritis. This  
CC is the amino acid sequence of a novel human PRO protein.  
XX Sequence 123 AA;

Query Match 100.0%; Score 123; DB 24; Length 123;

Best Local Similarity 100.0%; Pred. No. 4.8e-117;

Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MACRCLSLMLMGTFSLVSQTVLAQLDALLVPPQVACLCTLSQHVTHIDYGVSYQQR 60  
Db 1 MACRCLSLMLMGTFSLVSQTVLAQLDALLVPPQVACLCTLSQHVTHIDYGVSYQQR 60  
QY 61 AGSAPRYLLYYRSEEDHRRPADI PDRFSAAKDEAHNAACVLTISPQPEDDADYYCVSYG 120  
Db 61 AGSAPRYLLYYRSEEDHRRPADI PDRFSAAKDEAHNAACVLTISPQPEDDADYYCVSYG 120  
QY 121 FSP 123  
Db 121 FSP 123

RESULT 10

ABU59218

ID ABU59218 standard; Protein; 123 AA.

XX ABU59218;

AC ABU59218;

XX 22-APR-2003 (first entry)

XX Human secreted/transmembrane protein, #43.

Human; PRO; secreted; transmembrane; pharmaceutical;  
diagnostic; biosensor; bioreactor; tumour; therapeutic;  
gene therapy; tumour-associated antigenic target; TAG; ADEPT;  
antibody-dependent enzyme mediated prodrug therapy; cytostatic.

Homo sapiens.

US2003027162-A1.

06-FEB-2003.

15-NOV-2001; 2001US-0997428.

05-NOV-1997; 97WO-US20069.

16-SEP-1998; 98WO-US19330.

17-SEP-1998; 98WO-US19437.

07-OCT-1998; 98WO-US21141.

01-DEC-1998; 98WO-US25108.

05-JAN-1999; 99WO-US00106.

08-MAR-1999; 99WO-US05028.

02-JUN-1999; 99WO-US12252.

15-SEP-1999; 99WO-US21090.

15-SEP-1999; 99WO-US211547.

30-NOV-1999; 99WO-US28313.

01-DEC-1999; 99WO-US28301.

01-DEC-1999; 99WO-US28334.

16-DEC-1999; 99WO-US30095.

20-DEC-1999; 99WO-US30911.

05-JAN-2000; 2000WO-US00219.

06-JAN-2000; 2000WO-US00376.

11-FEB-2000; 2000WO-US03565.

18-FEB-2000; 2000WO-US04341.

22-FEB-2000; 2000WO-US04414.

24-FEB-2000; 2000WO-US04914.

24-FEB-2000; 2000WO-US05004.

02-MAR-2000; 2000WO-US05841.

10-MAR-2000; 2000WO-US06319.

15-MAR-2000; 2000WO-US06684.

20-MAR-2000; 2000WO-US07377.

30-MAR-2000; 2000WO-US08439.

15-MAY-2000; 2000WO-US13358.

17-MAY-2000; 2000WO-US13705.

22-MAY-2000; 2000WO-US14042.

30-MAY-2000; 2000WO-US14941.

02-JUN-2000; 2000WO-US15264.

28-JUL-2000; 2000WO-US20710.

11-AUG-2000; 2000WO-US22031.

23-AUG-2000; 2000WO-US23522.

24-AUG-2000; 2000WO-US23328.

08-NOV-2000; 2000WO-US30952.

01-DEC-2000; 2000WO-US32678.

28-FEB-2001; 2001WO-US06520.

01-JUN-2001; 2001WO-US17800.

20-JUN-2001; 2001WO-US19692.

29-JUN-2001; 2001WO-US21066.

09-JUL-2001; 2001WO-US21735.

16-JUN-1997; 97US-049787P.

17-OCT-1997; 97US-062250P.

12-NOV-1997; 97US-065186P.

13-NOV-1997; 97US-065311P.

24-NOV-1997; 97US-066770P.

25-FEB-1998; 98US-075945P.

20-MAR-1998; 98US-076910P.

28-APR-1998; 98US-083322P.

07-MAY-1998; 98US-084600P.

28-MAY-1998; 98US-087106P.

02-JUN-1998; 98US-087607P.

02-JUN-1998; 98US-087609P.

02-JUN-1998; 98US-087759P.

03-JUN-1998; 98US-087827P.

04-JUN-1998; 98US-088021P.

04-JUN-1998; 98US-088025P.

04-JUN-1998; 98US-088026P.

PR 04-JUN-1998; 98US-088028P.  
PR 04-JUN-1998; 98US-088029P.  
PR 04-JUN-1998; 98US-088030P.  
PR 04-JUN-1998; 98US-088033P.  
PR 04-JUN-1998; 98US-088225P.  
PR 05-JUN-1998; 98US-088167P.  
PR 05-JUN-1998; 98US-088202P.  
PR 05-JUN-1998; 98US-088212P.  
PR 05-JUN-1998; 98US-088217P.  
PR 09-JUN-1998; 98US-088655P.  
PR 10-JUN-1998; 98US-088734P.  
PR 10-JUN-1998; 98US-088738P.  
PR 10-JUN-1998; 98US-088742P.  
PR 10-JUN-1998; 98US-088810P.  
PR 10-JUN-1998; 98US-088824P.  
PR 10-JUN-1998; 98US-088826P.  
PR 11-JUN-1998; 98US-088858P.  
PR 11-JUN-1998; 98US-088861P.  
PR 11-JUN-1998; 98US-088876P.  
PR 12-JUN-1998; 98US-089105P.  
PR 16-JUN-1998; 98US-089440P.  
PR 16-JUN-1998; 98US-089512P.  
PR 16-JUN-1998; 98US-089514P.  
PR 17-JUN-1998; 98US-089532P.  
PR 17-JUN-1998; 98US-089538P.  
PR 17-JUN-1998; 98US-089598P.  
PR 17-JUN-1998; 98US-089599P.  
PR 17-JUN-1998; 98US-089600P.  
PR 17-JUN-1998; 98US-089653P.  
PR 18-JUN-1998; 98US-089801P.  
PR 18-JUN-1998; 98US-089907P.  
PR 18-JUN-1998; 98US-089908P.  
PR 19-JUN-1998; 98US-089947P.  
PR 19-JUN-1998; 98US-089948P.  
PR 19-JUN-1998; 98US-089952P.  
PR 22-JUN-1998; 98US-090246P.  
PR 22-JUN-1998; 98US-090252P.  
PR 22-JUN-1998; 98US-090254P.  
PR 23-JUN-1998; 98US-090349P.  
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DT 01-MAY-2003 (first entry)

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 pharmaceutical; diagnostic; therapeutic; gene therapy.  
 Homo sapiens.

US2002160384-A1.

31-OCT-2002.

14-NOV-2001; 2001US-0992598.

05-NOV-1997; 97WO-US200069.

16-SEP-1998; 98WO-US19330.

17-SEP-1998; 98WO-US19437.

07-OCT-1998; 98WO-US21141.

01-DEC-1998; 98WO-US25108.

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(GETH ) GENENTECH INC.

Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
 Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
 Roy MA, Stewart TA, Tamas D, Watanabe CK, Williams FM, Wood WI;  
 Zhang Z;

WPI; 2003-288106/28.

N-PSDB; ABX90174.

PT New transmembrane polypeptides and nucleic acids encoding the  
 polypeptides, useful in gene therapy, in chromosome identification, as  
 chromosome markers, or in generating probes -

Claim 12; Fig 68; 650pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides  
 comprising a sequence without signal peptide and the nucleic acid  
 encoding them. The polypeptides can be used to raise antibodies that  
 specifically bind to the PRO polypeptide, for linking a bioactive  
 molecule to a cell expressing a PRO protein and for modulating at least  
 one biological activity of a cell. The PRO polypeptides or  
 polynucleotides are also useful in gene therapy, in chromosome  
 identification, as chromosome markers, or in generating probes. The PRO  
 polypeptides are useful as molecular markers for protein  
 electrophoresis, and the isolated nucleic acids may be used for  
 recombinantly expressing those markers. The PRO polypeptides and nucleic  
 acids may also be used in tissue typing. Anti-PRO antibodies are useful  
 in diagnostic assays for PRO, and in affinity purification of PRO from  
 recombinant cell culture or natural sources. The sequences presented in  
 ABU60478-ABU60624 are the PRO polynucleotides of the invention.  
 Note: The sequence data for this patent is also available in electronic  
 format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).

Sequence 123 AA;

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db 121 RSP 123

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KW horse; cow; dog; cat; sheep; pig; goat; rabbit; ADFT;
KW antibody-dependent enzyme mediated prodrug therapy.
DS Homo sapiens.
EN US2003027163-A1.
PD 06-FEB-2003.
PF 15-NOV-2001; 2001US-0997666.
PR 05-NOV-1997; 97WO-US20069.
PR 16-SEP-1998; 98WO-US19330.
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R 30-JUL-1998; 98US-094651P.
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R 04-AUG-1998; 98US-095285P.
R 04-AUG-1998; 98US-095301P.
R 04-AUG-1998; 98US-095302P.
R 04-AUG-1998; 98US-095318P.
R 04-AUG-1998; 98US-095321P.
R 04-AUG-1998; 98US-095321P.
R 04-AUG-1998; 98US-095325P.
R 10-AUG-1998; 98US-095916P.
R 10-AUG-1998; 98US-095929P.
R 10-AUG-1998; 98US-096012P.
R 11-AUG-1998; 98US-096143P.
R 11-AUG-1998; 98US-096146P.
R 12-AUG-1998; 98US-096329P.
R 17-AUG-1998; 98US-096757P.
R 17-AUG-1998; 98US-096766P.
R 17-AUG-1998; 98US-096768P.
R 17-AUG-1998; 98US-096773P.
R 17-AUG-1998; 98US-096791P.
R 17-AUG-1998; 98US-096867P.
R 17-AUG-1998; 98US-096891P.
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R 17-AUG-1998; 98US-096897P.
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R 18-AUG-1998; 98US-096950P.
R 18-AUG-1998; 98US-096959P.
R 18-AUG-1998; 98US-096960P.
R 18-AUG-1998; 98US-097022P.
R 19-AUG-1998; 98US-097141P.
R 20-AUG-1998; 98US-097218P.
R 24-AUG-1998; 98US-097661P.
R 26-AUG-1998; 98US-097952P.
R 26-AUG-1998; 98US-097954P.
R 26-AUG-1998; 98US-097955P.
R 26-AUG-1998; 98US-097971P.
R 26-AUG-1998; 98US-097974P.
R 26-AUG-1998; 98US-097978P.
R 26-AUG-1998; 98US-097979P.
R 26-AUG-1998; 98US-097986P.
R 26-AUG-1998; 98US-098014P.
R 31-AUG-1998; 98US-098525P.
R 16-SEP-1998; 98US-100634P.
R 17-SEP-1998; 98US-100858P.
R 22-DEC-1998; 98US-113296P.
R 12-MAR-1999; 98US-123957P.
R 23-JUN-1999; 98US-141037P.
R 07-JUL-1999; 98US-143048P.

Query Match 100.0%; Score 123; DB 24; Length 123;

Best Local Similarity 100.0%; Pred. No. 4.9e-117;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MACRCLSFLLNGTSLVSQTVLAQLDALLVPPGVAQLSCTLSPPQHVITRDYGVSWYQQR 60
DB 1 MACRCLSFLLNGTSLVSQTVLAQLDALLVPPGVAQLSCTLSPPQHVITRDYGVSWYQQR 60
QY 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISFVQPEDDADYCVSGYG 120
DB 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISFVQPEDDADYCVSGYG 120
QY 121 FSP 123
DB 121 FSP 123

RESULT 14
ABUS8924
ID ABUS8924 standard; Protein, 123 AA.
XX
AC ABUS8924;
XX
DT 16-APR-2003 (first entry)
DE Human secreted/transmembrane protein, #43.
XX
KW Human; PRO; secreted; transmembrane; signal peptide;
KW Pharmaceutical; diagnostic; biosensor; bioindicator; tumour; therapeutic;
KW Colon cancer; lung cancer; breast cancer; cancer; gene therapy.
XX
OS Homo sapiens.
XX
PN US2002142961-A1.
PD 03-OCT-2002.
XX
PF 19-NOV-2001; 2001US-0989721.
XX
05-NOV-1997; 97WO-US20069.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 02-JUN-1999; 99WO-US12252.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 15-MAY-2000; 2000WO-US13358.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 26-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
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08-NOV-2000; 2000WO-US310952.  
01-DEC-2000; 2000WO-US32678.  
28-FEB-2001; 2001WO-US06520.  
01-JUN-2001; 2001WO-US17800.  
20-JUN-2001; 2001WO-US19692.  
09-JUL-2001; 2001WO-US21066.  
16-JUN-1997; 97US-04978735.  
12-OCT-1997; 97US-062250P.  
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13-NOV-1997; 97US-085311P.  
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25-FEB-1998; 98US-075945P.  
20-MAR-1998; 98US-078910P.  
28-APR-1998; 98US-083332P.  
07-MAY-1998; 98US-084600P.  
28-MAY-1998; 98US-087106P.  
02-JUN-1998; 98US-087607P.  
02-JUN-1998; 98US-087609P.  
02-JUN-1998; 98US-087759P.  
03-JUN-1998; 98US-087827P.  
04-JUN-1998; 98US-088021P.  
04-JUN-1998; 98US-088025P.  
04-JUN-1998; 98US-088026P.  
04-JUN-1998; 98US-088028P.  
04-JUN-1998; 98US-088029P.  
04-JUN-1998; 98US-088030P.  
04-JUN-1998; 98US-088033P.  
04-JUN-1998; 98US-088326P.  
05-JUN-1998; 98US-088167P.  
05-JUN-1998; 98US-088202P.  
05-JUN-1998; 98US-088212P.  
05-JUN-1998; 98US-088217P.  
09-JUN-1998; 98US-088655P.  
10-JUN-1998; 98US-088734P.  
10-JUN-1998; 98US-088738P.  
10-JUN-1998; 98US-088742P.  
10-JUN-1998; 98US-088810P.  
10-JUN-1998; 98US-088824P.  
10-JUN-1998; 98US-088826P.  
11-JUN-1998; 98US-088858P.  
11-JUN-1998; 98US-088861P.  
11-JUN-1998; 98US-088876P.  
12-JUN-1998; 98US-089105P.  
16-JUN-1998; 98US-089440P.  
16-JUN-1998; 98US-089512P.  
16-JUN-1998; 98US-089514P.  
17-JUN-1998; 98US-089532P.  
17-JUN-1998; 98US-089538P.  
17-JUN-1998; 98US-089598P.  
17-JUN-1998; 98US-089599P.  
17-JUN-1998; 98US-089600P.  
17-JUN-1998; 98US-089653P.  
18-JUN-1998; 98US-089801P.  
18-JUN-1998; 98US-089907P.  
18-JUN-1998; 98US-089908P.  
28-AUG-2001; 2001US-0941992.

(GETH ) GENENTECH INC.

Ashtenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
Grimaldi JC, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF;  
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams EM, Wood WI;  
Zhang Z;  
WPI; 2003-155950/15.

New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184, PRO361 or PRO846) useful as targets for therapeutic intervention in cancers (e.g. lung or breast cancers), or for diagnosing these cancers

Claim 12; Fig 68; 647pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides comprising a sequence without signal peptide and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. The PRO polypeptides or polynucleotides are also useful as pharmaceuticals, diagnostics, biosensors or bioreactors, for detecting or treating e.g. tumours in mammals, e.g. humans, dogs, cats, cattle, horses, sheep, goats or rabbits, as targets for therapeutic intervention in certain cancers (e.g. colon, lung or breast cancers) and diagnostic determination of the presence of these cancers. The PRO polypeptides are also useful as molecular weight markers or for chromosome identification. The PRO genes are useful as hybridisation probes or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequences presented in ABUS8900-ABUS9046 are the PRO polypeptides of the invention.

Sequence 123 AA;

Query Match 100.0%; Score 123; DB 24; Length 123;  
Best Local Similarity 100.0%; Pred. No. 4.8e-117;  
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MACRCLSFLMGTFLSVSQTLAQLDALLVFPQVAQLSCTLSPOHVTIRYGYSWYQQR 60  
Db 1 MACRCLSFLMGTFLSVSQTLAQLDALLVFPQVAQLSCTLSPOHVTIRYGYSWYQQR 60  
Qy 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISPVQPEDDADYCSVGYG 120  
Db 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAKDEAHNACVLTISPVQPEDDADYCSVGYG 120  
Qy 121 FSP 123  
Db 121 FSP 123

RESULT 15

ABU13884  
ID ABU13884 standard; Protein; 123 AA.  
XX AC ABU13884;  
XX DT 26-FEB-2003 (first entry)  
XX DE Human PRO619 polypeptide.  
XX KW Human; PRO polypeptide; secreted protein; transmembrane protein;  
XX KW genetic disorder; antibacterial; immunosuppressive.  
XX OS Homo sapiens.  
XX PN US2002103125-A1.  
XX PD 01-AUG-2002.  
XX PF 20-NOV-2001; 2001US-0989731.  
XX PR 05-NOV-1997; 97WO-US20069.  
XX PR 16-SEP-1998; 98WO-US19330.  
XX PR 17-SEP-1998; 98WO-US19437.  
XX PR 07-OCT-1998; 98WO-US21141.  
XX PR 01-DEC-1998; 98WO-US25108.  
XX PR 05-JAN-1999; 99WO-US00106.  
XX PR 08-MAR-1999; 99WO-US05028.  
XX PR 02-JUN-1999; 99WO-US12252.  
XX PR 15-SEP-1999; 99WO-US21090.  
XX PR 15-SEP-1999; 99WO-US21547.  
XX PR 30-NOV-1999; 99WO-US28313.  
XX PR 01-DEC-1999; 99WO-US28301.  
XX PR 01-DEC-1999; 99WO-US28634.

R 16-DEC-1999; 99WO-US30095.  
R 20-DEC-1999; 99WO-US30911.  
R 06-JAN-2000; 2000WO-US00219.  
R 08-JAN-2000; 2000WO-US00376.  
R 11-FEB-2000; 2000WO-US03565.  
R 18-FEB-2000; 2000WO-US04341.  
R 22-FEB-2000; 2000WO-US04414.  
R 24-FEB-2000; 2000WO-US04914.  
R 02-MAR-2000; 2000WO-US05004.  
R 10-MAR-2000; 2000WO-US05841.  
R 15-MAR-2000; 2000WO-US06319.  
R 20-MAR-2000; 2000WO-US06884.  
R 30-MAR-2000; 2000WO-US07377.  
R 15-MAY-2000; 2000WO-US08439.  
R 17-MAY-2000; 2000WO-US13358.  
R 22-MAY-2000; 2000WO-US13705.  
R 30-MAY-2000; 2000WO-US14042.  
R 02-JUN-2000; 2000WO-US14941.  
R 08-JUN-2000; 2000WO-US15264.  
R 28-JUL-2000; 2000WO-US20710.  
R 11-AUG-2000; 2000WO-US22031.  
R 23-AUG-2000; 2000WO-US23522.  
R 24-AUG-2000; 2000WO-US23328.  
R 08-NOV-2000; 2000WO-US30952.  
R 01-DEC-2000; 2000WO-US32678.  
R 28-FEB-2001; 2001WO-US06520.  
R 01-JUN-2001; 2001WO-US17800.  
R 20-JUN-2001; 2001WO-US19692.  
R 29-JUN-2001; 2001WO-US21066.  
R 09-JUL-2001; 2001WO-US21735.  
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R 20-MAR-1998; 98US-078910P.  
R 28-APR-1998; 98US-083322P.  
R 07-MAY-1998; 98US-084600P.  
R 28-MAY-1998; 98US-087106P.  
R 02-JUN-1998; 98US-087609P.  
R 02-JUN-1998; 98US-087759P.  
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R 04-JUN-1998; 98US-088021P.  
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R 04-JUN-1998; 98US-088026P.  
R 04-JUN-1998; 98US-088028P.  
R 04-JUN-1998; 98US-088029P.  
R 04-JUN-1998; 98US-088030P.  
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R 05-JUN-1998; 98US-088202P.  
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R 10-JUN-1998; 98US-088738P.  
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R 10-JUN-1998; 98US-088824P.  
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R 11-JUN-1998; 98US-088861P.  
R 12-JUN-1998; 98US-088876P.  
R 12-JUN-1998; 98US-089105P.  
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R 17-JUN-1998; 98US-089598P.

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PR 17-JUN-1998; 98US-089600P.  
PR 17-JUN-1998; 98US-089653P.  
PR 18-JUN-1998; 98US-089801P.  
PR 18-JUN-1998; 98US-089907P.  
PR 18-JUN-1998; 98US-089908P.  
PR 28-AUG-2001; 2001US-0941992.  
XX  
XX (GETH ) GENENTECH LTD.  
XX  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrera N, Fong S, Gerber H, Gerritsen WE, Goddard A, Godowski RJ;  
PI Grimaldi JC, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
XX  
XX WPI: 2003-102117/09.  
DR N-PSDB; ABX64020.  
XX  
XX Novel secreted and transmembrane polypeptide for modulating biological  
PT activity of cell expressing the polypeptide, identifying agonists or  
PT antagonists of polypeptide, and as molecular weight markers -  
XX  
PS Claim 12; Fig 68; 649pp; English.  
XX  
CC The present invention relates to the isolation of novel human PRO  
CC polypeptides, and the polynucleotide sequences encoding them. The  
CC PRO polypeptides are secreted and transmembrane proteins. The PRO  
CC polypeptides are useful for detecting other PRO polypeptides, for  
CC linking bioactive molecules to cells expressing PRO polypeptides,  
CC for modulating biological activities of cells expressing PRO  
CC polypeptides, and for identifying agonists or antagonists.  
CC The polynucleotide sequences encoding PRO polypeptides are useful as  
CC hybridisation probes, in chromosome and gene mapping, in the generation  
CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for  
CC generating transgenic animals or knockout animals, to construct  
CC hybridisation probes for mapping the gene which encodes the PRO  
CC polypeptide, and for the genetic analysis of individuals with genetic  
CC disorders, in gene therapy, for chromosome identification, as  
CC chromosome markers, and for generating probes for PCR, Northern  
CC analysis, Southern analysis and Western analysis. ABU13860-ABU14006  
CC represent the human PRO polypeptides of the invention.  
CC Note: The sequence data for this patent was obtained in electronic  
CC format directly from the USPTO web site at  
CC seqdata.uspto.gov/psipsdEntry.html.  
XX  
XX Sequence 123 AA;  
SQ  
Query Match 100.0%; Score 123; DB 24; Length 123;  
Best Local Similarity 100.0%; Pred. No. 4.8e-117;  
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MACRCLSFLMGTFILSVSOTVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQQR 60  
Db 1 MACRCLSFLMGTFILSVSOTVLAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQQR 60  
Qy 61 AGSAPRYLLYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYCSGVYG 120  
Db 61 AGSAPRYLLYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYCSGVYG 120  
Qy 121 FSP 123  
Db 121 FSP 123  
RESULT 16  
ABU10839  
ID ABU10839 standard; Protein; 123 AA.  
XX  
AC ABU10839;  
XX  
DT 04-FEB-2003 (first entry)  
XX

DE Human PRO polypeptide #25.  
CX Human; PRO; secreted polypeptide; transmembrane polypeptide;  
CX toxin; radiolabel; cell death; gene mapping; chromosome mapping;  
CW protein electrophoresis; Genetic disorder; immunosuppressive; cytostatic;  
CW antibacterial.  
CX Homo sapiens.  
CX US2002123463-A1.  
CX 05-SEP-2002.  
CX 19-NOV-2001; 2001US-0969732.  
CX 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 30-NOV-1999; 99WO-US21547.  
PR 01-DEC-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 06-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06894.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-049787P.  
PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-068770P.  
PR 25-FEB-1998; 98US-075545P.  
PR 20-MAR-1998; 98US-078910P.  
PR 28-APR-1998; 98US-083322P.  
PR 07-MAY-1998; 98US-084600P.  
PR 28-MAY-1998; 98US-087106P.  
PR 02-JUN-1998; 98US-087607P.  
PR 02-JUN-1998; 98US-087609P.  
PR 02-JUN-1998; 98US-087759P.  
PR 03-JUN-1998; 98US-087827P.  
PR 04-JUN-1998; 98US-088021P.

PR 04-JUN-1998; 98US-088025P.  
PR 04-JUN-1998; 98US-088026P.  
PR 04-JUN-1998; 98US-088028P.  
PR 04-JUN-1998; 98US-088029P.  
PR 04-JUN-1998; 98US-088030P.  
PR 04-JUN-1998; 98US-088033P.  
PR 04-JUN-1998; 98US-088326P.  
PR 05-JUN-1998; 98US-088167P.  
PR 05-JUN-1998; 98US-088202P.  
PR 05-JUN-1998; 98US-088212P.  
PR 05-JUN-1998; 98US-088217P.  
PR 09-JUN-1998; 98US-088655P.  
PR 10-JUN-1998; 98US-088734P.  
PR 10-JUN-1998; 98US-088738P.  
PR 10-JUN-1998; 98US-088742P.  
PR 10-JUN-1998; 98US-088810P.  
PR 10-JUN-1998; 98US-088824P.  
PR 10-JUN-1998; 98US-088826P.  
PR 11-JUN-1998; 98US-088858P.  
PR 11-JUN-1998; 98US-088861P.  
PR 11-JUN-1998; 98US-088876P.  
PR 12-JUN-1998; 98US-089105P.  
PR 16-JUN-1998; 98US-089440P.  
PR 16-JUN-1998; 98US-089512P.  
PR 16-JUN-1998; 98US-089514P.  
PR 17-JUN-1998; 98US-089532P.  
PR 17-JUN-1998; 98US-089538P.  
PR 17-JUN-1998; 98US-089598P.  
PR 17-JUN-1998; 98US-089599P.  
PR 17-JUN-1998; 98US-089600P.  
PR 17-JUN-1998; 98US-089653P.  
PR 18-JUN-1998; 98US-089801P.  
PR 18-JUN-1998; 98US-089907P.  
PR 18-JUN-1998; 98US-089908P.  
PR 28-AUG-2001; 2001US-0941992.  
XX (GETH ) GENENTECH INC.  
PA Atkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
XX Ferraz N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
XX WPI; 2003-066810/06.  
DR N-PSDB; ABX16984.  
XX Novel secreted and transmembrane polypeptide for modulating biological  
PT activity of cell expressing the polypeptide, identifying agonists or  
PT antagonists of polypeptide, and as molecular weight markers  
XX Claim 12; Fig 68; 655pp; English.

The invention relates to a secreted and transmembrane polypeptide, termed PRO polypeptide, and the polynucleotide encoding it. The polypeptide is useful for detecting PRO polypeptides and for linking a bioactive molecule to a cell expressing the above polypeptides, where the bioactive molecule is a toxin, radiolabel or an antibody. The bioactive material causes the death of the cell. The polypeptide is useful for identifying agonists or antagonists of the PRO polypeptide, for preparing variants of PRO, as a molecular weight marker for protein electrophoresis purposes and the PRO polynucleotide is also useful as a hybridisation probe, in markers. The polynucleotide is also useful as a hybridisation probe, in chromosome and gene mapping, in generation of antisense RNA and DNA, in the preparation of PRO polypeptide, for generating transgenic animals or knockout animals which in turn are useful in the development and screening of therapeutically useful reagents, to construct hybridisation probes for mapping the gene which encodes PRO and for the genetic analysis of individuals with genetic disorders, in gene therapy, for chromosome identification, as a chromosome marker and for generating probes for PCR, Northern analysis, Southern analysis and Western analysis. This sequence represents a human PRO polypeptide of the invention.

XX Sequence 123 AA;  
Query Match 100.0%; Score 123; DB 24; Length 123;  
Best Local Similarity 100.0%; Pred. No. 4.8e-117;  
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 MACRCFLMGTFLSVQTVAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQOR 60  
b 1 MACRCFLMGTFLSVQTVAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQOR 60

Y 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAAKDEAHNACVLTISPQPEDDADYCSVG 120  
b 61 AGSAPRYLLYRSEEDHRRPADIPDRFSAAKDEAHNACVLTISPQPEDDADYCSVG 120

Y 121 FSP 123  
b 121 FSP 123

RESULT 17  
IAM39690  
ID AM39690 standard; Protein; 141 AA.  
XX AC AM39690;  
XX DT 22-OCT-2001 (first entry)  
XX DE Human polypeptide SEQ ID NO 2835.  
XX KW Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia.  
XX OS Homo sapiens.  
XX PN WO200153312-A1.  
XX PD 26-JUL-2001.  
XX PF 26-DEC-2000; 2000WO-US34263.  
XX PR 21-JAN-2000; 2000US-0488725.  
XX PR 25-APR-2000; 2000US-0552317.  
XX PR 09-JUL-2000; 2000US-0598042.  
XX PR 19-JUL-2000; 2000US-0620312.  
XX PR 03-AUG-2000; 2000US-0653450.  
XX PR 14-SEP-2000; 2000US-0682191.  
XX PR 19-OCT-2000; 2000US-0693036.  
XX PR 29-NOV-2000; 2000US-0727344.  
XX PA (HYSEQ-) HYSEQ INC.  
XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;  
XX WPI; 2001-442253/47.  
XX DR N-PSDB; AAI58846.  
XX PT Novel nucleic acids and polypeptides, useful for treating disorders  
XX such as central nervous system injuries -  
XX Example 4; SEQ ID NO 2835; 10078pp; English.  
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and  
CC the encoded polypeptides (AAI38642-AAI42213) with nontropic,  
CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC of the invention may be used to treat diseases of the peripheral nervous

CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localised neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilisation of the activities such as: immune system suppression,  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification.

XX SQ Sequence 141 AA;  
Query Match 96.7%; Score 119; DB 22; Length 141;  
Best Local Similarity 100.0%; Pred. No. 6.3e-113;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CLSFLMGTFLSVQTVAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQORAGSA 64  
b 23 CLSFLMGTFLSVQTVAQLDALLVFPQVAQLSCTLSPOHVTIRDYGVSWYQORAGSA 82

QY 65 PRYLLYRSEEDHRRPADIPDRFSAAKDEAHNACVLTISPQPEDDADYCSVGFSF 123  
b 83 PRYLLYRSEEDHRRPADIPDRFSAAKDEAHNACVLTISPQPEDDADYCSVGFSF 141

RESULT 18  
AAM41476  
ID AAM41476 standard; Protein; 113 AA.  
XX AC AAM41476;  
XX DT 22-OCT-2001 (first entry)  
XX DE Human polypeptide SEQ ID NO 6407.  
XX KW Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia.  
XX OS Homo sapiens.  
XX PN WO200153312-A1.  
XX PD 26-JUL-2001.  
XX PF 26-DEC-2000; 2000WO-US34263.  
XX PR 21-JAN-2000; 2000US-0488725.  
XX PR 25-APR-2000; 2000US-0552317.  
XX PR 09-JUL-2000; 2000US-0598042.  
XX PR 19-JUL-2000; 2000US-0620312.  
XX PR 03-AUG-2000; 2000US-0653450.  
XX PR 14-SEP-2000; 2000US-0662191.  
XX PR 19-OCT-2000; 2000US-0693036.  
XX PR 29-NOV-2000; 2000US-0727344.  
XX PA (HYSEQ-) HYSEQ INC.  
XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;  
XX WPI; 2001-442253/47.  
XX DR N-PSDB; AAI60632.  
XX PT Novel nucleic acids and polypeptides, useful for treating disorders  
XX such as central nervous system injuries -

PS Example 2; SEQ ID NO 6407; 10078pp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and

CC the encoded polypeptides (AA386642-AA42213) with neurotropic,

CC immunosuppressant and cytostatic activity. The polypeptide or polynucleotide

CC of the invention may be used to treat diseases of the peripheral nervous

CC system, such as peripheral nervous injuries, peripheral neuropathy and

CC localised neuropathies and central nervous system diseases, such as

CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the

CC utilisation of the activities such as: Immune system suppression,

CC activation/inhibition activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,

CC assays for receptor activity, arthritis and inflammation, leukaemias and

CC C.N.S disorders.

CC Note: The sequence data for this patent did not form part of the printed

CC specification.

XX Sequence 113 AA;

SQ

Query Match 87.0%; Score 107; DB 22; Length 113;

Best Local Similarity 100.0%; Pred. No. 8.2e-101;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 VSQTVLAQIDALLVFPFGVQAQLSCTLSPOHVTIRDYGVSMTQQRAGSAPRYLLYRSEED 76

Db 7 VSQTVLAQIDALLVFPFGVQAQLSCTLSPOHVTIRDYGVSMTQQRAGSAPRYLLYRSEED 66

QY 77 HRPADIPDRFSAKDEAHNACVLTISVPQEDDADYYCYSVGYGFSP 123

Db 67 HRPADIPDRFSAKDEAHNACVLTISVPQEDDADYYCYSVGYGFSP 113

RESULT 19

ABP45354

ID ABP45354 standard; Protein; 258 AA.

XX

AC ABP45354;

XX

DT 19-AUG-2002 (first entry)

XX

DE Human BlyS binding scPv SEQ ID 1365.

XX

XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;

XX tumour necrosis factor; B cell proliferation; B cell differentiation;

XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;

XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

XX common variable immunodeficiency; acquired immunodeficiency syndrome.

XX

OS Homo sapiens.

XX

PN WO200202641-A1.

XX

PD 10-JAN-2002.

XX

PF 15-JUN-2001; 2001WO-US19110.

XX

PR 16-JUN-2000; 2000US-212210P.

PR 17-OCT-2000; 2000US-240816P.

PR 16-MAR-2001; 2001US-276248P.

PR 21-MAR-2001; 2001US-277379P.

PR 25-MAY-2001; 2001US-293499P.

XX

XX (HUMA-) HUMAN GENOME SCI INC.

PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

PI WPI; 2002-114799/15.

XX

XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for

PT

PT the diagnosis and treatment of cancers and immune disorders -

XX Claim 1; Page 2031-2032; 3148pp; English.

XX

XX This invention describes novel antibodies that immunospecifically bind to

CC B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the

CC tumour necrosis factor (TNF) super family and induces B cell

CC proliferation and differentiation. The antibodies of the invention have

CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,

CC antirheumatic and antiAIDS activity and can be used in vaccines to

CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS in

CC and so may be used to detect and quantitate the presence of BlyS in

CC biological samples and may be used in this way to diagnose disease

CC associated with aberrant expression of BlyS. They may also be

CC administered to treat diseases associated with aberrant BlyS expression

CC and activity such as cancer, immune, and autoimmune disorders and

CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,

CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and

CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent

CC the antibodies and fragments of the antibodies described in the method

CC of the invention.

XX

SQ Sequence 258 AA;

Query Match 7.3%; Score 9; DB 23; Length 258;

Best Local Similarity 100.0%; Pred. No. 0.76;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 EDDADYYCS 116

Db 230 EDDADYYCS 238

RESULT 20

AA38953

ID AA38953 standard; Protein; 235 AA.

XX

AC AA38953;

XX

DT 22-OCT-2001 (first entry)

XX

DE Human polypeptide SEQ ID NO 2098.

XX

XX Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;

XX peripheral nervous system; neuropathy; central nervous system; CNS;

XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

XX leukaemia.

XX

OS Homo sapiens.

XX

PN WO200153312-A1.

XX

PD 26-JUL-2001.

XX

PF 26-DEC-2000; 2000WO-US34263.

XX

PR 21-JAN-2000; 2000US-0488725.

PR 25-APR-2000; 2000US-0582317.

PR 09-JUL-2000; 2000US-0596042.

PR 19-JUL-2000; 2000US-0620312.

PR 03-AUG-2000; 2000US-0653450.

PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000; 2000US-0693036.

PR 29-NOV-2000; 2000US-0727344.

XX

XX (HYSE-) HYSEQ INC.

PA

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX





CC The invention relates to human novel polynucleotides and associated  
 CC polypeptides. The polynucleotides and polypeptides are useful for  
 CC treating inflammatory conditions such as arthritis, nephritis, Crohn's  
 CC disease, ischaemia-reperfusion injury, shock, sepsis, immune responses  
 CC and cancer and for promoting wound healing. The sequences are used to  
 CC induce the proliferation of neural cells and regeneration of nerve and  
 CC brain tissue, and are useful for the treatment of central and peripheral  
 CC nervous system diseases and neuropathies, such as Alzheimer's disease,  
 CC Parkinson's disease, Huntington's disease and amyotrophic lateral  
 CC sclerosis. The sequences are involved in chemotactic or chemokinetic  
 CC activity, regulation of haematopoiesis, treatment of myeloid or lymphoid  
 CC cell disorders and platelet disorders such as thrombocytopenia,  
 CC regeneration of bone, cartilage, tendon, ligament and/or nerve tissue  
 CC growth, tissue repair, healing of burns, incisions, ulcers, treatment of  
 CC osteoporosis, osteoarthritis, bone degenerative disorders and periodontal  
 CC disease. The sequences of the invention are also useful for gut  
 CC protection or regeneration and treatment of lung or liver fibrosis,  
 CC including severe combined immunodeficiency (SCID), bacterial or fungal  
 CC infections, autoimmune disorders e.g. multiple sclerosis and myasthenia  
 CC gravis, allergic conditions such as asthma, thrombolytic or thrombotic  
 CC and coagulation disorders. Sequences ABG66666-ABG66758 represent human  
 CC novel polypeptides of the invention.

XX Sequence 526 AA;  
 SQ

Query Match 6.5%; Score 8; DB 23; Length 526;  
 Best Local Similarity 100.0%; Pred. No. 15;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 TISPVQPE 108  
 DB 96 TISPVQPE 103  
 |||||

RESULT 23  
 ABG66689  
 ID ABG66689 standard; Protein; 588 AA.

AC ABG66689;

XX 30-AUG-2002 (first entry)

DE Human novel polypeptide #24.

XX Human; inflammatory condition; shock; sepsis; immune response;  
 KW cancer; wound healing; central nervous system disease; haematopoiesis;  
 KW peripheral nervous system disease; amyotrophic lateral sclerosis; tendon;  
 KW myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone;  
 KW cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis;  
 KW bone degenerative disorder; periodontal disease; reperfusion injury;  
 KW lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection;  
 KW allergic condition; thrombolytic; thrombosis; coagulation disorder;  
 KW fungal infection.

XX Homo sapiens.

XX WO200244340-A2.

XX 06-JUN-2002.

XX 30-NOV-2001; 2001WO-US47004.

XX 30-NOV-2000; 2000US-0028952.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Wang J, Wang D;

PI Yamazaki V, Ujwal ML, Dmanac RT;

XX WPI; 2002-508509/54.

DR N-PSDB; ABK94913.

XX

PT Novel nucleic acids and polypeptides for diagnosis, treatment of  
 PT inflammatory, autoimmune, nervous system, myeloid or lymphoid cell  
 PT disorders, cancer and promoting wound healing -  
 XX Claim 10; Page 590-591; 672pp; English.

XX The invention relates to human novel polynucleotides and associated  
 CC polypeptides. The polynucleotides and polypeptides are useful for  
 CC treating inflammatory conditions such as arthritis, nephritis, Crohn's  
 CC disease, ischaemia-reperfusion injury, shock, sepsis, immune responses  
 CC and cancer and for promoting wound healing. The sequences are used to  
 CC induce the proliferation of neural cells and regeneration of nerve and  
 CC brain tissue, and are useful for the treatment of central and peripheral  
 CC nervous system diseases and neuropathies, such as Alzheimer's disease,  
 CC Parkinson's disease, Huntington's disease and amyotrophic lateral  
 CC sclerosis. The sequences are involved in chemotactic or chemokinetic  
 CC activity, regulation of haematopoiesis, treatment of myeloid or lymphoid  
 CC cell disorders and platelet disorders such as thrombocytopenia, and  
 CC regeneration of bone, cartilage, tendon, ligament and/or nerve tissue  
 CC growth, tissue repair, healing of burns, incisions, ulcers, treatment of  
 CC osteoporosis, osteoarthritis, bone degenerative disorders and periodontal  
 CC disease. The sequences of the invention are also useful for gut  
 CC protection or regeneration and treatment of lung or liver fibrosis,  
 CC including severe combined immunodeficiency (SCID), bacterial or fungal  
 CC infections, autoimmune disorders e.g. multiple sclerosis and myasthenia  
 CC gravis, allergic conditions such as asthma, thrombolytic or thrombotic  
 CC and coagulation disorders. Sequences ABG66666-ABG66758 represent human  
 CC novel polypeptides of the invention.

SQ Sequence 588 AA;

Query Match 6.5%; Score 8; DB 23; Length 588;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 TISPVQPE 108  
 DB 96 TISPVQPE 103  
 |||||

RESULT 24

AAE01020

ID AAE01020 standard; Protein; 689 AA.

XX AAE01020;

XX 17-JUL-2001 (first entry)

DT Human pif-1 type helicase protein.

DE Human; pif-1 type helicase; cytostatic; antiinflammatory; antiviral;  
 KW antisense therapy; telomerase; cellular senescence; cancer; tumour;  
 KW lymphoma; leukaemia; viral replication disease; retroviral disease.

XX Homo sapiens.

XX WO200130986-A2.

XX 03-MAY-2001.

XX 18-OCT-2000; 2000WO-US28780.

XX 22-OCT-1999; 99US-0425335.

XX (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX Weinmann R, Yang W;

PI WPI; 2001-300502/31.

DR N-PSDB; AAD04757.

XX

PT Novel human homolog of yeast helicase, Pif-1 useful for generating

antibodies for detection of hPif1 protein for diagnostic or clinical purposes, and for screening drugs which either modulate helicase activity

Claim 9; Fig 2; 57pp; English.

The present protein sequence is human homologue of yeast helicase, Pif-1. Pif-1 type helicase affects the formation or elongation of telomerase and/or interaction with components of the replication machinery. They are also involved in Arp binding or hydrolysis. Pif-1 modulators are useful for modulating a disorder which are characterised by the presence of cells exhibiting elevated helicase activity or decreased telomerase activity, or vice versa. Pif-1 or Pif-1 modulators are used to treat cellular senescence, cancer, tumours (e.g. solid tumours, lymphomas, leukaemia), viral replication diseases (including DNA and RNA viral replication diseases such as retroviral diseases and herpes) and inflammatory responses. Pif-1 is useful for generating antibodies for detection of human Pif-1 (hPif-1) protein for diagnostic or clinical purposes, and for screening drugs which either increase or decrease the activity of Pif-1. Pif-1 DNA is useful in antisense therapy.

Sequence 689 AA;

Query Match 6.5%; Score 8; DB 22; Length 689;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

101 TISPVQPE 108  
149 TISPVQPE 156

RESULT 25  
ABG21666  
ID ABG21666 standard; Protein; 1249 AA.

AC ABG21666;

18-FEB-2002 (first entry)

Novel human diagnostic protein #21657.

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

Homo sapiens.

WO200175067-A2.

11-OCT-2001.

30-MAR-2001; 2001WO-US08631.

31-MAR-2000; 2000US-0540217.

23-AUG-2000; 2000US-0649167.

(HYSE-) HYSEQ INC.

Drmanac RT, Liu C, Tang YT;

WPI; 2001-639362/73.

N-PGDB; AAS85853.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity

Claim 20; SEQ ID No 52025; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes,

polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.  
Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 1249 AA;

Query Match 6.5%; Score 8; DB 22; Length 1249;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 RCLSFLLM 11  
1037 RCLSFLLM 1044

RESULT 26

ABP76447

ID ABP76447 standard; Peptide; 14 AA.

AC ABP76447;

24-FEB-2003 (first entry)

Peptidomimetic antimicrobial peptide related peptide SEQ ID NO:79.

Template-fixed peptidomimetic; antimicrobial; beta-hairpin; cytostatic; antibacterial; infection; cystic fibrosis; lung infection; malignant; cancer; disinfectant; preservative.

Synthetic.

WO200270547-A1.

12-SEP-2002.

18-FEB-2002; 2002WO-EF01711.

23-FEB-2001; 2001WO-EF02072.

(POLY-) POLYPHOS LTD.

(UVZU-) UNIV ZUERICH.

Obrecht D, Robinson JA, Vrijbloed JW;

WPI; 2003-103173/09.

New beta-hairpin peptidomimetic compounds, useful for treating infections, especially cystic fibrosis lung infections and cancer, and as disinfectants/preservatives for e.g. foodstuffs or cosmetics

Example; Page 159; 262pp; English.

The present invention describes template-fixed beta-hairpin peptidomimetic compounds (I) and (II). Also described: (1) preparation of (I) and (II); and (2) a modification of the preparation in which enantiomers or all chiral starting materials are used. (I) and (II) have antibacterial and cytostatic activities. The peptidomimetic compounds

CC are useful for treating or preventing infections or diseases related to  
 CC such infections, especially cystic fibrosis lung infections; for  
 CC preparing medicaments useful against malignant cells for treatment of  
 CC cancer; as disinfectants or preservatives for foodstuffs, cosmetics,  
 CC medicaments and other nutrient-containing materials; and for preventing  
 CC microbial colonisation of surfaces. ABP76369 to ABP76677 represent  
 CC peptide sequences used in the exemplification of the present invention.  
 CC  
 XX Sequence 14 AA;

Query Match 5.7%; Score 7; DB 24; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 6.4;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 66 RYLLYYR 72  
 DB 8 RYLLYYR 14

RESULT 27  
 ABP76448  
 ID ABP76448 standard; Peptide; 14 AA.  
 XX  
 AC ABP76448;  
 XX  
 DT 24-FEB-2003 (first entry)  
 XX  
 DE Peptidomimetic antimicrobial peptide related peptide SEQ ID NO:80.  
 XX  
 KW Template-fixed peptidomimetic; antimicrobial; beta-hairpin; cytostatic;  
 KW antibacterial; infection; cystic fibrosis; lung infection; malignant;  
 KW cancer; disinfectant; preservative.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200270547-A1.  
 XX  
 PD 12-SEP-2002.  
 XX  
 PF 18-FEB-2002; 2002WO-EP01711.  
 XX  
 PR 23-FEB-2001; 2001WO-EP02072.  
 XX  
 PA (POLY-) POLYPHOS LTD.  
 PA (UYZU-) UNIV ZUERICH.  
 XX  
 XX Obrecht D, Robinson JA, Vrijbloed JW;  
 PI WPI; 2003-103173/09.  
 XX  
 DR New beta-hairpin peptidomimetic compounds, useful for treating  
 PT infections, especially cystic fibrosis lung infections and cancer, and  
 PT as disinfectants/preservatives for e.g. foodstuffs or cosmetics -  
 XX  
 PS Example; Page 159; 262pp; English.

The present invention describes template-fixed beta-hairpin  
 peptidomimetic compounds (I) and (II). Also described: (i) preparation  
 of (I) and (II); and (2) a modification of the preparation in which  
 enantiomers or all chiral starting materials are used. (I) and (II) have  
 antibacterial and cytostatic activities. The peptidomimetic compounds  
 are useful for treating or preventing infections or diseases related to  
 such infections, especially cystic fibrosis lung infections; for  
 preparing medicaments useful against malignant cells for treatment of  
 cancer; as disinfectants or preservatives for foodstuffs, cosmetics,  
 medicaments and other nutrient-containing materials; and for preventing  
 microbial colonisation of surfaces. ABP76369 to ABP76677 represent  
 peptide sequences used in the exemplification of the present invention.

Query Match 5.7%; Score 7; DB 24; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 6.4;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 66 RYLLYYR 72  
 DB 8 RYLLYYR 14

RESULT 28  
 AAR80091  
 ID AAR80091 standard; Protein; 103 AA.  
 XX  
 AC AAR80091;  
 XX  
 DT 23-MAY-1996 (first entry)  
 XX  
 DE Human derived light chain RT3 phage antibody.  
 XX  
 KW Light chain; RT3; human; catalytic antibody; bacteriophage.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..16  
 FT /note= "framework region 1"  
 FT Region 17..27  
 FT /note= "complementarity determining region 1"  
 FT Region 28..43  
 FT /note= "framework region 2"  
 FT Region 44..49  
 FT /note= "complementarity determining region 2"  
 FT Region 50..82  
 FT /note= "framework region 3"  
 FT Region 83..92  
 FT /note= "complementarity determining region 3"  
 FT Region 93..103  
 FT /note= "framework region 4"

WO9527045-A1.  
 12-OCT-1995.  
 30-MAR-1994; 94WO-US03420.  
 30-MAR-1994; 94WO-US03420.  
 (IGEN-) IGEN INC.  
 Chiswell D, Daraley MJ, Fitzgerald K, Kenten JH;  
 Martin MT, McCafferty J, Smith RG, Titmas RC, Williams RO;  
 WPI; 1995-358624/46.  
 N-PSDB; AAT04638.  
 Production of catalytic antibodies displayed on phage - by  
 generating a gene library of antibody-derived domains and expressing  
 it in phage vectors  
 Disclosure; Fig 20; 133pp; English.  
 AAT04638 encodes AAR80091 human derived light chain RT3 phage antibody.  
 The DNA was used in the prepn. of catalytic antibody (CA) producing  
 bacteriophage. The CAs can be used to activate/deactivate a  
 biological function in an animal by enhancing the rate of cleavage,  
 or formation of a specific bond within a mol. in vivo.

Query Match 5.7%; Score 7; DB 16; Length 103;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 83 IPDRFSA 89

Db 51 IPDRFSA 57

RESULT 29  
AAW95489  
ID AAW95489 standard; Protein; 103 AA.  
AC AAW95489;  
XX  
XX  
XX 29-MAR-1999 (first entry)  
XX Human-derived RT3 phage antibody light chain genetic sequence.  
XX Catalytic; antibody; phage display; immunising; phage expression vector;  
KW produg; scfv; RT3.  
XX  
XX Homo sapiens.  
XX  
XX US5855885-A.  
XX  
XX 05-JAN-1999.  
XX  
XX 14-JUL-1994; 94US-0273146.  
XX  
XX 22-JAN-1993; 93US-0007684.  
XX  
XX 14-JUL-1994; 94US-0273146.  
XX  
XX (CHIS/) CHISWELL D.  
XX (DARS/) DARSLEY M J.  
XX (FITZ/) FITZGERALD K.  
XX (KENT/) KENTEN J H.  
XX (MART/) MARTIN M T.  
XX (MCCA/) MCCAFFERTY J.  
XX (SMIT/) SMITH R.  
XX (TITM/) TITMAS R C.  
XX (WILL/) WILLIAMS R O.  
XX  
XX Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;  
XX Martin MT, McCafferty J, Smith R, Titmas RC, Williams RO;  
XX WPI: 1999-105036/09.  
XX N-PSDB; AAX00888.  
XX  
XX Production of catalytic antibodies displayed on bacteriophages -  
XX comprises generating a gene library of antibody-derived domains  
XX inserting coding into a phage expression vector and isolating the  
XX catalytic antibodies  
XX Examples; Fig 20F; 117pp; English.  
XX  
XX The invention relates to methods for producing catalytic antibodies  
XX displayed on a phage. The method comprises: (a) generating a gene  
XX library of antibody-derived domains; (b) inserting coding for the domains  
XX into a phage expression vector; and (c) isolating the catalytic  
XX antibodies. The phage expression vector incorporates a histidine peptide  
XX in tandem with a myc peptide. The catalytic antibodies can be isolated by  
XX preparing an antigen; optionally immunising an animal with the antigen;  
XX generating a library of VH and VL domains from the immunised animal;  
XX cloning the VH and VL domains into a phage expression vector to generate  
XX phage display antibodies; selecting phage display antibodies which bind  
XX specifically to the antigen; screening the selected phage display  
XX antibodies for catalytic activity to substrate; and isolating the  
XX catalytic antibodies, where the phage expression vector incorporates a  
XX histidine peptide in tandem with a myc peptide. The processes are used to  
XX produce catalytic antibodies, which can be used for in vivo activation of  
XX a produg. Sequences AAW95484-489 represent genetic sequences of heavy  
XX and light chains of RT3 specific phage antibodies selected from a naive  
XX human phage antibody library.  
XX  
XX Sequence 103 AA;  
XX  
XX Query Match 5.7%; Score 7; DB 20; Length 103;  
XX Best Local Similarity 100.0%; Pred. No. 37;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 IPDRFSA 89  
| | | | |  
Db 51 IPDRFSA 57

RESULT 30  
AAR26962  
ID AAR26962 standard; Protein; 104 AA.  
XX  
XX AAR26962;  
XX  
XX 25-MAR-2003 (updated)  
XX 11-FEB-1993 (first entry)  
XX Human T lymphocyte receptor V-beta w23 subfamily segment.  
XX  
XX TCR; IGR b 04; variable region; immunomodulation;  
XX polymerase chain reaction; T cell receptor.  
XX  
XX Homo sapiens.  
XX  
XX WO9213950-A2.  
XX  
XX 20-AUG-1992.  
XX  
XX 12-FEB-1992; 92WO-FR00130.  
XX  
XX 12-FEB-1991; 91FR-0001613.  
XX 12-APR-1991; 91FR-0004523.  
XX  
XX (ROUS) ROUSSEL-UCLAF.  
XX  
XX Ferradini L, Hercend T, Roman-Roman S, Triebel F;  
XX WPI: 1992-300036/36.  
XX N-PSDB; AAQ28175.  
XX  
XX Variable regions of b-chain of T-lymphocyte receptors and their  
XX DNA - useful as immuno:modulant(s) and for diagnosing immune  
XX disorders  
XX  
XX Claim 7; Page 39; 75pp; French.  
XX  
XX RNA was isolated from peripheral lymphocytes and converted to cDNA  
XX using a C-beta-specific primer. The cDNA was amplified by anchored  
XX PCR using C-beta and polyC primers, then amplified again using a  
XX different C-beta specific primer. The amplified product was SacII-  
XX restricted, inserted into Bluescript SK+ vector and used to transform  
XX E.coli XL-1blue. Transformants were screened with a C-beta specific  
XX probe and DNA from positive clones was sequenced in the C-beta  
XX region. The sequence designated "IGR b 04" is a consensus sequence  
XX from 4 distinct cDNA clones. The sequence has an homology of 75.7%  
XX with the sequence Vb12A1 (see Leiden J.M., et al., Proc. Natl. Acad.  
XX Sci. USA, 83:4456, 1986) but has a homology of less than 75% with  
XX other members of the Vbeta 5 subfamily. IGR b 04 is, therefore, not  
XX a member of the Vbeta 5 subfamily. The peptide encoded by it can be  
XX used to block T cell epitopes and in vaccines.  
XX See also AAQ28173-Q28228.  
XX (Updated on 25-MAR-2003 to correct PN field.)  
XX  
XX Sequence 104 AA;  
XX  
XX Query Match 5.7%; Score 7; DB 13; Length 104;  
XX Best Local Similarity 100.0%; Pred. No. 37;  
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 IPDRFSA 89  
| | | | |  
Db 70 IPDRFSA 76

RESULT 31  
AARS4313  
ID AARS4313 standard; protein; 104 AA.

XX AC AARS4313;  
XX DT 25-MAR-2003 (updated)  
XX DT 10-NOV-1994 (first entry)  
XX DE Anti-HIV gp120 immunoglobulin light chain variable region s3.  
XX KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;  
XX KW neutralisation; monoclonal antibody; kappa light chain;  
XX KW variable region; framework; complementarity determining region.  
XX OS Homo sapiens.

XX	Key	Location/Qualifiers
XX	Region	1..18
XX	FT	/label= FR1
XX	FT	19..30
XX	FT	/label= CDR1
XX	FT	31..45
XX	FT	/label= FR2
XX	FT	46..52
XX	FT	/label= CDR2
XX	FT	53..84
XX	FT	/label= FR3
XX	FT	85..93
XX	FT	/label= CDR3
XX	FT	94..104
XX	FT	/label= FR4

WO9407922-A1.

PN 14-APR-1994.

XX PD 30-SEP-1993; 93WO-US09328.

XX PF 30-SEP-1992; 92US-0954148.

XX PR (SRI ) SCRIPPS RES INST.

XX PA Barbas CF, Burton DR, Lerner RA;

XX PI WPI; 1994-135516/16.

XX DR New human monoclonal antibodies neutralising HIV - react with  
XX PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo  
XX PT or in vitro diagnosis and for passive immuno-therapy

XX PS Example; Page 181-182; 248pp; English.

XX CC Lymphocyte mRNA was converted to cDNA and subjected to PCR  
XX CC amplification using primers specific for heavy and light chain  
XX CC variable regions. The amplification products were inserted into a  
XX CC dicistronic vector to produce a library of fragments. E.coli XL1  
XX CC Blue cells were transformed with the library. Filamentous phage were  
XX CC produced which expressed the MAb regions on their surface. Panning  
XX CC with gp120 and gp41 resulted in the recovery of immunoreactive  
XX CC clones. The light chain VK region sequence AARS4313 is from a gp120-  
XX CC specific clone.  
XX CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 104 AA;

Query Match 5.7%; Score 7; DB 15; Length 104;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 DIPDRFS 88

DB 53 DIPDRFS 59

RESULT 32  
AAW01271  
ID AAW01271 standard; Protein; 104 AA.

XX AC AAW01271;  
XX DT 28-JAN-1997 (first entry)  
XX DE VL region of HIV neutralising MAb, clone s3.  
XX KW Heavy chain; light chain; variable region; VH; monoclonal antibody;  
XX KW Mab; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;  
XX KW virus infectivity assay; precursor gp160; immunocompetence; human;  
XX KW anti-HIV antibody; detection; HIV infection.

XX	Key	Location/Qualifiers
XX	Region	1..18
XX	FT	/label= FR1
XX	FT	19..30
XX	FT	/label= CDR1
XX	FT	31..45
XX	FT	/label= FR2
XX	FT	46..52
XX	FT	/label= CDR2
XX	FT	53..84
XX	FT	/label= FR3
XX	FT	85..93
XX	FT	/label= CDR3
XX	FT	94..104
XX	FT	/label= FR4

WO9602273-A1.

XX PN 01-FEB-1996.

XX PF 11-JUL-1995; 95WO-US08743.

XX PR 18-JUL-1994; 94US-0276852.

XX PA (SRI ) SCRIPPS RES INST.

XX PI Barbas CF, Burton DR, Lerner RA;

XX WPI; 1996-179601/16.

XX DR Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in  
XX PT passive immuno-therapy and detection of HIV infection.

XX PS Example; Fig 11; 366pp; English.

XX CC The sequences given in AAW01261-92 represent the light chain variable  
XX CC regions (VL) of a series of monoclonal antibodies (MAbs) which are  
XX CC immunoreactive with HIV glycoprotein gp120 and are capable of  
XX CC neutralising HIV. This sequence represents the sequence of the JK2  
XX CC gene clone, s3. A MAb containing this VL sequence has the capacity  
XX CC to reduce HIV infectivity titre in an in vivo virus infectivity assay  
XX CC by 50 % at a concentration of less than 700 ng of antibody/ml. The MAb  
XX CC binds mature gp120 preferentially over the precursor gp160. The MAb  
XX CC may be used for determining immunocompetence of a human anti-HIV  
XX CC antibody and in the detection of HIV infection.

XX SQ Sequence 104 AA;

Query Match 5.7%; Score 7; DB 17; Length 104;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 DIPDRFS 88

db 53 DIPDRFS 59

RESULT 33  
AY95123  
ID AAY95123 standard; Protein; 104 AA.

AC AAY95123;  
AT 30-JUN-2000 (first entry)

DE Anti-gp120 antibody light chain variable region from clone s3.

KW Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;  
KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;  
KW glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.

OS Homo sapiens.

PN AU9948756-A.

PD 17-FEB-2000.

PF 16-SEP-1999; 99AU-0048756.

PR 16-SEP-1999; 99AU-0048756.

PA (SCRI ) SCRIPPS RES INST.

PI Burton DR, Barbas CF, Lerner RA;

PI WPI; 2000-293393/26.

PT Novel human monoclonal antibodies which immunoreact with and neutralise  
PT human immunodeficiency virus useful for treating HIV infections -

PS Example 9; Figure 11; 366pp; English.

CC The present sequence represents a fragment of an anti-human  
CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to  
CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV  
CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein  
CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an  
CC in vitro virus infectivity assay by 50%, at a concentration of less than  
CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and  
CC immunotherapy of HIV induced disease. They are useful as neutralising  
CC field isolates and provide useful information regarding the  
CC immunocompetence of an immune response in HIV infected patients. The  
CC monoclonal antibodies are useful for producing anti-idiotypic antibodies  
CC which can be used to screen human monoclonal antibodies to identify  
CC whether the antibody has the same binding specificity as the antibodies  
CC of the invention. The neutralising antibodies define new epitopes on the  
CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new  
CC immunotherapeutic human monoclonal antibodies. A major advantage of the  
CC monoclonal antibodies derives from the fact that they are encoded by a  
CC human polynucleotide sequence. Thus in vivo use of the monoclonal  
CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly  
CC reduces the problems of significant host immune response to the passively  
CC administered antibodies which is a problem commonly encountered when  
CC monoclonal antibodies of xenogenic or chimeric derivation are utilized.  
CC An additional major advantage of the monoclonal antibodies described  
CC derives from the fact that they immunoreact with a unique determinant  
CC present on mature HIV glycoprotein gp120. This class of antibodies is  
CC particularly effective at neutralising field isolates of HIV.

XX Sequence 104 AA;

Query Match 5.7%; Score 7; DB 21; Length 104;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 DIPDRFS 88

|||||

Db 53 DIPDRFS 59

RESULT 34  
AAY98232  
ID AAY98232 standard; Protein; 104 AA.

AC AAY98232;

DT 04-JUL-2000 (first entry)

DE Anti-gp120 antibody light chain variable region from clone s3.

KW Antibody; anti-HIV monoclonal antibody; glycoprotein-120;  
KW human immunodeficiency virus type 1; HIV-1; infectivity titre;  
KW passive immunotherapy; reduce severity; HIV-induced disease;  
KW immunocompetence; active immunisation.

OS Homo sapiens.

PN AU9948754-A.

PD 17-FEB-2000.

PF 16-SEP-1999; 99AU-0048754.

PR 16-SEP-1999; 99AU-0048754.

PA (SCRI ) SCRIPPS RES INST.

PI Burton DR, Barbas CF, Lerner RA;

PI WPI; 2000-246867/22.

PT Human neutralising monoclonal antibodies to human immunodeficiency  
PT virus (HIV) used for providing passive immunotherapy to HIV are  
PT specific for glycoprotein-120 -

PS Example 9; Figure 11; 374pp; English.

CC This sequence represents a fragment of the antibodies of the invention.  
CC The invention relates to the production of an anti-HIV (human  
CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody  
CC capable of reducing an HIV infectivity titre in an in vitro virus  
CC infectivity assay by 50% at a concentration of less than 70 ng/ml. The  
CC method for the production of the antibody comprises:  
CC (a) providing a first polynucleotide encoding a heavy chain  
CC immunoglobulin amino acid sequence (which does not comprise the sequence  
CC represented by AAY98206) and a second polynucleotide encoding a light  
CC chain immunoglobulin amino acid sequence;  
CC (b) inserting the first and second polynucleotide sequences into a host  
CC cell;

CC (c) maintaining the host cell in conditions which allow the amino acid  
CC sequences encoded by the polynucleotides to be expressed in the host  
CC cell; and  
CC (d) isolating the antibody comprising the heavy and light chain  
CC immunoglobulin amino acid sequences from the host cell.

CC The anti-HIV gp-120 monoclonal antibody is used for providing passive  
CC immunotherapy to HIV in a human. They can be administered to high-risk  
CC patients to reduce the likelihood and/or severity of HIV-induced disease  
CC and to patients who are already HIV-infected. The antibodies are used  
CC for neutralising field isolates which provides information about the  
CC immunocompetence of an immune response in HIV patients, for detecting  
CC HIV in a biological fluid or tissue sample e.g. by radioimmunoassay, for  
CC producing anti-idiotypic antibodies which can be used for active  
CC immunisation and to screen human monoclonal antibodies to identify those  
CC with the same binding specificity and to monitor the course of HIV  
CC disease therapy by measuring the changes in concentration of HIV present  
CC in the body or in body fluids by immunoassay. The anti-HIV gp-120  
CC monoclonal antibodies are encoded by a human polynucleotide sequence and  
CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease  
CC reduce the problems of significant host immune response to the  
CC antibodies associated with monoclonal antibodies of xenogeneic or

CC chimeric derivation.

SQ Sequence 104 AA;

Query Match 5.7%; Score 7; DB 21; Length 104;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 DIPDRFS 88

Db 53 DIPDRFS 59

RESULT 35

ABG22849

ID ABG22849 standard; Protein; 105 AA.

XX AC ABG22849;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #22840.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Dmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS97036.

XX PT New isolated polynucleotide and encoded polypeptides, useful in

XX PT diagnostics, forensic, gene mapping, identification of mutations

XX PT responsible for genetic disorders or other traits and to assess

XX PT biodiversity

XX PS Claim 20; SEQ ID No 53208; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and

XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,

XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

XX CC and gene mapping, and in recombinant production of (II). The

XX CC polynucleotides are also used in diagnostics as expressed sequence tags

XX CC for identifying expressed genes. (I) is useful in gene therapy techniques

XX CC to restore normal activity of (II) or to treat disease states involving

XX CC (II). (II) is useful for generating antibodies against it, detecting or

XX CC quantitating a polypeptide in tissue, as molecular weight markers and as

XX CC a food supplement. (II) and its binding partners are useful in medical

XX CC imaging of sites expressing (II). (I) and (II) are useful for treating

XX CC disorders involving aberrant protein expression or biological activity.

XX CC The polypeptide and polynucleotide sequences have applications in

XX CC diagnostics, forensic, gene mapping, identification of mutations

XX CC responsible for genetic disorders or other traits to assess biodiversity

XX CC and to produce other types of data and products dependent on DNA and

XX CC amino acid sequences. ABG0010-ABG30377 represent novel human

XX CC diagnostic amino acid sequences of the invention.

XX CC Note: The sequence data for this patent did not appear in the printed

XX CC specification, but was obtained in electronic format directly from WIPO

XX CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX CC

SQ Sequence 105 AA;

Query Match 5.7%; Score 7; DB 22; Length 105;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 PRYLLYY 71

Db 46 PRYLLYY 52

RESULT 36

AAR50217

ID AAR50217 standard; Protein; 109 AA.

XX AC AAR50217;

XX DT 25-MAR-2003 (updated)

XX DT 31-OCT-1994 (first entry)

XX DE HSV glycoprotein F binding MAB clone rev6/11/21/22L VH/VL domain.

XX KW Complementarity determination region; CDR3; human; bronchiolitis;

XX KW monoclonal antibody; epitope; glycoprotein F; influenza virus;

XX KW respiratory syncytial virus; RSV; disease; rhinovirus; coronavirus;

XX KW lung; pneumonia.

XX OS Synthetic.

XX PH Key

XX FT Region

XX FT /label= FR1

XX FT Region

XX FT /label= CDR1

XX FT Region

XX FT /label= FR2

XX FT Region

XX FT /label= CDR2

XX FT Region

XX FT /label= FR3

XX FT Region

XX FT /label= CDR3

XX FT Region

XX FT /label= FR4

XX FT

XX PN WO9406448-A1.

XX XD 31-MAR-1994.

XX XX 16-SEP-1993; 93WO-US08786.

XX PR 16-SEP-1992; 92US-0945515.

XX PA (SCRI) SCRIPPS RES INST.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Barbas CF, Burton DR, Chanock RM, Crowe JE, Murphy BR;

XX WPI; 1994-118147/14.

XX XX Human neutralising monoclonal antibodies to respiratory syncytial

XX PT virus - for treatment prophylaxis and diagnosis of RSV and other

XX PT diseases of the respiratory tract

XX PS Disclosure; Fig 4; 104pp; English.

XX CC The sequences given in AAR50215-19 represent the heavy and light chain

XX CC variable domains of various clones of a human monoclonal antibody

XX CC which binds to an epitope on glycoprotein F of respiratory syncytial

XX CC virus (RSV). These antibodies may be used as a reagent for the

XX CC diagnosis of RSV disease and other viral mucosal diseases, eg.

XX CC influenza virus, rhinovirus and coronavirus. They are particularly

XX CC useful in ameliorating RSV when delivered directly to the lungs, and

XX CC



CC may also be used for treating pneumonia and bronchiolitis.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX

SQ Sequence 109 AA;

Query Match 5.7%; Score 7; DB 15; Length 109;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 82 DIPDRFS 88  
|||||

DB 58 DIPDRFS 64  
|||||

RESULT 37

AAB98230  
ID AAB98230 standard; Protein; 109 AA.

AC AAB98230;

20-AUG-2001 (first entry)

Rabbit anti-A33 antigen antibody VL1 polypeptide SEQ ID NO:21.

Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;  
immunoglobulin; complementarity determining region; CDR; cancer;  
cytostatic; anticancer; colon cancer; stomach cancer.

Oryctolagus cuniculus.

Homo sapiens.

WO200130393-A2.

03-MAY-2001.

20-OCT-2000; 2000WO-US29289.

22-OCT-1999; 99US-0425638.

04-APR-2000; 2000US-0543004.

(LUDW-) LUDWIG INST CANCER RES.

(SLOK) SLOAN KETTERING INST CANCER RES.

(SCRI) SCRIPPS RES INST.

Barbas CF, Rader C, Ritter G, Welt S, Old LJ;

WPI; 2001-328613/34.

Treating cancers, particularly of stomach and colon, that express A33  
antigen by administering conjugate of anticancer agent with specific  
immunoglobulin product.

Example 3; Fig 1; 85pp; English.

The present invention describes a method for treating cancers that  
express the A33 antigen. The method comprises administering an  
anticancer agent (I) conjugated to an immunoglobulin product (II) that  
binds specifically to A33 and contains one or more of 13 specified  
complementarity determining regions (CDRs), given in AAB98262 to  
AAB98274. (I) has cytostatic activity. The method can be used for  
treating colon and stomach cancers. (II), or the nucleic acid encoding  
it, can be used directly, in unconjugated form, for immunotherapy of  
cancer, and, when labeled, for detection or diagnosis of diseases  
associated with A33 expression. AAH22218 to AAH22254 and AAB98230 to  
AAB98321 represent sequences used in the exemplification of the  
present invention.

SQ Sequence 109 AA;

Query Match 5.7%; Score 7; DB 22; Length 109;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 GVSQYQQ 59  
|||||  
Db 32 GVSQYQQ 38

RESULT 38

AAB98231  
ID AAB98231 standard; Protein; 109 AA.

AC AAB98231;

20-AUG-2001 (first entry)

Rabbit anti-A33 antigen antibody VL2 polypeptide SEQ ID NO:22.

Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;  
immunoglobulin; complementarity determining region; CDR; cancer;  
cytostatic; anticancer; colon cancer; stomach cancer.

Oryctolagus cuniculus.

Homo sapiens.

WO200130393-A2.

03-MAY-2001.

20-OCT-2000; 2000WO-US29289.

22-OCT-1999; 99US-0425638.

04-APR-2000; 2000US-0543004.

(LUDW-) LUDWIG INST CANCER RES.

(SLOK) SLOAN KETTERING INST CANCER RES.

(SCRI) SCRIPPS RES INST.

Barbas CF, Rader C, Ritter G, Welt S, Old LJ;

WPI; 2001-328613/34.

Treating cancers, particularly of stomach and colon, that express A33  
antigen by administering conjugate of anticancer agent with specific  
immunoglobulin product.

Example 3; Fig 1; 85pp; English.

The present invention describes a method for treating cancers that  
express the A33 antigen. The method comprises administering an  
anticancer agent (I) conjugated to an immunoglobulin product (II) that  
binds specifically to A33 and contains one or more of 13 specified  
complementarity determining regions (CDRs), given in AAB98262 to  
AAB98274. (I) has cytostatic activity. The method can be used for  
treating colon and stomach cancers. (II), or the nucleic acid encoding  
it, can be used directly, in unconjugated form, for immunotherapy of  
cancer, and, when labeled, for detection or diagnosis of diseases  
associated with A33 expression. AAH22218 to AAH22254 and AAB98230 to  
AAB98321 represent sequences used in the exemplification of the  
present invention.

SQ Sequence 109 AA;

Query Match 5.7%; Score 7; DB 22; Length 109;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 GVSQYQQ 59  
|||||  
Db 32 GVSQYQQ 38

RESULT 39

AAB98232  
ID AAB98232 standard; Protein; 109 AA.

XX

```
AC AAB98232;
XX
XX 20-AUG-2001 (first entry)
XX
XX Rabbit anti-A33 antigen antibody VLB polypeptide SEQ ID NO:23.
XX
XX Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;
XX immunoglobulin; complementarity determining region; CDR; cancer;
XX cytostatic; anticancer; colon cancer; stomach cancer.
XX
XX Oryctolagus cuniculus.
XX Homo sapiens.
XX WO200130393-A2.
XX
XX 03-MAY-2001.
XX
XX 20-OCT-2000; 2000WO-US29289.
XX
XX 22-OCT-1999; 99US-0425638.
XX
XX 04-APR-2000; 2000US-0543004.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX (SLOK) SLOAN KETTERING INST-CANCER RES.
XX (SCRI) SCRIPPS RES INST.
XX
XX Barbas CF, Rader C, Ritter G, Welt S, Old LJ;
XX
XX WPI; 2001-328613/34.
XX
XX Treating cancers, particularly of stomach and colon, that express A33
XX antigen by administering conjugate of anticancer agent with specific
XX immunoglobulin product.
XX
XX Example 3; Fig 1; 85pp; English.
XX
XX The present invention describes a method for treating cancers that
XX express the A33 antigen. The method comprises administering an
XX anticancer agent (I) conjugated to an immunoglobulin product (II) that
XX binds specifically to A33 and contains one or more of 13 specified
XX complementarity determining regions (CDRs), given in AAB98262 to
XX AAB98274. (I) has cytostatic activity. The method can be used for
XX treating colon and stomach cancers. (II), or the nucleic acid encoding
XX it, can be used directly, in unconjugated form, for immunotherapy of
XX cancer, and, when labeled, for detection or diagnosis of diseases
XX associated with A33 expression. AAH22218 to AAH22254 and AAB98230 to
XX AAB98321 represent sequences used in the exemplification of the
XX present invention.
XX
XX Sequence 109 AA;
XX
XX Query Match 5.7%; Score 7; DB 22; Length 109;
XX Best Local Similarity 100.0%; Pred. No. 39;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 53 GVSWYQQ 59
XX |||||
XX Db 32 GVSWYQQ 38
XX
XX RESULT 40
XX AAB98233
XX ID AAB98233 standard; Protein; 109 AA.
XX
XX AC AAB98233;
XX
XX 20-AUG-2001 (first entry)
XX
XX Humanised anti-A33 antigen antibody VLA polypeptide SEQ ID NO:39.
XX
XX Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;
XX immunoglobulin; complementarity determining region; CDR; cancer;
XX cytostatic; anticancer; colon cancer; stomach cancer.
XX
```

```
XX OS Homo sapiens.
XX WO200130393-A2.
XX
XX 03-MAY-2001.
XX
XX 20-OCT-2000; 2000WO-US29289.
XX
XX 22-OCT-1999; 99US-0425638.
XX
XX 04-APR-2000; 2000US-0543004.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX (SLOK) SLOAN KETTERING INST CANCER RES.
XX (SCRI) SCRIPPS RES INST.
XX
XX Barbas CF, Rader C, Ritter G, Welt S, Old LJ;
XX
XX WPI; 2001-328613/34.
XX
XX Treating cancers, particularly of stomach and colon, that express A33
XX antigen by administering conjugate of anticancer agent with specific
XX immunoglobulin product.
XX
XX Example 5; Fig 1; 85pp; English.
XX
XX The present invention describes a method for treating cancers that
XX express the A33 antigen. The method comprises administering an
XX anticancer agent (I) conjugated to an immunoglobulin product (II) that
XX binds specifically to A33 and contains one or more of 13 specified
XX complementarity determining regions (CDRs), given in AAB98262 to
XX AAB98274. (I) has cytostatic activity. The method can be used for
XX treating colon and stomach cancers. (II), or the nucleic acid encoding
XX it, can be used directly, in unconjugated form, for immunotherapy of
XX cancer, and, when labeled, for detection or diagnosis of diseases
XX associated with A33 expression. AAH22218 to AAH22254 and AAB98230 to
XX AAB98321 represent sequences used in the exemplification of the
XX present invention.
XX
XX Sequence 109 AA;
XX
XX Query Match 5.7%; Score 7; DB 22; Length 109;
XX Best Local Similarity 100.0%; Pred. No. 39;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 53 GVSWYQQ 59
XX |||||
XX Db 32 GVSWYQQ 38
XX
XX RESULT 41
XX AAB98234
XX ID AAB98234 standard; Protein; 109 AA.
XX
XX AC AAB98234;
XX
XX 20-AUG-2001 (first entry)
XX
XX Humanised anti-A33 antigen antibody VLB polypeptide SEQ ID NO:40.
XX
XX Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;
XX immunoglobulin; complementarity determining region; CDR; cancer;
XX cytostatic; anticancer; colon cancer; stomach cancer.
XX
XX Homo sapiens.
XX
XX WO200130393-A2.
XX
XX 03-MAY-2001.
XX
XX 20-OCT-2000; 2000WO-US29289.
XX
XX 22-OCT-1999; 99US-0425638.
```

2R 04-APR-2000; 2000US-0543004.  
 3A (LUDW-) LUDWIG INST CANCER RES.  
 3A (SLOK) SLOAN KETTERING INST CANCER RES.  
 3A (SCRI) SCRIPPS RES INST.  
 3I Barbas CF, Rader C, Ritter G, Welt S, Old LJ;  
 3X WPI; 2001-328613/34.  
 3R Treating cancers, particularly of stomach and colon, that express A33  
 3T antigen by administering conjugate of anticancer agent with specific  
 3T immunoglobulin product -  
 3X Example 5; Fig 1; 85pp; English.  
 3X The present invention describes a method for treating cancers that  
 3C express the A33 antigen. The method comprises administering an  
 3C anticancer agent (I) conjugated to an immunoglobulin product (II) that  
 3C binds specifically to A33 and contains one or more of 13 specified  
 3C complementarity determining regions (CDRs), given in AAB98262 to  
 3C AAB98274. (I) has cytostatic activity. The method can be used for  
 3C treating colon and stomach cancers. (II), or the nucleic acid encoding  
 3C it, can be used directly, in unconjugated form, for immunotherapy of  
 3C cancer, and, when labeled, for detection or diagnosis of diseases  
 3C associated with A33 expression. AAH22218 to AAH22254 and AAB98230 to  
 3C AAB98321 represent sequences used in the exemplification of the  
 3C present invention.  
 3X Sequence 109 AA;

Query Match 5.7%; Score 7; DB 22; Length 109;  
 Best Local Similarity 100.0%; Pred. No. 39;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3Y 53 GVSWMYQQ 59  
 |||||  
 3b 32 GVSWMYQQ 38

RESULT 42  
 AAB98235  
 ID AAB98235 standard; Protein; 109 AA.  
 AC AAB98235;  
 20-AUG-2001 (first entry)  
 Humanised anti-A33 antigen antibody VLC polypeptide SEQ ID NO:41.  
 Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;  
 immunoglobulin; complementarity determining region; CDR; cancer;  
 cytostatic; anticancer; colon cancer; stomach cancer.

OS Homo sapiens.  
 XX WO200130393-A2.  
 03-MAY-2001.  
 20-OCT-2000; 2000WO-US29289.  
 22-OCT-1999; 99US-0425638.  
 04-APR-2000; 2000US-0543004.  
 (LUDW-) LUDWIG INST CANCER RES.  
 (SLOK) SLOAN KETTERING INST CANCER RES.  
 (SCRI) SCRIPPS RES INST.  
 Barbas CF, Rader C, Ritter G, Welt S, Old LJ;  
 WPI; 2001-328613/34.

PT Treating cancers, particularly of stomach and colon, that express A33  
 PT antigen by administering conjugate of anticancer agent with specific  
 XX immunoglobulin product -  
 PS Example 5; Fig 1; 85pp; English.  
 XX The present invention describes a method for treating cancers that  
 CC express the A33 antigen. The method comprises administering an  
 CC anticancer agent (I) conjugated to an immunoglobulin product (II) that  
 CC binds specifically to A33 and contains one or more of 13 specified  
 CC complementarity determining regions (CDRs), given in AAB98262 to  
 CC AAB98274. (I) has cytostatic activity. The method can be used for  
 CC treating colon and stomach cancers. (II), or the nucleic acid encoding  
 CC it, can be used directly, in unconjugated form, for immunotherapy of  
 CC cancer, and, when labeled, for detection or diagnosis of diseases  
 CC associated with A33 expression. AAH22218 to AAH22254 and AAB98230 to  
 CC AAB98321 represent sequences used in the exemplification of the  
 CC present invention.  
 XX Sequence 109 AA;

Query Match 5.7%; Score 7; DB 22; Length 109;  
 Best Local Similarity 100.0%; Pred. No. 39;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 GVSWMYQQ 59  
 |||||  
 Db 32 GVSWMYQQ 38

RESULT 43  
 AAB98236  
 ID AAB98236 standard; Protein; 109 AA.  
 AC AAB98236;  
 20-AUG-2001 (first entry)  
 Humanised anti-A33 antigen antibody VLD polypeptide SEQ ID NO:42.  
 Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;  
 immunoglobulin; complementarity determining region; CDR; cancer;  
 cytostatic; anticancer; colon cancer; stomach cancer.

OS Homo sapiens.  
 XX WO200130393-A2.  
 03-MAY-2001.  
 20-OCT-2000; 2000WO-US29289.  
 22-OCT-1999; 99US-0425638.  
 04-APR-2000; 2000US-0543004.  
 (LUDW-) LUDWIG INST CANCER RES.  
 (SLOK) SLOAN KETTERING INST CANCER RES.  
 (SCRI) SCRIPPS RES INST.  
 Barbas CF, Rader C, Ritter G, Welt S, Old LJ;  
 WPI; 2001-328613/34.

Treating cancers, particularly of stomach and colon, that express A33  
 antigen by administering conjugate of anticancer agent with specific  
 immunoglobulin product -  
 Example 5; Fig 1; 85pp; English.

The present invention describes a method for treating cancers that  
 express the A33 antigen. The method comprises administering an  
 anticancer agent (I) conjugated to an immunoglobulin product (II) that  
 binds specifically to A33 and contains one or more of 13 specified

CC complementarity determining regions (CDRs), given in AAB98262 to  
CC AAB98274. (I) has cytotostatic activity. The method can be used for  
CC treating colon and stomach cancers. (II), or the nucleic acid encoding  
CC it, can be used directly, in unconjugated form, for immunotherapy of  
CC cancer, and, when labeled, for detection or diagnosis of diseases  
CC associated with A33 expression. AAH22218 to AAH22254 and AAB98230 to  
CC AAB98321 represent sequences used in the exemplification of the  
CC present invention.  
XX  
SQ Sequence 109 AA;  
  
Query Match 5.7%; Score 7; DB 22; Length 109;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 53 GVSQYQQ 59  
DB 32 GVSQYQQ 38  
  
RESULT 44  
AAB98237  
ID AAB98237 standard; Protein; 109 AA.  
XX  
AC AAB98237;  
XX  
DT 20-AUG-2001 (first entry)  
XX  
DE Humanised anti-A33 antigen antibody VLE polypeptide SEQ ID NO:43.  
XX  
KW Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;  
KW immunoglobulin; complementarity determining region; CDR; cancer;  
KW cytotostatic; anticancer; colon cancer; stomach cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO200130393-A2.  
XX  
PD 03-MAY-2001.  
XX  
PF 20-OCT-2000; 2000WO-US29289.  
XX  
PR 22-OCT-1999; 99US-0425638.  
XX  
PR 04-APR-2000; 2000US-0543004.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (SLOK) SLOAN KETTERING INST CANCER RES.  
PA (SCRI) SCRIPPS RES INST.  
XX  
PI Barbas CF, Rader C, Ritter G, Welt S, Old LJ;  
XX  
DR WPI; 2001-328613/34.  
XX  
PT Treating cancers, particularly of stomach and colon, that express A33  
PT antigen by administering conjugate of anticancer agent with specific  
PT immunoglobulin product -  
XX  
PS Example 5; Fig 1; 85pp; English.  
XX  
CC The present invention describes a method for treating cancers that  
CC express the A33 antigen. The method comprises administering an  
CC anticancer agent (I) conjugated to an immunoglobulin product (II) that  
CC binds specifically to A33 and contains one or more of 13 specified  
CC complementarity determining regions (CDRs), given in AAB98262 to  
CC AAB98274. (I) has cytotostatic activity. The method can be used for  
CC treating colon and stomach cancers. (II), or the nucleic acid encoding  
CC it, can be used directly, in unconjugated form, for immunotherapy of  
CC cancer, and, when labeled, for detection or diagnosis of diseases  
CC associated with A33 expression. AAH22218 to AAH22254 and AAB98230 to  
CC AAB98321 represent sequences used in the exemplification of the  
CC present invention.  
XX  
SQ Sequence 109 AA;  
  
Query Match 5.7%; Score 7; DB 22; Length 109;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 53 GVSQYQQ 59  
DB 32 GVSQYQQ 38

Query Match 5.7%; Score 7; DB 22; Length 109;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 53 GVSQYQQ 59  
DB 32 GVSQYQQ 38  
  
RESULT 45  
AAB98238  
ID AAB98238 standard; Protein; 109 AA.  
XX  
AC AAB98238;  
XX  
DT 20-AUG-2001 (first entry)  
XX  
DE Humanised anti-A33 antigen antibody VLF polypeptide SEQ ID NO:44.  
XX  
KW Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;  
KW immunoglobulin; complementarity determining region; CDR; cancer;  
KW cytotostatic; anticancer; colon cancer; stomach cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO200130393-A2.  
XX  
PD 03-MAY-2001.  
XX  
PF 20-OCT-2000; 2000WO-US29289.  
XX  
PR 22-OCT-1999; 99US-0425638.  
XX  
PR 04-APR-2000; 2000US-0543004.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (SLOK) SLOAN KETTERING INST CANCER RES.  
PA (SCRI) SCRIPPS RES INST.  
XX  
PI Barbas CF, Rader C, Ritter G, Welt S, Old LJ;  
XX  
DR WPI; 2001-328613/34.  
XX  
PT Treating cancers, particularly of stomach and colon, that express A33  
PT antigen by administering conjugate of anticancer agent with specific  
PT immunoglobulin product -  
XX  
PS Example 5; Fig 1; 85pp; English.  
XX  
CC The present invention describes a method for treating cancers that  
CC express the A33 antigen. The method comprises administering an  
CC anticancer agent (I) conjugated to an immunoglobulin product (II) that  
CC binds specifically to A33 and contains one or more of 13 specified  
CC complementarity determining regions (CDRs), given in AAB98262 to  
CC AAB98274. (I) has cytotostatic activity. The method can be used for  
CC treating colon and stomach cancers. (II), or the nucleic acid encoding  
CC it, can be used directly, in unconjugated form, for immunotherapy of  
CC cancer, and, when labeled, for detection or diagnosis of diseases  
CC associated with A33 expression. AAH22218 to AAH22254 and AAB98230 to  
CC AAB98321 represent sequences used in the exemplification of the  
CC present invention.  
XX  
SQ Sequence 109 AA;  
  
Query Match 5.7%; Score 7; DB 22; Length 109;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 53 GVSQYQQ 59  
DB 32 GVSQYQQ 38

RESULT 46  
AAB98239  
ID AAB98239 standard; Protein; 109 AA.  
XX  
AC AAB98239;  
XX  
DT 20-AUG-2001 (first entry)  
XX  
DE Humanised anti-A33 antigen antibody VL polypeptide SEQ ID NO:45.  
XX  
KW Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;  
KW immunoglobulin; complementarity determining region; CDR; cancer;  
KW cytostatic; anticancer; colon cancer; stomach cancer.  
XX  
CS Homo sapiens.  
XX  
XX WO200130393-A2.  
XX  
XX 03-MAY-2001.  
XX  
XX 20-OCT-2000; 200WO-US29289.  
XX  
XX 22-OCT-1999; 99US-0425638.  
XX  
XX 04-APR-2000; 2000US-0543004.  
XX  
XX (LUDW-) LUDWIG INST CANCER RES.  
XX  
XX (SLOK) SLOAN KETTERING INST CANCER RES.  
XX  
XX (SCRI) SCRIPPS RES INST.  
XX  
XX Barbas CF, Rader C, Ritter G, Weit S, Old LJ;  
XX  
XX WPI; 2001-328613/34.  
XX  
XX Treating cancers, particularly of stomach and colon, that express A33  
XX antigen by administering conjugate of anticancer agent with specific  
XX immunoglobulin product -  
XX  
XX Example 5; Fig 1; 85pp; English.  
XX  
XX The present invention describes a method for treating cancers that  
XX express the A33 antigen. The method comprises administering an  
XX anticancer agent (I) conjugated to an immunoglobulin product (II) that  
XX binds specifically to A33 and contains one or more of 13 specified  
XX complementarity determining regions (CDRs), given in AAB98262 to  
XX AAB98274. (I) has cytostatic activity. The method can be used for  
XX treating colon and stomach cancers. (II), or the nucleic acid encoding  
XX it, can be used directly, in unconjugated form, for immunotherapy of  
XX cancer, and, when labeled, for detection or diagnosis of diseases  
XX associated with A33 expression. AAH2218 to AAH2254 and AAB98230 to  
XX AAB98321 represent sequences used in the exemplification of the  
XX present invention.  
XX  
SQ Sequence 109 AA;  
Query Match 5.7%; Score 7; DB 22; Length 109;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 53 GVSWMYQQ 59  
Db 32 GVSWMYQQ 38  
RESULT 47  
AAB75149  
ID AAB75149 standard; Protein; 109 AA.  
XX  
XX AAB75149;  
XX  
XX 08-AUG-2001 (first entry)  
XX  
XX Rabbit anti A33 antigen antibody V region VL1 SEQ ID NO:20.  
XX

KW Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;  
KW immunoreact; anti A33 antigen antibody.  
XX  
OS Oryctolagus cuniculus.  
XX  
XX  
FH Key Location/Qualifiers  
FT Region 1..23  
FT /label= FR1  
FT Region 24..34  
FT /label= CDR1  
FT Region 35..49  
FT /label= FR2  
FT Region 50..56  
FT /label= CDR2  
FT Region 57..88  
FT /label= FR3  
FT Region 89..99  
FT /label= CDR3  
FT Region 100..109  
FT /label= FR4  
XX  
XX WO200131065-A1.  
XX  
XX 03-MAY-2001.  
XX  
XX 20-OCT-2000; 2000WO-US29026.  
XX  
XX 22-OCT-1999; 99US-0425638.  
XX  
XX 04-APR-2000; 2000US-0543004.  
XX  
XX (SCRI) SCRIPPS RES INST.  
XX  
XX Barbas CF, Rader C;  
XX  
XX WPI; 2001-328657/34.  
XX  
XX Preparing humanized rabbit antibodies that specifically immunoreact  
XX with a particular antigen using display technology for expressing  
XX libraries of antibody domains and fine tuning variable domain regions -  
XX  
XX Example 4; Fig 1A; 62pp; English.  
XX  
XX The present invention describes a method for preparing a humanised rabbit  
XX antibody that specifically immunoreacts with a particular antigen. The  
XX method comprises expressing a library of antibodies comprising one or  
XX more complementarity determining region (CDR) from the variable domain  
XX sequences that specifically immunoreact with the antigen grafted into  
XX framework regions from humans, and selecting the antibodies that react  
XX with the antigen. The method is useful for humanising non-human  
XX mammalian antibodies, which can be used for the treatment of a variety  
XX of diseases. The present sequence represents a rabbit anti A33 antigen  
XX antibody V region protein sequence which is given in an example from the  
XX present invention.  
XX  
SQ Sequence 109 AA;  
Query Match 5.7%; Score 7; DB 22; Length 109;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 53 GVSWMYQQ 59  
Db 32 GVSWMYQQ 38  
RESULT 48  
AAB75150  
ID AAB75150 standard; Protein; 109 AA.  
XX  
XX AAB75150;  
XX  
XX 08-AUG-2001 (first entry)  
XX  
XX

DE Rabbit anti A33 antigen antibody V region VL2 SEQ ID NO:21.  
XX Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;  
KW immunoreact; anti A33 antigen antibody.  
XX Cryptolagus cuniculus.  
XX Key Location/Qualifiers  
FH Region 1..23 /label= FR1  
FT Region 24..34 /label= CDR1  
FT Region 35..49 /label= FR2  
FT Region 50..56 /label= CDR2  
FT Region 57..88 /label= FR3  
FT Region 89..99 /label= CDR3  
FT Region 100..109 /label= FR4  
XX WO200131065-A1.  
XX 03-MAY-2001.  
XX 20-OCT-2000; 2000WO-US29026.  
XX 22-OCT-1999; 99US-0425638.  
XX 04-APR-2000; 2000US-0543004.  
XX (SCRI ) SCRIPPS RES INST.  
XX Barbas CF, Rader C;  
XX WPI; 2001-328657/34.  
XX Preparing humanized rabbit antibodies that specifically immunoreact  
PT with a particular antigen using display technology for expressing  
PT libraries of antibody domains and fine tuning variable domain regions -  
XX Example 4; Fig 1A; 62pp; English.  
XX The present invention describes a method for preparing a humanised rabbit  
CC antibody that specifically immunoreacts with a particular antigen. The  
CC method comprises expressing a library of antibodies comprising one or  
CC more complementarity determining region (CDR) from the variable domain  
CC sequences that specifically immunoreact with the antigen grafted into  
CC framework regions from humans, and selecting the antibodies that react  
CC with the antigen. The method is useful for humanising non-human  
CC mammalian antibodies, which can be used for the treatment of a variety  
CC of diseases. The present sequence represents a rabbit anti A33 antigen  
CC antibody V region protein sequence which is given in an example from the  
XX present invention.  
XX Sequence 109 AA;  
SQ Query Match 5.7%; Score 7; DB 22; Length 109;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 53 GVSQYQQ 59  
DB 32 GVSQYQQ 38  
RESULT 49  
AAB75151  
ID AAB75151 standard; Protein; 109 AA.  
XX  
AC AAB75151;  
XX

DT 08-AUG-2001 (first entry)  
XX Rabbit anti A33 antigen antibody V region VL3 SEQ ID NO:22.  
DE Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;  
KW immunoreact; anti A33 antigen antibody.  
XX Cryptolagus cuniculus.  
XX Key Location/Qualifiers  
FH Region 1..23 /label= FR1  
FT Region 24..34 /label= CDR1  
FT Region 35..49 /label= FR2  
FT Region 50..56 /label= CDR2  
FT Region 57..88 /label= FR3  
FT Region 89..99 /label= CDR3  
FT Region 100..109 /label= FR4  
XX WO200131065-A1.  
XX 03-MAY-2001.  
XX 20-OCT-2000; 2000WO-US29026.  
XX 22-OCT-1999; 99US-0425638.  
XX 04-APR-2000; 2000US-0543004.  
XX (SCRI ) SCRIPPS RES INST.  
XX Barbas CF, Rader C;  
XX WPI; 2001-328657/34.  
XX Preparing humanized rabbit antibodies that specifically immunoreact  
PT with a particular antigen using display technology for expressing  
PT libraries of antibody domains and fine tuning variable domain regions -  
XX Example 4; Fig 1A; 62pp; English.  
XX The present invention describes a method for preparing a humanised rabbit  
CC antibody that specifically immunoreacts with a particular antigen. The  
CC method comprises expressing a library of antibodies comprising one or  
CC more complementarity determining region (CDR) from the variable domain  
CC sequences that specifically immunoreact with the antigen grafted into  
CC framework regions from humans, and selecting the antibodies that react  
CC with the antigen. The method is useful for humanising non-human  
CC mammalian antibodies, which can be used for the treatment of a variety  
CC of diseases. The present sequence represents a rabbit anti A33 antigen  
CC antibody V region protein sequence which is given in an example from the  
XX present invention.  
XX Sequence 109 AA;  
SQ Query Match 5.7%; Score 7; DB 22; Length 109;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 53 GVSQYQQ 59  
DB 32 GVSQYQQ 38  
RESULT 50  
AAB75152  
ID AAB75152 standard; Protein; 109 AA.  
XX

IC AAB75152;  
XX 08-AUG-2001 (first entry)  
XX Humanised rabbit anti A33 antigen antibody V region VL SEQ ID NO:45.  
XX Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;  
XX immunoreact; anti A33 antigen antibody.  
XX Oryctolagus cuniculus.  
XX Synthetic.  
XX Key Location/Qualifiers  
XX TH Region 1..23  
XX TT /label= FR1  
XX TT Region 24..34  
XX TT /label= CDR1  
XX TT Region 35..49  
XX TT /label= FR2  
XX TT Region 50..56  
XX TT /label= CDR2  
XX TT Region 57..88  
XX TT /label= FR3  
XX TT Region 89..99  
XX TT /label= CDR3  
XX TT Region 100..109  
XX TT /label= FR4  
XX WO200131065-A1.  
XX 03-MAY-2001.  
XX 20-OCT-2000; 2000WO-US29026.  
XX 22-OCT-1999; 99US-0425638.  
XX 04-APR-2000; 2000US-0543004.  
XX (SCRI ) SCRIPPS RES INST.  
XX Barbas CF, Rader C;  
XX WPI; 2001-328657/34.  
XX Preparing humanized rabbit antibodies that specifically immunoreact  
XX with a particular antigen using display technology for expressing  
XX libraries of antibody domains and fine tuning variable domain regions -  
XX Example 6; Fig 1A; 62pp; English.  
XX The present invention describes a method for preparing a humanised rabbit  
XX antibody that specifically immunoreacts with a particular antigen. The  
XX method comprises expressing a library of antibodies comprising one or  
XX sequences that specifically immunoreact with the antigen grafted into  
XX framework regions from humans, and selecting the antibodies that react  
XX with the antigen. The method is useful for humanising non-human  
XX mammalian antibodies, which can be used for the treatment of a variety  
XX of diseases. The present sequence represents a humanised rabbit anti A33  
XX antigen antibody V region protein sequence which is given in an example  
XX from the present invention.  
SQ Sequence 109 AA;  
Query Match 5.7%; Score 7; DB 22; Length 109;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 53 GVSWTQQ 59  
DB 32 GVSWTQQ 38  
RESULT 51

AAB75153  
ID AAB75153 standard; Protein; 109 AA.  
XX  
XX AAB75153;  
XX 08-AUG-2001 (first entry)  
XX Human anti A33 antigen antibody V region VLA SEQ ID NO:39.  
XX Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;  
XX immunoreact; anti A33 antigen antibody.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
XX TH Region 1..23  
XX TT /label= FR1  
XX TT Region 24..34  
XX TT /label= CDR1  
XX TT Region 35..49  
XX TT /label= FR2  
XX TT Region 50..56  
XX TT /label= CDR2  
XX TT Region 57..88  
XX TT /label= FR3  
XX TT Region 89..99  
XX TT /label= CDR3  
XX TT Region 100..109  
XX TT /label= FR4  
XX WO200131065-A1.  
XX 03-MAY-2001.  
XX 20-OCT-2000; 2000WO-US29026.  
XX 22-OCT-1999; 99US-0425638.  
XX 04-APR-2000; 2000US-0543004.  
XX (SCRI ) SCRIPPS RES INST.  
XX Barbas CF, Rader C;  
XX WPI; 2001-328657/34.  
XX Preparing humanized rabbit antibodies that specifically immunoreact  
XX with a particular antigen using display technology for expressing  
XX libraries of antibody domains and fine tuning variable domain regions -  
XX Example 6; Fig 1A; 62pp; English.  
XX The present invention describes a method for preparing a humanised rabbit  
XX antibody that specifically immunoreacts with a particular antigen. The  
XX method comprises expressing a library of antibodies comprising one or  
XX sequences that specifically immunoreact with the antigen grafted into  
XX framework regions from humans, and selecting the antibodies that react  
XX with the antigen. The method is useful for humanising non-human  
XX mammalian antibodies, which can be used for the treatment of a variety  
XX of diseases. The present sequence represents a human anti A33 antigen  
XX antibody V region protein sequence which is given in an example from the  
XX present invention.  
SQ Sequence 109 AA;  
Query Match 5.7%; Score 7; DB 22; Length 109;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 53 GVSWTQQ 59  
DB 32 GVSWTQQ 38

RESULT 52  
LAB75154  
ID AAB75154 standard; Protein; 109 AA.  
AC AAB75154;  
XX  
XX  
XX 08-AUG-2001 (first entry)  
DE Human anti A33 antigen antibody V region VLB SEQ ID NO:40.  
XX  
XX Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;  
XX immunoreact; anti A33 antigen antibody.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX 1..23  
XX Region /label= FR1  
XX 24..34  
XX Region /label= CDR1  
XX 35..49  
XX Region /label= FR2  
XX 50..56  
XX Region /label= CDR2  
XX 57..88  
XX Region /label= FR3  
XX 89..99  
XX Region /label= CDR3  
XX 100..109  
XX Region /label= FR4  
XX  
XX WO200131065-A1.  
XX  
XX 03-MAY-2001.  
XX  
XX 20-OCT-2000; 2000WO-US29026.  
XX  
XX 22-OCT-1999; 99US-0425638.  
XX  
XX 04-APR-2000; 2000US-0543004.  
XX  
XX (SCRI ) SCRIPPS RES INST.  
XX  
XX Barbas CF, Rader C;  
XX  
XX WPI; 2001-328657/34.  
XX  
XX Preparing humanized rabbit antibodies that specifically immunoreact  
XX with a particular antigen using display technology for expressing  
XX libraries of antibody domains and fine tuning variable domain regions -  
XX  
XX Example 6; Fig 1A; 62pp; English.  
XX  
XX The present invention describes a method for preparing a humanised rabbit  
XX antibody that specifically immunoreacts with a particular antigen. The  
XX method comprises expressing a library of antibodies comprising one or  
XX more complementarity determining region (CDR) from the variable domain  
XX sequences that specifically immunoreact with the antigen grafted into  
XX framework regions from humans, and selecting the antibodies that react  
XX with the antigen. The method is useful for humanising non-human  
XX mammalian antibodies, which can be used for the treatment of a variety  
XX of diseases. The present sequence represents a human anti A33 antigen  
XX antibody V region protein sequence which is given in an example from the  
XX present invention.  
XX  
XX Sequence 109 AA;  
SQ  
Query Match 5.7%; Score 7; DB 22; Length 109;  
Best Local Similarity 100.0%; Pred.No. 39;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 53 GVSQYQQ 59  
|||||

Db 32 GVSQYQQ 38  
RESULT 53  
AAB75155  
ID AAB75155 standard; Protein; 109 AA.  
XX  
XX AAB75155;  
XX  
XX 08-AUG-2001 (first entry)  
XX  
XX Human anti A33 antigen antibody V region VLC SEQ ID NO:41.  
XX  
XX Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;  
XX immunoreact; anti A33 antigen antibody.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX 1..23  
XX Region /label= FR1  
XX 24..34  
XX Region /label= CDR1  
XX 35..49  
XX Region /label= FR2  
XX 50..56  
XX Region /label= CDR2  
XX 57..88  
XX Region /label= FR3  
XX 89..99  
XX Region /label= CDR3  
XX 100..109  
XX Region /label= FR4  
XX  
XX WO200131065-A1.  
XX  
XX 03-MAY-2001.  
XX  
XX 20-OCT-2000; 2000WO-US29026.  
XX  
XX 22-OCT-1999; 99US-0425638.  
XX  
XX 04-APR-2000; 2000US-0543004.  
XX  
XX (SCRI ) SCRIPPS RES INST.  
XX  
XX Barbas CF, Rader C;  
XX  
XX WPI; 2001-328657/34.  
XX  
XX Preparing humanized rabbit antibodies that specifically immunoreact  
XX with a particular antigen using display technology for expressing  
XX libraries of antibody domains and fine tuning variable domain regions -  
XX  
XX Example 6; Fig 1A; 62pp; English.  
XX  
XX The present invention describes a method for preparing a humanised rabbit  
XX antibody that specifically immunoreacts with a particular antigen. The  
XX method comprises expressing a library of antibodies comprising one or  
XX more complementarity determining region (CDR) from the variable domain  
XX sequences that specifically immunoreact with the antigen grafted into  
XX framework regions from humans, and selecting the antibodies that react  
XX with the antigen. The method is useful for humanising non-human  
XX mammalian antibodies, which can be used for the treatment of a variety  
XX of diseases. The present sequence represents a human anti A33 antigen  
XX antibody V region protein sequence which is given in an example from the  
XX present invention.  
XX  
XX Sequence 109 AA;  
SQ  
Query Match 5.7%; Score 7; DB 22; Length 109;  
Best Local Similarity 100.0%; Pred.No. 39;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Y 53 GVSXYQQ 59  
b 32 GVSXYQQ 38

RESULT 54  
AB75156  
D AAB75156 standard; Protein; 109 AA.

C AAB75156;

T 08-AUG-2001 (first entry)

E Human anti A33 antigen antibody V region VLD SEQ ID NO:42.

X Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;  
W immunoreact; anti A33 antigen antibody.

X Homo sapiens.

H Key Location/Qualifiers

T 1..23 /label= FR1

T 24..34 /label= CDR1

T 35..49 /label= FR2

T 50..56 /label= CDR2

T 57..88 /label= FR3

T 89..99 /label= CDR3

T 100..109 /label= FR4

N WO200131065-A1.

D 03-MAY-2001.

X 20-OCT-2000; 2000WO-US29026.

F 22-OCT-1999; 99US-0425638.

R 04-APR-2000; 2000US-0543004.

R (SCRI ) SCRIPPS RES INST.

A Barbas CF, Rader C;

I WPI; 2001-328657/34.

X Preparing humanized rabbit antibodies that specifically immunoreact  
T with a particular antigen using display technology for expressing

T Libraries of antibody domains and fine tuning variable domain regions -  
X Example 6; Fig 1A; 62pp; English.

X The present invention describes a method for preparing a humanised rabbit  
X antibody that specifically immunoreacts with a particular antigen. The  
X method comprises expressing a library of antibodies comprising one or  
X more complementarity determining region (CDR) from the variable domain  
X sequences that specifically immunoreact with the antigen grafted into  
X framework regions from humans, and selecting the antibodies that react  
X with the antigen. The method is useful for humanising non-human  
X mammalian antibodies, which can be used for the treatment of a variety  
X of diseases. The present sequence represents a human anti A33 antigen  
X antibody V region protein sequence which is given in an example from the  
X present invention.

X Sequence 109 AA;

Query Match 5.7%; Score 7; DB 22; Length 109;  
Best Local Similarity 100.0%; Pred. No. 39;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 53 GVSXYQQ 59  
Db 32 GVSXYQQ 38

RESULT 55  
AAB75157  
ID AAB75157 standard; Protein; 109 AA.

XX AAB75157;

XX 08-AUG-2001 (first entry)

XX Human anti A33 antigen antibody V region VLE SEQ ID NO:43.

XX Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;  
KW immunoreact; anti A33 antigen antibody.

XX Homo sapiens.

XX Key Location/Qualifiers

FT 1..23 /label= FR1

FT 24..34 /label= CDR1

FT 35..49 /label= FR2

FT 50..56 /label= CDR2

FT 57..88 /label= FR3

FT 89..99 /label= CDR3

FT 100..109 /label= FR4

XX WO200131065-A1.

XX 03-MAY-2001.

XX 20-OCT-2000; 2000WO-US29026.

XX 22-OCT-1999; 99US-0425638.

XX 04-APR-2000; 2000US-0543004.

XX (SCRI ) SCRIPPS RES INST.

XX Barbas CF, Rader C;

XX WPI; 2001-328657/34.

XX Preparing humanized rabbit antibodies that specifically immunoreact  
PT with a particular antigen using display technology for expressing

PT Libraries of antibody domains and fine tuning variable domain regions -  
XX Example 6; Fig 1A; 62pp; English.

PS The present invention describes a method for preparing a humanised rabbit  
XX antibody that specifically immunoreacts with a particular antigen. The  
XX method comprises expressing a library of antibodies comprising one or  
XX more complementarity determining region (CDR) from the variable domain  
XX sequences that specifically immunoreact with the antigen grafted into  
XX framework regions from humans, and selecting the antibodies that react  
XX with the antigen. The method is useful for humanising non-human  
XX mammalian antibodies, which can be used for the treatment of a variety  
XX of diseases. The present sequence represents a human anti A33 antigen  
XX antibody V region protein sequence which is given in an example from the  
XX present invention.

XX Sequence 109 AA;

Query Match 5.7%; Score 7; DB 22; Length 109;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

53 GVSUWYQQ 59  
| | | | |  
32 GVSUWYQQ 38

RESULT 56  
AB75158  
D AAB75158 standard; Protein; 109 AA.  
X  
C AAB75158;  
X  
X  
X 08-AUG-2001 (first entry)  
X  
X Human anti A33 antigen antibody V region VLP SEQ ID NO:44.  
X  
X Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;  
X immunoreact; anti A33 antigen antibody.  
X  
X Homo sapiens.  
X  
X  
X Key Location/Qualifiers  
X Region 1..23  
X /label= FR1  
X Region 24..34  
X /label= CDR1  
X Region 35..49  
X /label= FR2  
X Region 50..56  
X /label= CDR2  
X Region 57..88  
X /label= FR3  
X Region 89..99  
X /label= CDR3  
X Region 100..109  
X /label= FR4  
X  
X WO200131065-A1.  
X  
X 03-MAY-2001.  
X  
X 20-OCT-2000; 2000WO-US29026.  
X  
X 22-OCT-1999; 99US-0425638.  
X PR 04-APR-2000; 2000US-0543004.  
X  
X (SCRI ) SCRIPPS RES INST.  
X  
X Barbas CF, Rader C;  
X  
X WPI; 2001-328657/34.  
X  
X Preparing humanized rabbit antibodies that specifically immunoreact  
X with a particular antigen using display technology for expressing  
X libraries of antibody domains and fine tuning variable domain regions -  
X  
X Example 6; Fig 1A; 62pp; English.  
X  
X The present invention describes a method for preparing a humanised rabbit  
X antibody that specifically immunoreacts with a particular antigen. The  
X method comprises expressing a library of antibodies comprising one or  
X more complementarity determining region (CDR) from the variable domain  
X sequences that specifically immunoreact with the antigen grafted into  
X framework regions from humans, and selecting the antibodies that react  
X with the antigen. The method is useful for humanising non-human  
X mammalian antibodies, which can be used for the treatment of a variety  
X of diseases. The present sequence represents a human anti A33 antigen  
X antibody V region protein sequence which is given in an example from the  
X present invention.

SQ Sequence 109 AA;  
Query Match 5.7%; Score 7; DB 22; Length 109;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

53 GVSUWYQQ 59  
| | | | |  
32 GVSUWYQQ 38

RESULT 57  
AAR54277  
ID AAR54277 standard; protein; 111 AA.  
X  
X AAR54277;  
X  
X 25-MAR-2003 (updated)  
X DT 10-NOV-1994 (first entry)  
X  
X Anti-HIV gp41 immunoglobulin light chain V region clone GL 41 1.  
X  
X Human immunodeficiency virus; HIV1; glycoprotein gp41; epitope;  
X neutralisation; monoclonal antibody; light chain; variable region;  
X framework region; complementarity determining region.  
X  
X Homo sapiens.  
X  
X Key Location/Qualifiers  
X Region 1..23  
X /label= FR1  
X Region 24..35  
X /label= CDR1  
X Region 36..50  
X /label= FR2  
X Region 51..57  
X /label= CDR2  
X Region 58..89  
X /label= FR3  
X Region 90..97  
X /label= CDR3  
X Region 98..111  
X /label= FR4  
X  
X WO9407922-A1.  
X  
X 14-APR-1994.  
X  
X 30-SEP-1993; 93WO-US09328.  
X  
X 30-SEP-1992; 92US-0954148.  
X  
X (SCRI ) SCRIPPS RES INST.  
X  
X Barbas CF, Burton DR, Lerner RA;  
X  
X WPI; 1994-135516/16.  
X  
X New human monoclonal antibodies neutralising HIV - react with  
X gp120 or gp41 and nucleic acid encoding them, useful for in vivo  
X or in vitro diagnosis and for passive immuno-therapy  
X  
X Claim 11; Page 217; 248pp; English.  
X  
X Lymphocyte mRNA was converted to cDNA and subjected to PCR  
X amplification using primers specific for heavy and light chain  
X variable regions. The amplification products were inserted into a  
X digastronic vector to produce a library of fragments. E.coli XL1  
X Blue cells were transformed with the library. Filamentous phage were  
X produced which expressed the MAb regions on their surface. Panning  
X with gp120 and gp41 resulted in the recovery of immunoreactive  
X clones. The light chain VL region sequence AAR54277 neutralises HIV1  
X gp41.



CC capacity to reduce HIV infectivity titre in an in vivo virus infectivity assay by 50 % at a concentration of less than 700 ng of antibody/ml.  
 CC The MAb may be used for determining immunocompetence of a human anti-HIV antibody and in the detection of HIV infection.

XX Sequence 111 AA;

Query Match 5.7%; Score 7; DB 17; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 39;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YY 82 DIPDRFS 88

YY 58 DIPDRFS 64

RESULT 60

AAW08738

ID AAW08738 standard; Protein; 111 AA.

XX AAW08738;

XX 08-AUG-1997 (first entry)

XX Human anti-HIV Fab amino acid sequence tat16(VL1).

XX Gene therapy; antibody; immunisation; human immunodeficiency virus;

XX HIV; human T-cell leukaemia virus.

XX Human Immunodeficiency Virus Type-1.

XX Key Location/Qualifiers

XX Region 1..20

XX /label= FR1

XX Region 21..33

XX /label= CDR1

XX Region 34..48

XX /label= FR2

XX Region 49..55

XX /label= CDR2

XX Region 56..87

XX /label= FR3

XX Region 87..100

XX /label= CDR3

XX Region 101..111

XX /label= FR4

XX Misc-difference 42

XX /label= Unspecified

XX WO9637234-A1.

XX 28-NOV-1996.

XX 23-MAY-1996; 96WO-US07393.

XX 23-MAY-1995; 95US-0447610.

XX (UVEJ-) UNIV JEFFERSON THOMAS.

XX Duan L, Pomerantz RJ;

XX WPI; 1997-020948/02.

XX Improved gene therapy using recombinant gene coding for an antibody

XX - for intracellular immunisation against pathogens recognised by the

XX antibody, esp. human immunodeficiency virus HIV-1

XX Example 11; Page 58; 213pp; English.

XX The present sequence is a human anti-HIV Fab light chain VL sequence.

XX A novel gene therapy method has been produced, where a recombinant

XX (rec) gene is introduced into the cells of a mammal. The method is

XX improved by using a rec gene encoding an antibody (Ab) (e.g. the

XX

XX

XX

XX

XX

CC present sequence) that is selectively specific for an intracellular (IC) antigen associated with a disease. The method is used to prevent or halt the progress of a disease by IC immunisation. Specifically, the Ab can be used to inhibit the replication of a virus, such as human T-cell leukaemia virus or especially HIV-1, or of other pathogens, e.g. bacteria, fungi. The method provides immunity before or after the development of the disease and can be used to control the severity of the disease.

XX Sequence 111 AA;

Query Match 5.7%; Score 7; DB 18; Length 111;

Best Local Similarity 100.0%; Pred. No. 39;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 83 IPDRFSA 89

OY 57 IPDRFSA 63

RESULT 61

AAAY95172

ID AAY95172 standard; Protein; 111 AA.

XX AAY95172;

XX 30-JUN-2000 (first entry)

XX Anti-gp41 light chain variable region from clone DL 41 1.

XX Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;

XX reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;

XX glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.

XX Homo sapiens.

XX AU9948756-A.

XX 17-FEB-2000.

XX 16-SEP-1999; 99AU-0048756.

XX 16-SEP-1999; 99AU-0048756.

XX (SCRI ) SCRIPPS RES INST.

XX Burton DR, Barbas CF, Lerner RA;

XX WPI; 2000-293393/26.

XX Novel human monoclonal antibodies which immunoreact with and neutralise

XX human immunodeficiency virus useful for treating HIV infections

XX Disclosure; Figure 19; 366pp; English.

XX The present sequence represents a fragment of an anti-human immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV mature glycoprotein gp120 preferentially over HIV precursor glycoprotein gp160 and neutralises HIV and which reduces HIV infectivity titre in an in vitro virus infectivity assay by 50%, at a concentration of less than 700 ng/ml. The antibodies are used as reagents for the diagnosis and immunotherapy of HIV induced disease. They are useful as neutralising field isolates and provide useful information regarding the immunocompetence of an immune response in HIV infected patients. The monoclonal antibodies are useful for producing anti-idiotypic antibodies which can be used to screen human monoclonal antibodies to identify whether the antibody has the same binding specificity as the antibodies of the invention. The neutralising antibodies define new epitopes on the HIV gp120 and gp41 glycoproteins, thus increasing the availability of new immunotherapeutic human monoclonal antibodies. A major advantage of the monoclonal antibodies derives from the fact that they are encoded by a human polynucleotide sequence. Thus in vivo use of the monoclonal

antibodies for diagnosis and immunotherapy of HIV induced disease greatly reduces the problems of significant host immune response to the passively administered antibodies which is a problem commonly encountered when monoclonal antibodies of xenogeneic or chimeric derivation are utilized. An additional major advantage of the monoclonal antibodies described derives from the fact that they immunoreact with a unique determinant present on mature HIV glycoprotein gp120. This class of antibodies is particularly effective at neutralising field isolates of HIV.

Sequence 111 AA;

Query Match 5.7%; Score 7; DB 21; Length 111;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 82 DIPDRFS 88  
|||||  
b 58 DIPDRFS 64

RESULT 62

AA98281  
D AAY98281 standard; Protein; 111 AA.

X C AAY98281;

T 04-JUL-2000 (first entry)

X Anti-gp41 light chain variable region from clone DL 41 1.

X Antibody; anti-HIV monoclonal antibody; glycoprotein-120;  
W human immunodeficiency virus type 1; HIV-1; infectivity titre;  
W passive immunotherapy; reduce severity; HIV-induced disease;  
W immunocompetence; active immunisation.

X Homo sapiens.

X AU9948754-A.

X 17-FEB-2000.

X 16-SEP-1999; 99AU-0048754.

X 16-SEP-1999; 99AU-0048754.

X (SCRI) SCRIPPS RES INST.

X Burton DR, Barbas CF, Lerner RA;

X WPI; 2000-246867/22.

X Human neutralizing monoclonal antibodies to human immunodeficiency virus (HIV) used for providing passive immunotherapy to HIV are specific for glycoprotein-120

PS Disclosure; Figure 19; 374pp; English.

CC This sequence represents a fragment of the antibodies of the invention.  
CC The invention relates to the production of an anti-HIV (human  
CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody  
CC capable of reducing an HIV infectivity titre in an in vitro virus  
CC infectivity assay by 50% at a concentration of less than 70 ng/ml. The  
CC method for the production of the antibody comprises:

CC (a) providing a first polynucleotide encoding a heavy chain  
CC immunoglobulin amino acid sequence (which does not comprise the sequence  
CC represented by AAY98206) and a second polynucleotide encoding a light  
CC chain immunoglobulin amino acid sequence;  
CC (b) inserting the first and second polynucleotide sequences into a host  
CC cell;

CC (c) maintaining the host cell in conditions which allow the amino acid  
CC sequences encoded by the polynucleotides to be expressed in the host  
CC cell; and  
CC (d) isolating the antibody comprising the heavy and light chain

CC immunoglobulin amino acid sequences from the host cell.  
CC The anti-HIV gp-120 monoclonal antibody is used for providing passive  
CC immunotherapy to HIV in a human. They can be administered to high-risk  
CC patients to reduce the likelihood and/or severity of HIV-induced disease  
CC and to patients who are already HIV-infected. The antibodies are used  
CC for neutralising field isolates which provides information about the  
CC immunocompetence of an immune response in HIV patients, for detecting  
CC HIV in a biological fluid or tissue sample e.g. by radioimmunoassay, for  
CC producing anti-idiotypic antibodies which can be used for active  
CC immunisation and to screen human monoclonal antibodies to identify those  
CC with the same binding specificity and to monitor the course of HIV  
CC disease therapy by measuring the changes in concentration of HIV present  
CC in the body or in body fluids by immunoassay. The anti-HIV gp-120  
CC monoclonal antibodies are encoded by a human polynucleotide sequence and  
CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease  
CC reduce the problems of significant host immune response to the  
CC antibodies associated with monoclonal antibodies of xenogeneic or  
CC chimeric derivation.

SQ Sequence 111 AA;

Query Match 5.7%; Score 7; DB 21; Length 111;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 DIPDRFS 88

DB 58 DIPDRFS 64

RESULT 63

ABG64978

ID ABG64978 standard; Protein; 120 AA.

XX AC ABG64978;

DT 27-AUG-2002 (first entry)

DE Human albumin fusion protein #1653.

XX Albumin fusion protein; therapeutic protein X; human albumin; HA;  
KW human serum albumin; HSA; cancer; reproductive disorder;  
KW digestive disorder; immune disorder; endocrine disorder;  
KW haematopoietic disorder; neural disorder; connective disorder;  
KW cytostatic; antifertility; antiinflammatory; antitumor;  
KW immunomodulator; anti-HIV; antidiabetic; haemostatic; neuroleptic;  
KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;  
KW osteopathic; antiarthritic.

OS Homo sapiens.

OS Synthetic.

PN WO200177137-A1.

XX 18-OCT-2001.

XX 12-APR-2001; 2001WO-US11988.

XX 12-APR-2000; 2000US-229358P.

XX 25-APR-2000; 2000US-159384P.

XX 21-DEC-2000; 2000US-256931P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Haseltine WA;

XX WPI; 2002-010886/01.

XX New fusion protein for treating disease e.g. diabetes comprises an  
PT albumin fused to a therapeutic protein

PS Claim 1; Page 1651; 2102pp; English.

CC The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA), also known as human serum albumin (HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological C in vitro/in vivo activity. The protein is useful for treating and C diagnosing disorders such as cancer, reproductive disorders, digestive C disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders C (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders C (e.g. diabetes), haematopoietic disorders, neural disorders C (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease, C encephalomyelitis, meningitis, schizophrenia), and connective disorders C (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin C fusion proteins of the invention.

XX Sequence 120 AA;

Query Match 5.7%; Score 7; DB 23; Length 120;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 28 LLVFPQG 34  
D 11 LLVFPQG 17

RESULT 64  
ABG64980  
D ABG64980 standard; Protein; 120 AA.

XX ABG64980;

DT 27-AUG-2002 (first entry)

DE Human albumin fusion protein #1655.

CC Albumin fusion protein; therapeutic protein X; human albumin; HA;  
CC human serum albumin; HSA; cancer; reproductive disorder;  
CC digestive disorder; immune disorder; endocrine disorder;  
CC haematopoietic disorder; neural disorder; connective disorder;  
CC cytostatic; anti-fertility; anti-inflammatory; anti-ulcer;  
CC immunomodulator; anti-HIV; antidiabetic; haemostatic; neurotropic;  
CC neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;  
CC osteopathic; antiarthritic.

DS Homo sapiens.

DS Synthetic.

XX WO200177137-A1.

PD 18-OCT-2001.

PF 12-APR-2001; 2001WO-US11988.

PR 12-APR-2000; 2000US-229358P.

PR 25-APR-2000; 2000US-19384P.

PR 21-DEC-2000; 2000US-256531P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Haseltine WA;

XX WPI; 2002-010886/01.

XX New fusion protein for treating disease e.g. diabetes comprises an  
PT albumin fused to a therapeutic protein -

PS Claim 1; Page 1652; 2102pp; English.

CC The present invention relates to albumin fusion proteins comprising a  
CC therapeutic protein X and human albumin (HA), also known as human serum  
CC albumin, HSA). The proteins are useful for treating a disease or  
CC disorder that may be modulated by therapeutic protein X. The albumin

CC extends the shelf-life of protein X, and may increase its biological  
CC in vitro/in vivo activity. The protein is useful for treating and  
CC diagnosing disorders such as cancer, reproductive disorders, digestive  
CC disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders  
CC (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders  
CC (e.g. diabetes), haematopoietic disorders, neural disorders  
CC (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease,  
CC encephalomyelitis, meningitis, schizophrenia), and connective disorders  
CC (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin  
CC fusion proteins of the invention.

XX Sequence 120 AA;

Query Match 5.7%; Score 7; DB 23; Length 120;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 LLVFPQG 34  
Db 11 LLVFPQG 17

RESULT 65  
AAE21465  
ID AAE21465 standard; Protein; 120 AA.

XX AAE21465;

DT 01-JUL-2002 (first entry)

DE Human gene 14 encoded secreted protein HDPXL05, SEQ ID NO:81.

CC Human; secreted protein; gene therapy; autoimmune disease; vitamin;  
CC rheumatoid arthritis; hyperproliferative disorder; neoplasm; breast;  
CC liver; cardiovascular; cardiac arrest; cerebrovascular; infection;  
CC cerebral ischaemia; angiogenesis; nervous system; Alzheimer's disease;  
CC ocular; corneal infection; wound healing; neuroprotective; skin aging;  
CC transplantation; chemotaxis; food additive; preservative; vulnerary;  
CC storage capability; mineral; cofactor; immunosuppressive; cytostatic;  
CC antiproliferative; cardiant; vasotropic; cerebroprotective; neurotropic;  
CC fungicide; opthalmological; sunburn; virucide; antibacterial.

OS Homo sapiens.

XX Location/Qualifiers

Key 1..20

FT Peptide /label= Signal\_peptide

FT Protein 21..120

FT /label= Mature\_secreted\_protein

XX WO200224719-A1.

XX 28-MAR-2002.

XX 17-JAN-2001; 2001WO-US01565.

XX 20-SEP-2000; 2000US-234210P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR, Olsen HS;  
PI Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH, Fiscella M,  
PI Ni J;

XX WPI; 2002-258042/30.

XX N-PSDB; RAD33825.

PT New nucleic acid molecules encoding 21 human secreted proteins for  
PT diagnosing or treating e.g. autoimmune diseases, hyperproliferative  
PT disorders, and cardiovascular disorders, and used as food additives or  
PT preservatives -

PS Claim 11; Page 477; 519pp; English.

XX AAD33812-AAD33868 represent cDNAs corresponding to 21 human secreted  
XX protein genes, and AAE21452-AAE21508 represent the proteins they encode.  
XX AAE21509-AAE21517 represent human secreted protein fragments. The genes  
XX and their corresponding secreted proteins are useful for preventing,  
XX treating or ameliorating medical conditions, e.g., by protein or gene  
XX therapy. Pathological conditions can be diagnosed by determining the  
XX amount of the new protein in a sample or by determining the presence of  
XX mutations in the new genes. Specific uses are described for each of the  
XX 21 genes, based on the tissues in which they are most highly expressed,  
XX disorders such as autoimmune diseases e.g. rheumatoid arthritis,  
XX hyperproliferative disorders e.g. neoplasms of the breast or liver,  
XX cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders  
XX e.g. cerebral ischaemia, angiodenesis, nervous system disorders e.g.  
XX Alzheimer's disease, infections caused by bacteria, viruses and fungi  
XX and ocular disorders e.g. corneal infection. The polypeptides of the  
XX invention can also be used to aid wound healing and epithelial cell  
XX proliferation, to prevent skin aging due to sunburn, to maintain organs  
XX before transplantation, for supporting cell culture of primary tissues,  
XX to regenerate tissues and in chemotaxis. They can also be used as a food  
XX additive or preservative to increase or decrease storage capabilities,  
XX fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors  
XX and other nutritional components. The present sequence represents a  
XX human secreted protein of the invention.

XX Sequence 120 AA;  
XX Query Match 5.7%; Score 7; DB 23; Length 120;  
XX Best Local Similarity 100.0%; Pred. No. 42;  
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 28 LLVFPQG 34  
XX |||||  
XX 11 LLVFPQG 17

RESULT 66  
AAE21495  
ID AAE21495 standard; Protein; 120 AA.  
AC AAE21495;  
XX 01-JUL-2002 (first entry)  
XX Human gene 14 encoded secreted protein HDPXL05, SEQ ID NO:111.  
XX Human; secreted protein; gene therapy; autoimmune disease; vitamin;  
XX rheumatoid arthritis; hyperproliferative disorder; neoplasm; breast;  
XX liver; cardiovascular; cardiac arrest; cerebrovascular; infection;  
XX cerebral ischaemia; angiodenesis; nervous system; Alzheimer's disease;  
XX ocular; corneal infection; wound healing; neuroprotective; skin aging;  
XX transplantation; chemotaxis; food additive; preservative; vulnerable;  
XX storage capability; mineral; cofactor; immunosuppressive; cytostatic;  
XX antiproliferative; cardiant; vasotropic; cerebroprotective; nootropic;  
XX fungicide; ophthalmological; sunburn; virucide; antibacterial.

XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX Peptide 1..20  
XX /label= Signal\_peptide  
XX Protein 21..120  
XX /note= "Human mature secreted protein"  
XX Misc-difference 116  
XX /label= Unknown  
XX /note= "Encoded by TGS"  
XX Misc-difference 120  
XX /label= Unknown  
XX /note= "Encoded by KTA"  
XX  
XX W0200224719-A1.

PD 28-MAR-2002.  
XX 17-JAN-2001; 2001WO-US01565.  
XX 20-SEP-2000; 2000US-234210P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Rosen CA, Konatsoulis GA, Baker KP, Birse CE, Soppet DR, Olsen HS;  
XX Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH, Fiscella M;  
XX Ni J;  
XX WPI; 2002-258042/30.  
XX N-PSDB; AAD33855.  
XX New nucleic acid molecules encoding 21 human secreted proteins for  
XX diagnosing or treating e.g. autoimmune diseases, hyperproliferative  
XX disorders, and cardiovascular disorders, and used as food additives or  
XX preservatives -  
XX Claim 11; Page 496-497; 519pp; English.  
XX AAD33812-AAD33868 represent cDNAs corresponding to 21 human secreted  
XX protein genes, and AAE21452-AAE21508 represent the proteins they encode.  
XX AAE21509-AAE21517 represent human secreted protein fragments. The genes  
XX and their corresponding secreted proteins are useful for preventing,  
XX treating or ameliorating medical conditions, e.g., by protein or gene  
XX therapy. Pathological conditions can be diagnosed by determining the  
XX amount of the new protein in a sample or by determining the presence of  
XX mutations in the new genes. Specific uses are described for each of the  
XX 21 genes, based on the tissues in which they are most highly expressed,  
XX disorders such as autoimmune diseases e.g. rheumatoid arthritis,  
XX hyperproliferative disorders e.g. neoplasms of the breast or liver,  
XX cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders  
XX e.g. cerebral ischaemia, angiodenesis, nervous system disorders e.g.  
XX Alzheimer's disease, infections caused by bacteria, viruses and fungi  
XX and ocular disorders e.g. corneal infection. The polypeptides of the  
XX invention can also be used to aid wound healing and epithelial cell  
XX proliferation, to prevent skin aging due to sunburn, to maintain organs  
XX before transplantation, for supporting cell culture of primary tissues,  
XX to regenerate tissues and in chemotaxis. They can also be used as a food  
XX additive or preservative to increase or decrease storage capabilities,  
XX fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors  
XX and other nutritional components. The present sequence represents a human  
XX secreted protein of the invention.

XX Sequence 120 AA;  
XX Query Match 5.7%; Score 7; DB 23; Length 120;  
XX Best Local Similarity 100.0%; Pred. No. 42;  
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 28 LLVFPQG 34  
XX |||||  
XX 11 LLVFPQG 17

RESULT 67  
AAU17887  
ID AAU17887 standard; Protein; 121 AA.  
AC AAU17887;  
XX 07-NOV-2001 (first entry)  
XX Novel human respiratory antigen #203.  
XX Human; respiratory antigen; respiratory disorder; throat disorder;  
XX lung disorder; nose disorder; lung cancer; gene therapy; cytostatic;  
XX anti allergic; anti asthmatic; anti inflammatory; olfactory;  
XX respiratory active.

DS Homo sapiens.  
PX KN WO200155448-A1.  
PX KX 02-AUG-2001.  
PX KX 17-JAN-2001; 2001WO-US01333.  
PX KX 31-JAN-2000; 2000US-0179065.  
PX PR 04-FEB-2000; 2000US-0180628.  
PX PR 24-FEB-2000; 2000US-0184664.  
PX PR 02-MAR-2000; 2000US-0186350.  
PX PR 16-MAR-2000; 2000US-0189874.  
PX PR 17-MAR-2000; 2000US-0190076.  
PX PR 18-APR-2000; 2000US-0198123.  
PX PR 19-MAY-2000; 2000US-0205515.  
PX PR 07-JUN-2000; 2000US-0209467.  
PX PR 28-JUN-2000; 2000US-0214886.  
PX PR 30-JUN-2000; 2000US-0215135.  
PX PR 07-JUL-2000; 2000US-0216647.  
PX PR 07-JUL-2000; 2000US-0216880.  
PX PR 11-JUL-2000; 2000US-0217487.  
PX PR 11-JUL-2000; 2000US-0217496.  
PX PR 14-JUL-2000; 2000US-0218290.  
PX PR 26-JUL-2000; 2000US-0220963.  
PX PR 26-JUL-2000; 2000US-0220964.  
PX PR 14-AUG-2000; 2000US-0224518.  
PX PR 14-AUG-2000; 2000US-0224519.  
PX PR 14-AUG-2000; 2000US-0225213.  
PX PR 14-AUG-2000; 2000US-0225214.  
PX PR 14-AUG-2000; 2000US-0225266.  
PX PR 14-AUG-2000; 2000US-0225267.  
PX PR 14-AUG-2000; 2000US-0225270.  
PX PR 14-AUG-2000; 2000US-0225447.  
PX PR 14-AUG-2000; 2000US-0225757.  
PX PR 14-AUG-2000; 2000US-0235758.  
PX PR 14-AUG-2000; 2000US-0235759.  
PX PR 18-AUG-2000; 2000US-0226279.  
PX PR 22-AUG-2000; 2000US-0226681.  
PX PR 22-AUG-2000; 2000US-0226868.  
PX PR 22-AUG-2000; 2000US-0227182.  
PX PR 23-AUG-2000; 2000US-0227009.  
PX PR 30-AUG-2000; 2000US-0228924.  
PX PR 01-SEP-2000; 2000US-0229287.  
PX PR 01-SEP-2000; 2000US-0229343.  
PX PR 01-SEP-2000; 2000US-0229344.  
PX PR 01-SEP-2000; 2000US-0229345.  
PX PR 05-SEP-2000; 2000US-0229509.  
PX PR 06-SEP-2000; 2000US-0229513.  
PX PR 06-SEP-2000; 2000US-0230437.  
PX PR 06-SEP-2000; 2000US-0230438.  
PX PR 08-SEP-2000; 2000US-0231242.  
PX PR 08-SEP-2000; 2000US-0231243.  
PX PR 08-SEP-2000; 2000US-0231244.  
PX PR 08-SEP-2000; 2000US-0231413.  
PX PR 08-SEP-2000; 2000US-0231414.  
PX PR 08-SEP-2000; 2000US-0232080.  
PX PR 08-SEP-2000; 2000US-0232081.  
PX PR 12-SEP-2000; 2000US-0231968.  
PX PR 14-SEP-2000; 2000US-0232397.  
PX PR 14-SEP-2000; 2000US-0232398.  
PX PR 14-SEP-2000; 2000US-0232399.  
PX PR 14-SEP-2000; 2000US-0232400.  
PX PR 14-SEP-2000; 2000US-0232401.  
PX PR 14-SEP-2000; 2000US-0233063.  
PX PR 14-SEP-2000; 2000US-0233064.  
PX PR 14-SEP-2000; 2000US-0233065.  
PX PR 21-SEP-2000; 2000US-0234223.  
PX PR 21-SEP-2000; 2000US-0234274.  
PX PR 25-SEP-2000; 2000US-0234997.  
PX PR 25-SEP-2000; 2000US-0234998.  
PX PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241221.  
PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241808.  
PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241826.  
PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246478.  
PR 08-NOV-2000; 2000US-0246523.  
PR 08-NOV-2000; 2000US-0246524.  
PR 08-NOV-2000; 2000US-0246525.  
PR 08-NOV-2000; 2000US-0246526.  
PR 08-NOV-2000; 2000US-0246527.  
PR 08-NOV-2000; 2000US-0246528.  
PR 08-NOV-2000; 2000US-0246532.  
PR 08-NOV-2000; 2000US-0246609.  
PR 08-NOV-2000; 2000US-0246610.  
PR 08-NOV-2000; 2000US-0246611.  
PR 08-NOV-2000; 2000US-0246613.  
PR 17-NOV-2000; 2000US-0249207.  
PR 17-NOV-2000; 2000US-0249208.  
PR 17-NOV-2000; 2000US-0249209.  
PR 17-NOV-2000; 2000US-0249210.  
PR 17-NOV-2000; 2000US-0249211.  
PR 17-NOV-2000; 2000US-0249212.  
PR 17-NOV-2000; 2000US-0249213.  
PR 17-NOV-2000; 2000US-0249214.  
PR 17-NOV-2000; 2000US-0249215.  
PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.  
PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249244.  
PR 17-NOV-2000; 2000US-0249245.  
PR 17-NOV-2000; 2000US-0249264.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250160.  
PR 01-DEC-2000; 2000US-0250391.  
PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
PR 05-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.  
PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251868.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
XX XX (HUMA-) HUMAN GENOME SCI INC.  
PA



X I Rosen CA, Barash SC, Ruben SM;  
X R WPI; 2001-476224/51.  
X R N-PSDB; AAS28071.  
X T Isolated polypeptide for treating, preventing and/or prognosing  
X T disorders related to the respiratory system including respiratory  
X T cancers and also for testing and detection e.g. diagnosis -  
X S Claim 11; SEQ ID No 505; 546pp; English.  
X C The present invention relates to the isolation of novel human  
X C respiratory antigens, and cDNA (AAS27869-AAS28159) and genomic  
X C sequences encoding for these polypeptides. The sequences of the  
X C invention are useful for preventing, treating and/or prognosing  
X C disorders related to the respiratory system including throat  
X C disorders (e.g. vocal cord paralysis, tonsillitis, and laryngitis),  
X C lung disorders e.g. pneumonia, allergic disorders e.g. asthma,  
X C pleurisy, cystic fibrosis, emphysema, nose disorders and cancers of  
X C the respiratory tissues e.g. lung cancer. The polynucleotide sequences  
X C of the invention are useful in gene therapy and antisense therapy.  
X C AAU17685-AAU17975 represent novel human respiratory antigens.  
X C Note: The sequence data for this patent did not form part of the printed  
X C specification, but was obtained in electronic format directly from WIPO  
X C at ftp.wipo.int/pub/published\_pct\_sequences.

X Q Sequence 121 AA;  
Query Match 5.7%; Score 7; DB 22; Length 121;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 27 ALLVFFG 33  
b 55 ALLVFFG 61  
|||||

RESULT 68  
BG18228  
D ABG18228 standard; Protein; 122 AA.  
X C ABG18228;  
X T 18-FEB-2002 (first entry)  
X C Novel human diagnostic protein #18219.  
X Human; chromosome mapping; gene mapping; gene therapy; forensic;  
X food supplement; medical imaging; diagnostic; genetic disorder.  
X Homo sapiens.  
X WO200175067-A2.  
X 11-OCT-2001.  
X 30-MAR-2001; 2001WO-US08631.  
X 31-MAR-2000; 2000US-0540217.  
X 23-AUG-2000; 2000US-0649167.  
X (HYSE-) HYSEQ INC.  
X Drmanac RT, Liu C, Tang YT;  
X WPI; 2001-639362/73.  
X N-PSDB; AAS82415.  
X New isolated polynucleotide and encoded polypeptides, useful in  
X diagnostics, forensics, gene mapping, identification of mutations  
X responsible for genetic disorders or other traits and to assess  
X biodiversity -  
X Claim 20; SEQ ID No 43246; 103pp; English.

XX PS Claim 20; SEQ ID No 48587; 103pp; English.  
XX CC The invention relates to isolated polynucleotide (I) and  
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
XX CC and gene mapping, and in recombinant production of (II). The  
XX CC polynucleotides are also used in diagnostics as expressed sequence tags  
XX CC for identifying expressed genes. (I) is useful in gene therapy techniques  
XX CC to restore normal activity of (II) or to treat disease states involving  
XX CC (II). (II) is useful for generating antibodies against it, detecting or  
XX CC quantitating a polypeptide in tissue, as molecular weight markers and as  
XX CC a food supplement. (II) and its binding partners are useful for treating  
XX CC disorders involving aberrant protein expression or biological activity.  
XX CC The polypeptide and polynucleotide sequences have applications in  
XX CC diagnostics, forensics, gene mapping, identification of mutations  
XX CC responsible for genetic disorders or other traits to assess biodiversity  
XX CC and to produce other types of data and products dependent on DNA and  
XX CC amino acid sequences. ABG00010-ABG30377 represent novel human  
XX CC diagnostic amino acid sequences of the invention.  
XX CC Note: The sequence data for this patent did not appear in the printed  
XX CC specification, but was obtained in electronic format directly from WIPO  
XX CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Q Sequence 122 AA;  
Query Match 5.7%; Score 7; DB 22; Length 122;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 APRYLLY 70  
Db 103 APRYLLY 109  
|||||

RESULT 69  
ABG12887  
ID ABG12887 standard; Protein; 161 AA.  
XX AC ABG12887;  
XX DT 13-FEB-2002 (first entry)  
XX DE Novel human diagnostic protein #12878.  
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
XX food supplement; medical imaging; diagnostic; genetic disorder.  
XX Homo sapiens.  
XX WO200175067-A2.  
XX 11-OCT-2001.  
XX 30-MAR-2001; 2001WO-US08631.  
XX 31-MAR-2000; 2000US-0540217.  
XX 23-AUG-2000; 2000US-0649167.  
XX (HYSE-) HYSEQ INC.  
XX Drmanac RT, Liu C, Tang YT;  
XX WPI; 2001-639362/73.  
XX N-PSDB; AAS77074.  
XX New isolated polynucleotide and encoded polypeptides, useful in  
XX diagnostics, forensics, gene mapping, identification of mutations  
XX responsible for genetic disorders or other traits and to assess  
XX biodiversity -  
XX Claim 20; SEQ ID No 43246; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) is useful for generating antibodies against it, detecting or  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 161 AA;  
 CC Query Match 5.7%; Score 7; DB 22; Length 161;  
 CC Best Local Similarity 100.0%; Pred. No. 54;  
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 VSWYQQR 60  
 DB 75 VSWYQQR 81  
 |||||

RESULT 70  
 ABE19759  
 ID ABG19759 standard; Protein; 182 AA.

XX AC ABG19759;  
 XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #19750.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX FR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS93946.

XX New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity -

XX Claim 20; SEQ ID No 50118; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and

CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 182 AA;

Query Match 5.7%; Score 7; DB 22; Length 182;  
 Best Local Similarity 100.0%; Pred. No. 60;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 PRYLLEY 71

DB 65 PRYLLEY 71  
 |||||

RESULT 71  
 ABB11775  
 ID ABB11775 standard; peptide; 211 AA.

XX AC ABB11775;

XX DT 11-JAN-2002 (first entry)

XX DE Human 14274 receptor protein homologue, SEQ ID NO:2145.

XX Human; cytokine; cell proliferation; cell differentiation; growth factor;  
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;  
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;  
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;  
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;  
 KW chronic inflammatory condition; proliferative retinopathy;  
 KW atherosclerosis; coronary heart disease; arterial ischaemia;  
 KW bone disorder; osteoporosis; vascular growth disorder;  
 KW tissue regeneration; wound healing; infection; immune disorder;  
 KW cell culture; drug screening; gene therapy; antiinflammatory;  
 KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;  
 KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;  
 KW antifungal; vulnery; antiulcer.

XX OS Homo sapiens.

XX PN WO200157188-A2.

XX PD 09-AUG-2001.

XX PF 05-FEB-2001; 2001WO-US03800.

XX PR 03-FEB-2000; 2000US-0496914.

XX PR 27-APR-2000; 2000US-0560875.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX DR WPI; 2001-457740/49.

XX DR N-PSDB; ABA09019.

Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -

Claim 20; Page 244; 1963pp; English.

Sequences ABB10981-ABB21330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides, or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; haematopoietic regulatory activity; tissue growth activity; immunomodulatory activity; activin- or inhibin-related activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis. Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention.

Sequence 211 AA;

Query Match 5.7%; Score 7; DB 22; Length 211;  
Best Local Similarity 100.0%; Pred. No. 69;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0

2y 28 LLVFPQG 34  
|||||  
74 LLVFPQG 80

RESULT 72  
AAW45517  
ID AAW45517 standard; peptide; 214 AA.  
CX AAW45517;  
AC  
CX  
15-JUN-1998 (first entry)  
CX  
CX NANUC-2 light chain, an ulcerative colitis pANCA monoclonal antibody.  
DE  
CX  
CX ulcerative colitis; inflammatory bowel disease; diagnosis; human histone;  
CX perinuclear anti-neutrophil cytoplasmic antibody; pANCA; antibody;  
CX tolerogenic fragment; H1S-1; NANUC-2 light chain.  
CX  
CX Homo sapiens.  
CX  
CX W09738713-A1.  
CX

```

XX      23-OCT-1997.
PD
XX      11-APR-1997;   97WO-US06987.
PF
XX      12-APR-1996;   96US-0630671.
PR
XX      (CEDA-) CEDARS SINAI MEDICAL CENT.
PA      (REGC) UNIV CALIFORNIA.
XX
XX      Braun J, Eggens M, Targan SR;
PI      WPI; 1997-526206/48.
XX      N-PSDB; AAT86667.
DR
XX
XX      Diagnosis of ulcerative colitis from presence of perinuclear
PT      anti-neutrophil cytoplasmic antibodies reactive with histone H1 -
PT      also treatment and prevention using H1 or its fragments
XX
XX      Example 1; Pages 54-55; 77pp; English.
PS
XX      This sequence represents NANUC-2 light chain, an ulcerative colitis
CC      PANCA monoclonal antibody. The invention relates to diagnosis
CC      of ulcerative colitis, which comprises treating a patient's sample with
CC      human histone H1, or its perinuclear anti-neutrophil cytoplasmic
CC      antibody (PANCA)-reactive fragments and detecting formation of a complex
CC      between this and antibodies to human H1. The same method can also be
CC      used to determine susceptibility to ulcerative colitis. The invention
CC      also relates to: (1) inducing tolerance in a PANCA-positive ulcerative
CC      colitis subject by: (a) administration of H1, or its tolerogenic
CC      fragments;or (b) ex vivo treatment of serum with H1, or its PANCA-
CC      reactive fragments, removing the complex formed and returning the
CC      treated serum to the patient; (2) composition comprising H1, or its
CC      fragments, plus a tolerance-inducing agent; (3) prevention of ulcerative
CC      colitis by administration of H1 or tolerance-inducing fragments
CC      (particularly to subjects, including neonates diagnosed as being
CC      susceptible). The method is specifically used to diagnose the PANCA-
CC      positive clinical subtype of ulcerative colitis. The invention is based
CC      on the discovery that PANCA, present in most ulcerative colitis
CC      patients, are directed against H1.
XX
XX      Sequence 214 AA;
SQ
Query Match          5.7%; Score 7; DB 18; Length 214;
Best Local Similarity 100.0%; Pred.No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      83 IPDRFSA 89
        |||||
DB       58 IPDRFSA 64

RESULT 73
AAW07615
ID      AAW07615 standard; Protein; 214 AA.
XX
XX      AAW07615;
AC
XX
XX      27-FEB-1997 (first entry)
DT
XX
XX      Ulcerative colitis-associated PANCA Fab 5-3 light chain.
DE
XX
XX      Ulcerative colitis; anti-neutrophil cytoplasmic antibody; ANCA;
KW      PANCA; UCPANCA; antibody engineering; phage display; diagnosis.
XX
XX      Homo sapiens.
OS
XX
XX      Key Location/Qualifiers
FH      1..233
FT      Protein /note= "ANCA 5-3 kappa light chain "
FT      Peptide 1
FT      /label= N-terminal tag

```

PT Protein 2..107 /note= "preferred light chain for use in constructs  
 TT /note= Of the invention (Claim 15)"  
 TT Domain 2..95 /label= VKSEGMENT  
 TT Domain 96..108 /note= "variable segment of the kappa light chain"  
 TT /label= JK  
 TT Domain 109..213 /note= "kappa light chain joining segment"  
 TT /label= CK  
 TT Region /note= "kappa light chain constant segment"  
 TT 2..22 /label= FR1  
 TT Region /note= "framework region 1"  
 TT 23..34 /label= CDR1  
 TT /note= "complementarity determining region 1"  
 TT 35..49 /label= FR2  
 TT /note= "framework region 2"  
 TT 50..56 /label= CDR2  
 TT /note= "complementarity determining region 2"  
 TT 57..88 /label= FR3  
 TT /note= "framework region 3"  
 TT 89..97 /label= CDR3  
 TT /note= "complementarity determining region 3"  
 TT 98..108 /label= FR4  
 TT /note= "framework region 4"  
 TT  
 CX WO9639186-A1.  
 PX 12-DEC-1996.  
 PX 05-JUN-1996; 96WO-US08756.  
 PX 06-JUN-1995; 95US-0472688.  
 PX (CEDA-) CEDARS SINAI MEDICAL CENT.  
 PX (REGC ) UNIV CALIFORNIA.  
 PX Braun J, Eggens MP, Targan SR;  
 CX WPI; 1997-042866/04.  
 CX N-PSDB; AAT44090.  
 CX Antibody material associated with ulcerative colitis - comprising  
 PT anti-neutrophil cytoplasmic antibody, characterised by perinuclear  
 PT neutrophil staining pattern  
 CX Disclosure; Page 117-118; 145pp; English.  
 CX A polypeptide (AAW07615) comprises the light chain of recombinant  
 CC UCPANCA Fab clone 5-3. Anti-neutrophil cytoplasmic antibodies  
 CC characterised by perinuclear neutrophil staining pattern (PANCA)  
 CC associated with ulcerative colitis (UC) were recombinantly produced  
 CC and characterised using a phase display technique. Libraries of VH-  
 CC and VL-encoding DNA homologues having the immunoreactivity of  
 CC UCPANCA antigen were created. Recombinant UCPANCA Fab clones 5-3  
 CC and 5-4 were generated (see also AAW07613-16). These can be used in  
 CC methods for screening for UCPANCA and for isolating UCPANCA  
 CC antigens.  
 CX Sequence 214 AA;

Query Match 5.7%; Score 7; DB 18; Length 214;  
 Best Local Similarity 100.0%; Pred. No. 70;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFSA 89  
 DB 58 IPDRFSA 64  
 RESULT 74  
 AAW64671  
 ID AAW64671 standard; Protein; 214 AA.  
 CX AAW64671;  
 CX 11-NOV-1998 (first entry)  
 CX Human UC pANCA monoclonal antibody NANUC-1 light chain.  
 CX NANUC-1; NANUC-2; UC pANCA; monoclonal antibody; ulcerative colitis;  
 CX UC pANCA secretory vesicle antigen; secretory vesicle membrane; UC;  
 CX mast cell; neuroendocrine cell; tolerogenic; autoantibody.  
 CX Homo sapiens.  
 CX WO9837415-A1.  
 CX 27-AUG-1998.  
 CX 06-AUG-1997; 97WO-US13059.  
 CX 20-FEB-1997; 97US-0804106.  
 CX (CEDA-) CEDARS SINAI MEDICAL CENT.  
 CX (REGC ) UNIV CALIFORNIA.  
 CX Braun J, Eggens M, Gordon LK, Targan SR;  
 CX WPI; 1998-467728/40.  
 CX N-PSDB; AAV51395.  
 CX New ulcerative colitis pANCA secretory vesicle antigen - is  
 PT immuno-reactive with NANUC-1 and NANUC-2 and is expressed in  
 PT secretory vesicle membrane  
 CX Disclosure; Pages 62-63; 83pp; English.  
 CX This represents the light chain of human NANUC-1, a representative  
 CC UC pANCA monoclonal antibody. The invention provides a pure ulcerative  
 CC colitis (UC) pANCA secretory vesicle antigen, comprising a protein  
 CC immunoreactive with NANUC-1 and NANUC-2 antibodies, and characterised by  
 CC being selectively expressed in secretory vesicle membrane, in mast and/or  
 CC neuroendocrine cells. The UC pANCA secretory vesicle antigen can be used  
 CC in compositions or as tolerogenic fragment, combined with a tolerogenic  
 CC molecule for the diagnosis of UC, or for detecting susceptibility to UC.  
 CC Tolerance may be induced in a pANCA positive patient by administration of  
 CC a substantially pure UC pANCA secretory vesicle antigen or a tolerogenic  
 CC fragment, such that the level of autoantibodies reactive with the antigen  
 CC in the patient is reduced. Administration of this antigen prevents the  
 CC formation of UC.  
 CX Sequence 214 AA;  
 CX Query Match 5.7%; Score 7; DB 19; Length 214;  
 CX Best Local Similarity 100.0%; Pred. No. 70;  
 CX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 83 IPDRFSA 89  
 DB 58 IPDRFSA 64  
 RESULT 75  
 RAY34039  
 ID AAY34039 standard; Protein; 214 AA.  
 CX AAY34039;

X 23-NOV-1999 (first entry)  
X  
X NANUC-2 antibody light chain.  
X  
X Ulcerative colitis; histone; H1-like antigen; porin antigen; human;  
X Bacteroides antigen; inflammatory bowel disease; IBD; PANCA; diagnosis;  
X perinuclear anti-neutrophil cytoplasmic antibody; isoform; NANUC-2.  
X  
X Homo sapiens.  
X  
X WO9945955-A1.  
X  
X 16-SEP-1999.  
X  
X 12-MAR-1999; 99WO-US05492.  
X  
X 12-MAR-1998; 98US-0041889.  
X  
X (REGC ) UNIV CALIFORNIA.  
X  
X Braun J, Cohavy O;  
X  
X WPI; 1999-551215/46.  
X  
X N-PSDB; AAX91123.  
X  
X Use of histone H1, porin or Bacteroides antigens as targets for the  
X diagnosis, prevention and treatment of ulcerative colitis -  
X  
X Disclosure; Page 109-110; 134pp; English.  
X  
X The invention provides a method for the diagnosis, prevention and  
X treatment of ulcerative colitis (UC) using histone H1-like antigen, a  
X porin antigen or a Bacteroides antigen as a target antigen. The novel  
X method of diagnosing UC in a subject suspected of having inflammatory  
X bowel disease (IBD) comprises: (1) obtaining a sample from the subject;  
X (2) contacting the sample with a histone H1-like antigen, or perinuclear  
X anti-neutrophil cytoplasmic antibody (PANCA)-reactive fragment, to form a  
X complex of the histone H1-like antigen, or the PANCA-reactive fragment,  
X and antibody to the histone H1-like antigen; and (3) detecting the  
X presence or absence of the complex; where the presence of the complex  
X indicates that the subject has UC. The PANCA-reactive histone H1-like  
X antigen, porin antigen and Bacteroides antigen are useful in the  
X diagnosis, prevention and treatment of UC. The methods can also be used  
X for identifying agents useful for treating UC. The present sequence  
X represents the light chain of NANUC-2 antibody.  
X  
X Sequence 214 AA;  
X  
X Query Match 5.7%; Score 7; DB 20; Length 214;  
X Best Local Similarity 100.0%; Pred. No. 70;  
X Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
X  
X 83 IPDRFSA 89  
X |||||  
X 58 IPDRFSA 64

Search completed: February 9, 2004, 12:57:21  
Job time : 49 secs



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1 protein - protein search, using sw model

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247.821 Million cell updates/sec

title: US-09-981-876-200

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Issued Patents AA.\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	123	100.0	123	4	US-09-996-243-117
2	8	6.5	689	4	US-09-425-335-2
3	7	5.7	52	1	US-08-162-102C-43
4	7	5.7	103	2	US-08-273-146-71
5	7	5.7	104	1	US-08-276-852-92
6	7	5.7	104	1	US-08-899-575-92
7	5.7	104	1	US-08-899-575-92	
8	7	5.7	104	5	PCT-US95-08743-92
9	7	5.7	109	1	US-08-162-102C-23
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14	7	5.7	109	4	US-09-425-638A-40
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16	7	5.7	109	4	US-09-425-638A-42
17	7	5.7	109	4	US-09-425-638A-43
18	7	5.7	109	4	US-09-425-638A-44
19	7	5.7	109	4	US-09-425-638A-45
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					Sequence 22, Appl
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					Sequence 43, Appl

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31	7	5.7	111	1	US-08-276-852-149	Sequence 149, Appl
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35	7	5.7	214	2	US-08-480-753-6	Sequence 6, Appl
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37	7	5.7	214	4	US-09-417-264-11	Sequence 11, Appl
38	7	5.7	214	4	US-09-417-264-11	Sequence 6418, Appl
39	7	5.7	255	4	US-09-328-352-6418	Sequence 140, Appl
40	7	5.7	270	4	US-09-286-965-140	Sequence 21249, A
41	7	5.7	613	4	US-09-352-991A-21249	Sequence 2, Appl
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48	7	5.7	1010	4	US-09-708-200-13	Sequence 31, Appl
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50	6	4.9	12	3	US-08-747-599A-17	Sequence 17, Appl
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53	6	4.9	21	4	US-09-680-454-102	Sequence 102, Appl
54	6	4.9	53	1	US-08-162-102C-44	Sequence 44, Appl
55	6	4.9	54	3	US-08-851-843A-183	Sequence 183, Appl
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57	6	4.9	54	3	US-08-854-050-183	Sequence 183, Appl
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61	6	4.9	72	4	US-08-003-198A-17	Sequence 17, Appl
62	6	4.9	82	1	US-08-476-405A-25	Sequence 25, Appl
63	6	4.9	92	1	US-08-181-492B-27	Sequence 27, Appl
64	6	4.9	92	5	PCT-US95-00408-27	Sequence 27, Appl
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67	6	4.9	96	1	US-08-477-484B-158	Sequence 158, Appl
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72	6	4.9	96	2	US-08-082-842A-22	Sequence 22, Appl
73	6	4.9	96	3	US-08-839-765-158	Sequence 158, Appl
74	6	4.9	96	3	US-09-136-389-158	Sequence 158, Appl
75	6	4.9	96	4	US-09-610-838-158	Sequence 35, Appl
76	6	4.9	97	2	US-08-665-202-35	Sequence 35, Appl
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78	6	4.9	98	2	US-08-665-202-37	Sequence 37, Appl
79	6	4.9	98	4	US-09-315-574-37	Sequence 16637, A
80	6	4.9	99	4	US-09-253-991A-16637	Sequence 100, Appl
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82	6	4.9	104	1	US-08-488-113B-153	Sequence 153, Appl
83	6	4.9	104	1	US-08-477-484B-153	Sequence 153, Appl
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87	6	4.9	104	1	US-08-898-575-100	Sequence 100, Appl
88	6	4.9	104	2	US-08-477-531B-17	Sequence 17, Appl
89	6	4.9	104	2	US-08-646-360-153	Sequence 153, Appl
90	6	4.9	104	2	US-08-273-146-63	Sequence 63, Appl
91	6	4.9	104	2	US-08-082-842A-17	Sequence 17, Appl
92	6	4.9	104	3	US-08-839-765-153	Sequence 153, Appl
93	6	4.9	104	3	US-09-136-389-153	Sequence 153, Appl
94	6	4.9	104	3	US-09-240-274-49	Sequence 49, Appl
95	6	4.9	104	3	US-09-240-274-49	Sequence 69, Appl
96	6	4.9	104	4	US-08-793-450-2	Sequence 2, Appl
97	6	4.9	104	4	US-09-610-838-153	Sequence 153, Appl
98	6	4.9	104	5	PCT-US95-08743-100	Sequence 100, Appl
99	6	4.9	105	1	US-08-488-113B-157	Sequence 157, Appl
100	6	4.9	105	1	US-08-477-484B-157	Sequence 157, Appl

ALIGNMENTS

RESULT 1  
IS-09-996-243-117  
Sequence 117, Application US/09996243  
Patent No. 6478825  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gunney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C13  
CURRENT APPLICATION NUMBER: US/09/996,243  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087609  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087759  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087827  
PRIOR FILING DATE: 1998-06-03  
PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088025  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088026  
PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088028  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088029  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088030  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088033  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088326  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088167  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088202  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088212  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088217  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088655  
PRIOR FILING DATE: 1998-06-09  
PRIOR APPLICATION NUMBER: 60/088734  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088738  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088742  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088810  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088824  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088826  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088858  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088861  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088876  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089105  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089440  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089512  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089532  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089538  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089598  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089599  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089600  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089907  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089908  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089947  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089948  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089952  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/090246  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090252



PRIOR FILING DATE: 1998-06-22  
 PRIOR APPLICATION NUMBER: 60/090254  
 PRIOR FILING DATE: 1998-06-22  
 PRIOR APPLICATION NUMBER: 60/090349  
 PRIOR FILING DATE: 1998-06-23  
 PRIOR APPLICATION NUMBER: 60/090355  
 PRIOR FILING DATE: 1998-06-23  
 PRIOR APPLICATION NUMBER: 60/090429  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090431  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090435  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090444  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090445  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090472  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090535  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090540  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090542  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090557  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090676  
 PRIOR FILING DATE: 1998-06-25  
 PRIOR APPLICATION NUMBER: 60/090678  
 PRIOR FILING DATE: 1998-06-25  
 PRIOR APPLICATION NUMBER: 60/090690  
 PRIOR FILING DATE: 1998-06-25  
 PRIOR APPLICATION NUMBER: 60/090694  
 PRIOR FILING DATE: 1998-06-25  
 PRIOR APPLICATION NUMBER: 60/090695  
 PRIOR FILING DATE: 1998-06-25  
 PRIOR APPLICATION NUMBER: 60/090696  
 PRIOR FILING DATE: 1998-06-25  
 PRIOR APPLICATION NUMBER: 60/090862  
 PRIOR FILING DATE: 1998-06-26  
 PRIOR APPLICATION NUMBER: 60/090863  
 PRIOR FILING DATE: 1998-06-26  
 PRIOR APPLICATION NUMBER: 60/091360  
 PRIOR FILING DATE: 1998-07-01  
 PRIOR APPLICATION NUMBER: 60/091478  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091544  
 PRIOR FILING DATE: 1998-07-01  
 PRIOR APPLICATION NUMBER: 60/091519  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091626  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091633  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091978  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 123; DB 4; Length 123;  
 Best Local Similarity 100.0%; Pred.No. 3.6e-116;  
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 1 MACCLSLFLMGTSLVSQTVLQALDALLVPCQVQLSCTLSPOHVTIRDYGVSWYQOR 60  
 |||||  
 3b 1 MACCLSLFLMGTSLVSQTVLQALDALLVPCQVQLSCTLSPOHVTIRDYGVSWYQOR 60  
 |||||

2y 61 AGSAPRYLLYRSDEHRRPADIPDRFSAAKDEAHNACVLTISPVPEDDADYYCSVG 120  
 |||||  
 3b 61 AGSAPRYLLYRSDEHRRPADIPDRFSAAKDEAHNACVLTISPVPEDDADYYCSVG 120  
 |||||

QY 121 FSP 123  
 ||||  
 Db 121 FSP 123

RESULT 2  
 US-09-425-335-2  
 ; Sequence 2, Application US/09425335  
 ; Patent No. 6518052  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WEINMANN, ROBERTO  
 ; TITLE OF INVENTION: HUMAN HOMOLOGUE OF YEAST HELICASE AND USES THEREOF  
 ; FILE REFERENCE: db7 sequence  
 ; CURRENT APPLICATION NUMBER: US/09425.335  
 ; CURRENT FILING DATE: 1999-10-22  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 689  
 ; TYPE: PRT  
 ; ORGANISM: HUMAN  
 US-09-425-335-2

Query Match 6.5%; Score 8; DB 4; Length 689;  
 Best Local Similarity 100.0%; Pred.No. 6;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 TISPVQPE 108  
 |||||  
 Db 149 TISPVQPE 156

RESULT 3  
 US-08-162-102C-43  
 ; Sequence 43, Application US/08162102C  
 ; Patent No. 5762905  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Burton, Dennis R.  
 ; APPLICANT: Barbas, III, Carlos F.  
 ; APPLICANT: Chanock, Robert M.  
 ; APPLICANT: Murphy, Brian R.  
 ; APPLICANT: Crowe, Jr., James E.  
 ; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
 ; NUMBER OF SEQUENCES: 49  
 ; NUMBER OF INVENTIONS: TO RESPIRATORY SYNCYTIAL VIRUS  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fish & Richardson P.C.  
 ; STREET: 4225 Executive Square, Suite 1400  
 ; CITY: La Jolla  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 92037  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/162,102C  
 ; FILING DATE: 10-DEC-1993  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Halle, Ph.D., Lisa A.  
 ; REGISTRATION NUMBER: 38,347  
 ; REFERENCE/DOCKET NUMBER: 07300/007001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (619) 678-5070  
 ; TELEFAX: (619) 678-5099  
 ; INFORMATION FOR SEQ ID NO: 43:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 52 amino acids  
 ; TYPE: amino acid

STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
JS-08-162-102C-43

Query Match 5.7%; Score 7; DB 1; Length 52;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 DIPDRFS 88  
| | | | |  
DB 1 DIPDRFS 7

## RESULT 4

JS-08-273-146-71  
Sequence 71, Application US/08273146  
Patent No. 5855885

GENERAL INFORMATION:

APPLICANT: Smith, Rodger  
APPLICANT: McGafferty, John  
APPLICANT: Chiswell, David  
APPLICANT: Darsley, Michael J.  
APPLICANT: Fitzgerald, Kevin  
APPLICANT: Kenten, John H.  
APPLICANT: Martin, Mark T.  
APPLICANT: Titmas, Richard C.  
APPLICANT: Williams, Richard O.  
TITLE OF INVENTION: The Isolation and Production of  
NUMBER OF SEQUENCES: 71  
TITLE OF INVENTION: Catalytic Antibodies using Phage Technology  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IGEN, Inc.  
STREET: 1530 East Jefferson St.  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20852

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/273.146  
FILING DATE: 14-JUL-1994  
CLASSIFICATION: 435

## ATTORNEY/AGENT INFORMATION:

NAME: Ryan, John W.  
REGISTRATION NUMBER: 33,771  
REFERENCE/DOCKET NUMBER: 09000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-984-8000  
TELEFAX: 301-230-0158

INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 103 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-273-146-71.

Query Match 5.7%; Score 7; DB 2; Length 103;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFSA 89  
| | | | |  
DB 51 IPDRFSA 57

## RESULT 5

US-08-276-852-92

Sequence 92, Application US/08276852

Patent No. 5652138

GENERAL INFORMATION:

APPLICANT: Burton, Dennis R  
APPLICANT: Barbas, Carlos F  
APPLICANT: Lerner, Richard A  
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 170

CORRESPONDENCE ADDRESS:

ADDRESSEE: The Scripps Research Institute, Office of  
ADDRESSEE: Patent Counsel  
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/276,852  
FILING DATE: 18-JUL-1994  
CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/178,302

FILING DATE: 30-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/954,148

FILING DATE: 30-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: SC1452P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-554-2937

TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 92:

SEQUENCE CHARACTERISTICS:

LENGTH: 104 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-276-852-92

Query Match 5.7%; Score 7; DB 1; Length 104;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 DIPDRFS 88

| | | | |

DB 53 DIPDRFS 59

## RESULT 6

US-08-899-575-92

Sequence 92, Application US/08899575

Patent No. 5770440

GENERAL INFORMATION:

APPLICANT: Burton, Dennis R

APPLICANT: Barbas, Carlos F

APPLICANT: Lerner, Richard A

TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS

NUMBER OF SEQUENCES: 170

CORRESPONDENCE ADDRESS:

ADDRESSEE: The Scripps Research Institute, Office of

ADDRESSEE: Patent Counsel

STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

CITY: La Jolla  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 92037  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/899,575  
 FILING DATE: 24-JUL-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/276,852  
 FILING DATE: 18-JUL-1994  
 APPLICATION NUMBER: US 08/178,302  
 FILING DATE: 30-SEP-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/954,148  
 FILING DATE: 30-SEP-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fitting, Thomas  
 REGISTRATION NUMBER: 34,163  
 REFERENCE/DOCKET NUMBER: SCR1452P  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-554-2937  
 TELEFAX: 619-554-6312  
 INFORMATION FOR SEQ ID NO: 92:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 104 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 S-08-899-575-92

Query Match 5.7%; Score 7; DB 1; Length 104;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 82 DIPDRFS 88  
 |||||  
 b 53 DIPDRFS 59

RESULT 7  
 S-08-899-575-92  
 Sequence 92, Application US/08899575  
 Patent No. 580440  
 GENERAL INFORMATION:  
 APPLICANT: Dennis R.  
 APPLICANT: Burton, Dennis R.  
 APPLICANT: Barbas, Carlos F.  
 APPLICANT: Lerner, Richard A.  
 TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
 TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
 NUMBER OF SEQUENCES: 170  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: The Scripps Research Institute, Office of  
 ADDRESSEE: Patent Counsel  
 STREET: 10666 No. 580440th Torrey Pines Road, Suite 220,  
 STREET: Mail Drop 1PC8  
 CITY: La Jolla  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 92037  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/899,575  
 FILING DATE: 24-JUL-1997

CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/276,852  
 FILING DATE: 18-JUL-1994  
 APPLICATION NUMBER: US 08/178,302  
 FILING DATE: 30-SEP-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/954,148  
 FILING DATE: 30-SEP-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fitting, Thomas  
 REGISTRATION NUMBER: 34,163  
 REFERENCE/DOCKET NUMBER: SCR1452P  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-554-2937  
 TELEFAX: 619-554-6312  
 INFORMATION FOR SEQ ID NO: 92:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 104 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-899-575-92

Query Match 5.7%; Score 7; DB 1; Length 104;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 DIPDRFS 88  
 |||||  
 Db 53 DIPDRFS 59

RESULT 8  
 PCT-US95-08743-92  
 Sequence 92, Application PC/TUS9508743  
 GENERAL INFORMATION:  
 APPLICANT:  
 TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
 TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
 NUMBER OF SEQUENCES: 170  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/08743  
 FILING DATE: 11-JUL-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/276,852  
 FILING DATE: 18-JUL-1994  
 INFORMATION FOR SEQ ID NO: 92:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 104 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PCT-US95-08743-92

Query Match 5.7%; Score 7; DB 5; Length 104;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 DIPDRFS 88  
 |||||  
 Db 53 DIPDRFS 59

RESULT 9  
 US-08-162-102C-23  
 Sequence 23, Application US/08162102C  
 Patent No. 5762905

GENERAL INFORMATION:

APPLICANT: Burton, Dennis R.  
 APPLICANT: Barbas, III, Carlos F.  
 APPLICANT: Chanock, Robert M.  
 APPLICANT: Murphy, Brian R.  
 APPLICANT: Crowe, Jr., James E.  
 TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
 TITLE OF INVENTION: TO RESPIRATORY SYNCYTIAL VIRUS  
 NUMBER OF SEQUENCES: 49  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.  
 STREET: 4225 Executive Square, Suite 1400  
 CITY: La Jolla  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92037

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/162,102C  
 FILING DATE: 10-DEC-1993  
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:  
 NAME: Haile, Ph.D., Lisa A.  
 REGISTRATION NUMBER: 38,347  
 REFERENCE/DOCKET NUMBER: 07300/007001  
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 678-5070  
 TELEFAX: (619) 678-5099

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 109 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single

TOPOLOGY: linear  
 MOLECULE TYPE: peptide

IMMEDIATE SOURCE:  
 CLONE: rsv 6L; 11L; 21L; anad 22L

FEATURE:

NAME/KEY: Peptide  
 LOCATION: 1..109

IS-08-162-102C-23

Query Match 5.7%; Score 7; DB 1; Length 109;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 DIPDRFS 88  
 DB 58 DIPDRFS 64

RESULT 10

US-09-425-638A-20  
 ; Sequence 20, Application US/09425638A  
 ; Patent No. 6342587

GENERAL INFORMATION:

APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and  
 APPLICANT: Lloyd J. Old  
 TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF  
 FILE REFERENCE: LUD 5630  
 CURRENT APPLICATION NUMBER: US/09/425,638A  
 CURRENT FILING DATE: 1999-10-22  
 NUMBER OF SEQ ID NOS: 129

SEQ ID NO 20  
 LENGTH: 109  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:

IS-09-425-638A-20

Query Match 5.7%; Score 7; DB 4; Length 109;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 GVSQYQQ 59  
 DB 32 GVSQYQQ 38

RESULT 11

US-09-425-638A-21  
 ; Sequence 21, Application US/09425638A  
 ; Patent No. 6342587

GENERAL INFORMATION:

APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and  
 APPLICANT: Lloyd J. Old  
 TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF  
 FILE REFERENCE: LUD 5630  
 CURRENT APPLICATION NUMBER: US/09/425,638A  
 CURRENT FILING DATE: 1999-10-22  
 NUMBER OF SEQ ID NOS: 129

SEQ ID NO 21  
 LENGTH: 109  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:

US-09-425-638A-21

Query Match 5.7%; Score 7; DB 4; Length 109;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 GVSQYQQ 59  
 DB 32 GVSQYQQ 38

RESULT 12

US-09-425-638A-22  
 ; Sequence 22, Application US/09425638A  
 ; Patent No. 6342587

GENERAL INFORMATION:

APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and  
 APPLICANT: Lloyd J. Old  
 TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF  
 FILE REFERENCE: LUD 5630  
 CURRENT APPLICATION NUMBER: US/09/425,638A  
 CURRENT FILING DATE: 1999-10-22  
 NUMBER OF SEQ ID NOS: 129

SEQ ID NO 22  
 LENGTH: 109  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:

US-09-425-638A-22

Query Match 5.7%; Score 7; DB 4; Length 109;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 GVSQYQQ 59  
 DB 32 GVSQYQQ 38

RESULT 13

US-09-425-638A-39  
 ; Sequence 39, Application US/09425638A  
 ; Patent No. 6342587

GENERAL INFORMATION:

APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and  
 APPLICANT: Lloyd J. Old

```

TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREC
FILE REFERENCE: LUD 5630
CURRENT APPLICATION NUMBER: US/09/425,638A
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 129
SEQ ID NO 39
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
S-09-425-638A-39
Query Match 5.7%; Score 7; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 53 GVSQYQQ 59
b 32 GVSQYQQ 38
RESULT 14
US-09-425-638A-40
Sequence 40, Application US/09425638A
Patent No. 6342587
GENERAL INFORMATION:
APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
APPLICANT: Lloyd J. Old
TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREC
FILE REFERENCE: LUD 5630
CURRENT APPLICATION NUMBER: US/09/425,638A
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 129
SEQ ID NO 40
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
US-09-425-638A-40
Query Match 5.7%; Score 7; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 53 GVSQYQQ 59
b 32 GVSQYQQ 38
RESULT 15
US-09-425-638A-41
Sequence 41, Application US/09425638A
Patent No. 6342587
GENERAL INFORMATION:
APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
APPLICANT: Lloyd J. Old
TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREC
FILE REFERENCE: LUD 5630
CURRENT APPLICATION NUMBER: US/09/425,638A
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 129
SEQ ID NO 41
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
US-09-425-638A-41
Query Match 5.7%; Score 7; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 53 GVSQYQQ 59
b 32 GVSQYQQ 38
RESULT 16
US-09-425-638A-42
Sequence 42, Application US/09425638A
Patent No. 6342587
GENERAL INFORMATION:
APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
APPLICANT: Lloyd J. Old
TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREC
FILE REFERENCE: LUD 5630
CURRENT APPLICATION NUMBER: US/09/425,638A
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 129
SEQ ID NO 42
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
US-09-425-638A-42
Query Match 5.7%; Score 7; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 53 GVSQYQQ 59
b 32 GVSQYQQ 38
RESULT 17
US-09-425-638A-43
Sequence 43, Application US/09425638A
Patent No. 6342587
GENERAL INFORMATION:
APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
APPLICANT: Lloyd J. Old
TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREC
FILE REFERENCE: LUD 5630
CURRENT APPLICATION NUMBER: US/09/425,638A
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 129
SEQ ID NO 43
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
US-09-425-638A-43
Query Match 5.7%; Score 7; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 53 GVSQYQQ 59
b 32 GVSQYQQ 38
RESULT 18
US-09-425-638A-44
Sequence 44, Application US/09425638A
Patent No. 6342587
GENERAL INFORMATION:
APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
APPLICANT: Lloyd J. Old
TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREC
FILE REFERENCE: LUD 5630
CURRENT APPLICATION NUMBER: US/09/425,638A
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 129
SEQ ID NO 44
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
US-09-425-638A-44
Query Match 5.7%; Score 7; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 53 GVSQYQQ 59
b 32 GVSQYQQ 38

```

```
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
S-09-425-638A-44
Query Match      5.7%; Score 7; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
iy 53 GVSYYQQ 59
    |||||
ib 32 GVSYYQQ 38
    |||||

RESULT 19
US-09-425-638A-45
; Sequence 45, Application US/09425638A
; Patent No. 6342587
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREO
; FILE REFERENCE: LUD 5630
; CURRENT APPLICATION NUMBER: US/09/425,638A
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 45
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-425-638A-45
Query Match      5.7%; Score 7; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
iy 53 GVSYYQQ 59
    |||||
ib 32 GVSYYQQ 38
    |||||

RESULT 20
US-09-543-004-20
; Sequence 20, Application US/09543004
; Patent No. 6346249
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREO
; FILE REFERENCE: LUD 5630.1
; CURRENT APPLICATION NUMBER: US/09/543,004
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/425,638
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 20
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-543-004-20
Query Match      5.7%; Score 7; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
iy 53 GVSYYQQ 59
    |||||
ib 32 GVSYYQQ 38
    |||||

RESULT 21
US-09-543-004-21
; Sequence 21, Application US/09543004
; Patent No. 6346249
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREO
; FILE REFERENCE: LUD 5630.1
; CURRENT APPLICATION NUMBER: US/09/543,004
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/425,638
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 21
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-543-004-21
Query Match      5.7%; Score 7; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
iy 53 GVSYYQQ 59
    |||||
ib 32 GVSYYQQ 38
    |||||

RESULT 22
US-09-543-004-22
; Sequence 22, Application US/09543004
; Patent No. 6346249
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREO
; FILE REFERENCE: LUD 5630.1
; CURRENT APPLICATION NUMBER: US/09/543,004
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/425,638
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 22
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-543-004-22
Query Match      5.7%; Score 7; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
iy 53 GVSYYQQ 59
    |||||
ib 32 GVSYYQQ 38
    |||||

RESULT 23
US-09-543-004-39
; Sequence 39, Application US/09543004
; Patent No. 6346249
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREO
; FILE REFERENCE: LUD 5630.1
; CURRENT APPLICATION NUMBER: US/09/543,004
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/425,638
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 23
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-543-004-20
Query Match      5.7%; Score 7; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
iy 53 GVSYYQQ 59
    |||||
ib 32 GVSYYQQ 38
    |||||
```

NUMBER OF SEQ ID NOS: 129

SEQ ID NO 39

LENGTH: 109

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

S-09-543-004-39

Query Match

Best Local Similarity 5.7%; Score 7; DB 4; Length 109;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 53 GVSUWQQ 59

|||||

b 32 GVSUWQQ 38

RESULT 24

S-09-543-004-40

Sequence 40, Application US/09543004

Patent No. 6346249

GENERAL INFORMATION:

APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and

APPLICANT: Lloyd J. Old

TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREO

FILE REFERENCE: LUD 5630.1

CURRENT APPLICATION NUMBER: US/09/543,004

CURRENT FILING DATE: 2000-04-04

PRIOR APPLICATION NUMBER: 09/425,638

PRIOR FILING DATE: 1999-10-22

NUMBER OF SEQ ID NOS: 129

SEQ ID NO 40

LENGTH: 109

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

S-09-543-004-40

Query Match

Best Local Similarity 5.7%; Score 7; DB 4; Length 109;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 53 GVSUWQQ 59

|||||

b 32 GVSUWQQ 38

RESULT 25

S-09-543-004-41

Sequence 41, Application US/09543004

Patent No. 6346249

GENERAL INFORMATION:

APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and

APPLICANT: Lloyd J. Old

TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREO

FILE REFERENCE: LUD 5630.1

CURRENT APPLICATION NUMBER: US/09/543,004

CURRENT FILING DATE: 2000-04-04

PRIOR APPLICATION NUMBER: 09/425,638

PRIOR FILING DATE: 1999-10-22

NUMBER OF SEQ ID NOS: 129

SEQ ID NO 41

LENGTH: 109

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

S-09-543-004-41

Query Match

Best Local Similarity 5.7%; Score 7; DB 4; Length 109;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 53 GVSUWQQ 59

Db 32 GVSUWQQ 38

RESULT 26

US-09-543-004-42

Sequence 42, Application US/09543004

Patent No. 6346249

GENERAL INFORMATION:

APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and

APPLICANT: Lloyd J. Old

TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREO

FILE REFERENCE: LUD 5630.1

CURRENT APPLICATION NUMBER: US/09/543,004

CURRENT FILING DATE: 2000-04-04

PRIOR APPLICATION NUMBER: 09/425,638

PRIOR FILING DATE: 1999-10-22

NUMBER OF SEQ ID NOS: 129

SEQ ID NO 42

LENGTH: 109

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

US-09-543-004-42

Query Match

Best Local Similarity 5.7%; Score 7; DB 4; Length 109;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 GVSUWQQ 59

|||||

Db 32 GVSUWQQ 38

RESULT 27

US-09-543-004-43

Sequence 43, Application US/09543004

Patent No. 6346249

GENERAL INFORMATION:

APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and

APPLICANT: Lloyd J. Old

TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREO

FILE REFERENCE: LUD 5630.1

CURRENT APPLICATION NUMBER: US/09/543,004

CURRENT FILING DATE: 2000-04-04

PRIOR APPLICATION NUMBER: 09/425,638

PRIOR FILING DATE: 1999-10-22

NUMBER OF SEQ ID NOS: 129

SEQ ID NO 43

LENGTH: 109

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

US-09-543-004-43

Query Match

Best Local Similarity 5.7%; Score 7; DB 4; Length 109;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 GVSUWQQ 59

|||||

Db 32 GVSUWQQ 38

RESULT 28

US-09-543-004-44

Sequence 44, Application US/09543004

Patent No. 6346249

GENERAL INFORMATION:

APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and

APPLICANT: Lloyd J. Old

TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREO

FILE REFERENCE: LUD 5630.1

CURRENT APPLICATION NUMBER: US/09/543,004  
CURRENT FILING DATE: 2000-04-04  
PRIOR APPLICATION NUMBER: 09/425,638  
PRIOR FILING DATE: 1999-10-22  
NUMBER OF SEQ ID NOS: 129

SEQ ID NO 44

LENGTH: 109

TYPE: PRT

ORGANISM: Homo sapiens

FEATURES:

US-09-543-004-44

Query Match 5.7%; Score 7; DB 4; Length 109;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 53 GVSQYQQ 59

|||||

2b 32 GVSQYQQ 38

RESULT 29

US-09-543-004-45

Sequence 45, Application US/09543004

Patent No. 6346249

GENERAL INFORMATION:

APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and

APPLICANT: Lloyd J. Old

TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF

FILE REFERENCE: LUD 5630.1

CURRENT APPLICATION NUMBER: US/09/543,004

CURRENT FILING DATE: 2000-04-04

PRIOR APPLICATION NUMBER: 09/425,638

PRIOR FILING DATE: 1999-10-22

NUMBER OF SEQ ID NOS: 129

SEQ ID NO 45

LENGTH: 109

TYPE: PRT

ORGANISM: Homo sapiens

FEATURES:

US-09-543-004-45

Query Match 5.7%; Score 7; DB 4; Length 109;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 53 GVSQYQQ 59

|||||

2b 32 GVSQYQQ 38

RESULT 30

PCT-US93-08786-23

Sequence 23, Application PC/TUS9308786

GENERAL INFORMATION:

APPLICANT: Burton, Dennis R.

APPLICANT: Barbas, III, Carlos F.

APPLICANT: Chanock, Robert M.

APPLICANT: Murphy, Brian R.

APPLICANT: Crowe, Jr., James E.

TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

TITLE OF INVENTION: TO RESPIRATORY SYNCYTIAL VIRUS

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Spensley Horn Juba & Lubitz

STREET: 1880 Century Park East, Suite 500

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90067

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08786

FILING DATE: 16-SEP-1993

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Wetherell, Jr., Ph.D., John R.

REGISTRATION NUMBER: 31,678

REFERENCE/DOCKET NUMBER: FD-2791

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 455-5100

TELEFAX: (619) 455-5110

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 109 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE: rsv 6L; 11L; 21L; anad 22L

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..109

PCT-US93-08786-23

Query Match 5.7%; Score 7; DB 5; Length 109;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 DIPDRFS 88

|||||

Db 58 DIPDRFS 64

RESULT 31

US-08-276-852-149

Sequence 149, Application US/08276852

Patent No. 5652138

GENERAL INFORMATION:

APPLICANT: Burton, Dennis R.

APPLICANT: Barbas, Carlos F.

APPLICANT: Lerner, Richard A.

TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS

NUMBER OF SEQUENCES: 170

CORRESPONDENCE ADDRESS:

ADDRESSEE: The Scripps Research Institute, Office of

ADDRESSEE: Patent Counsel

STREET: 10686 No. 5652138th Torrey Pines Road, Suite 220,

STREET: Mail Drop TPC8

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/276,852

FILING DATE: 18-JUL-1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/178,302

FILING DATE: 30-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/954,148

FILING DATE: 30-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas



REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: SCR1452P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 149:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 111 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
S-08-276-852-149

Query Match 5.7%; Score 7; DB 1; Length 111;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 82 DIPDRFS 88  
b 58 DIPDRFS 64

RESULT 32  
S-08-899-575-149  
Sequence 149, Application US/08899575  
Patent No. 5770440  
GENERAL INFORMATION:  
APPLICANT: Burton, Dennis R  
APPLICANT: Barbas, Carlos F  
APPLICANT: Lerner, Richard A  
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 170  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute, Office of  
ADDRESSEE: Patent Counsel  
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,  
STREET: Mail Drop TPC8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/899,575  
FILING DATE: 24-JUL-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/276,852  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: US 08/178,302  
FILING DATE: 30-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/954,148  
FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: SCR1452P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 149:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 111 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
S-08-899-575-149

Query Match 5.7%; Score 7; DB 1; Length 111;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 DIPDRFS 88  
DB 58 DIPDRFS 64

RESULT 33  
US-08-899-575-149  
Sequence 149, Application US/08899575  
Patent No. 5804440  
GENERAL INFORMATION:  
APPLICANT: Burton, Dennis R  
APPLICANT: Barbas, Carlos F  
APPLICANT: Lerner, Richard A  
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 170  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute, Office of  
ADDRESSEE: Patent Counsel  
STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,  
STREET: Mail Drop TPC8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/899,575  
FILING DATE: 24-JUL-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/276,852  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: US 08/178,302  
FILING DATE: 30-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/954,148  
FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: SCR1452P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 149:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 111 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-899-575-149

Query Match 5.7%; Score 7; DB 1; Length 111;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 DIPDRFS 88  
DB 58 DIPDRFS 64

RESULT 34  
PCT-US95-08743-149

; Sequence 149, Application PC/TUS9508743  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
; NUMBER OF SEQUENCES: 170  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/08743  
; FILING DATE: 11-JUL-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/276,852  
; FILING DATE: 18-JUL-1994  
; INFORMATION FOR SEQ ID NO: 149:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 111 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US95-08743-149

Query Match 5.7%; Score 7; DB 5; Length 111;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 DIPDRFS 88  
DB 58 DIPDRFS 64

RESULT 35  
US-08-480-753-6  
; Sequence 6, Application US/08480753  
; Patent No. 5830675  
; GENERAL INFORMATION:  
; APPLICANT: Targan M.D., Stephan R.  
; APPLICANT: Vidulich Ph.D., Alda M.  
; TITLE OF INVENTION: METHODS FOR SELECTIVELY DETECTING  
; TITLE OF INVENTION: PERINUCLEAR ANTI-NEUTROPHIL CYTOPLASMIC ANTIBODY OF  
; TITLE OF INVENTION: ULCERATIVE COLITIS, PRIMARY SCLEROSING CHOLANGITIS, OR  
; TITLE OF INVENTION: TYPE I AUTOIMMUNE HEPATITIS  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wendy A. Whiteford, Esq.  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/480,753  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Whiteford, Wendy A.  
; REGISTRATION NUMBER: 36,964  
; REFERENCE/DOCKET NUMBER: P07 33571  
; TELEPHONE: (213) 622-7700  
; TELEFAX: (213) 489-4210  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 214 amino acids  
; TYPE: amino acid

; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-480-753-6  
Query Match 5.7%; Score 7; DB 2; Length 214;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFSA 89  
DB 58 IPDRFSA 64

RESULT 36  
US-09-041-889-11  
; Sequence 11, Application US/09041889  
; Patent No. 6033864  
; GENERAL INFORMATION:  
; APPLICANT: Braun, Jonathan  
; APPLICANT: Cohavy, Offer  
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of  
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using  
; TITLE OF INVENTION: Microbial UC PANCA antigens  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/041,889  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/837,058  
; FILING DATE: 11-APR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-PM 3006  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 214 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-041-889-11

Query Match 5.7%; Score 7; DB 3; Length 214;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFSA 89  
DB 58 IPDRFSA 64

RESULT 37  
US-08-837-058-11  
; Sequence 11, Application US/08837058  
; Patent No. 6074835  
; GENERAL INFORMATION:  
; APPLICANT: Braun, Jonathan

APPLICANT: Targan, Stephan R.  
APPLICANT: Eggena, Mark  
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of  
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using  
TITLE OF INVENTION: Histone H1  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/837,058  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-PM 2438  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 214 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-837-058-11

Query Match 5.7%; Score 7; DB 3; Length 214;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFSA 89  
| | | | |  
Db 58 IPDRFSA 64

RESULT 38  
US-09-417-264-11  
; Sequence 11, Application US/09417264  
; Patent No. 6537768  
; GENERAL INFORMATION:  
; APPLICANT: Braun, Jonathan  
; APPLICANT: Cohavy, Ofer  
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of  
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using  
; TITLE OF INVENTION: Microbial UC panCA antigens  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/417,264  
; FILING DATE:  
; CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/041,889  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-PM 3006  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 214 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-417-264-11

Query Match 5.7%; Score 7; DB 4; Length 214;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFSA 89  
| | | | |  
Db 58 IPDRFSA 64

RESULT 39  
US-09-328-352-6418  
; Sequence 6418, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gazy L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 6418  
; LENGTH: 255  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-6418

Query Match 5.7%; Score 7; DB 4; Length 255;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 VLAQLDA 27  
| | | | |  
Db 249 VLAQLDA 255

RESULT 40  
US-09-266-965-140  
; Sequence 140, Application US/09266965  
; Patent No. 6495348  
; GENERAL INFORMATION:  
; APPLICANT: Sherman, D  
; APPLICANT: Mac, Y  
; APPLICANT: Varoglu, M  
; APPLICANT: He, M  
; APPLICANT: Sheldon, P  
; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster  
; FILE REFERENCE: 600.456US1  
; CURRENT APPLICATION NUMBER: US/09/266,965  
; CURRENT FILING DATE: 1999-03-12  
; EARLIER APPLICATION NUMBER: US 08/624,447  
; EARLIER FILING DATE: 1996-08-19  
; EARLIER APPLICATION NUMBER: PCT/US94/11279  
; EARLIER FILING DATE: 1994-10-06  
; EARLIER APPLICATION NUMBER: US 08/133,963

```
; EARLIER FILING DATE: 1993-10-07
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 140
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Streptomyces lavendulae
US-09-266-965-140

Query Match          5.7%; Score 7; DB 4; Length 270;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      23 AQLDALL 29
DB      168 AQLDALL 174

RESULT 41
US-09-252-991A-21249
; Sequence 21249, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21249
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21249

Query Match          5.7%; Score 7; DB 4; Length 613;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      22 LAQLDAL 28
DB      44 LAQLDAL 50

RESULT 42
US-08-457-176-2
; Sequence 2, Application US/08457176
; Patent No. 5591826
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: de la Chappelle, Albert
; TITLE OF INVENTION: Mutator Gene and Hereditary
; TITLE OF INVENTION: No. 5591826-Polypsis Colorectal Cancer
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie, and Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,175
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 08/160295
; FILING DATE: 02-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.44900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202.508.9100
; TELEFAX: 202.508.9299
; CURRENT APPLICATION DATA:
```

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; APPLICATION NUMBER: US/08/457,176
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160295
; FILING DATE: 02-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.44900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202.508.9100
; TELEFAX: 202.508.9299
; TELEX: 197430 BEMB UT
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 934 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-457-176-2

Query Match          5.7%; Score 7; DB 1; Length 934;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      21 VLAQLDA 27
DB      598 VLAQLDA 604

RESULT 43
US-08-457-175-2
; Sequence 2, Application US/08457175
; Patent No. 5693470
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: de la Chappelle, Albert
; TITLE OF INVENTION: Mutator Gene and Hereditary
; TITLE OF INVENTION: No. 5693470-Polypsis Colorectal Cancer
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie, and Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,175
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 08/160295
; FILING DATE: 02-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.44900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202.508.9100
; TELEFAX: 202.508.9299
; CURRENT APPLICATION DATA:
```

TELEX: 197430 BBMB UT  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 934 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-457-175-2

Query Match 5.7%; Score 7; DB 1; Length 934;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 21 VLAQLDA 27  
|||  
b 598 VLAQLDA 604

## RESULT 44

US-08-709-784-1  
Sequence 1, Application US/08709784  
Patent No. 6048701  
GENERAL INFORMATION:

APPLICANT: The Johns Hopkins University  
TITLE OF INVENTION: Antibody Detection of Mismatch Repair  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Allegretti, Ltd.  
STREET: 1001 G Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20001-4597

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/709,784  
FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/480,351  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Kagan, Sarah A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 1107.57434  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 934 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

US-08-709-784-1

Query Match 5.7%; Score 7; DB 3; Length 934;  
Best Local Similarity 100.0%; Pred. No. 79;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 21 VLAQLDA 27  
|||  
Db 598 VLAQLDA 604

## RESULT 45

US-09-651-656-3  
Sequence 3, Application US/09651656  
Patent No. 6340566  
GENERAL INFORMATION:

APPLICANT: MCCUTHEN-MALONEY, SANDRA  
TITLE OF INVENTION: LAWRENCE LIVERMORE NATIONAL LABORATORY

TITLE OF INVENTION: DETECTION AND QUANTITATION OF SINGLE NUCLEOTIDE

TITLE OF INVENTION: POLYMORPHISMS, DNA SEQUENCE VARIATIONS, DNA MUTATIONS,

TITLE OF INVENTION: DNA DAMAGE AND DNA MISMATCHES

FILE REFERENCE: IL-10689

CURRENT APPLICATION NUMBER: US/09/651,656

CURRENT FILING DATE: 2000-08-29

PRIOR APPLICATION NUMBER: 60/192,764

PRIOR FILING DATE: 2000-03-28

NUMBER OF SEQ ID NOS: 106

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 3

LENGTH: 934

TYPE: PRT

ORGANISM: Homo sapiens

US-09-651-656-3

Query Match 5.7%; Score 7; DB 4; Length 934;

Best Local Similarity 100.0%; Pred. No. 79;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 VLAQLDA 27  
|||  
Db 598 VLAQLDA 604

## RESULT 46

US-09-650-855-3

Sequence 3, Application US/09650855

Patent No. 6365355

GENERAL INFORMATION:

APPLICANT: MCCUTHEN-MALONEY, SANDRA

APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY

TITLE OF INVENTION: CHIMERIC PROTEINS FOR DETECTION AND QUANTITATION OF DNA

TITLE OF INVENTION: MUTATIONS, DNA SEQUENCE VARIATIONS, DNA DAMAGE AND DNA

TITLE OF INVENTION: MISMATCHES

FILE REFERENCE: IL-10284

CURRENT APPLICATION NUMBER: US/09/650,855

CURRENT FILING DATE: 2000-08-29

PRIOR APPLICATION NUMBER: 60/192,764

PRIOR FILING DATE: 2000-03-28

NUMBER OF SEQ ID NOS: 106

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 3

LENGTH: 934

TYPE: PRT

ORGANISM: Homo sapiens

US-09-650-855-3

Query Match 5.7%; Score 7; DB 4; Length 934;

Best Local Similarity 100.0%; Pred. No. 79;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 VLAQLDA 27  
|||  
Db 598 VLAQLDA 604

## RESULT 47

US-09-708-200-13

; Sequence 13, Application US/09708200  
; Patent No. 6576468  
; GENERAL INFORMATION:  
; APPLICANT: Nicolaides, Nicholas C  
; APPLICANT: Grasso, Luigi  
; APPLICANT: Sasse, Philip M  
; TITLE OF INVENTION: METHODS FOR ISOLATING NOVEL ANTIMICROBIAL AGENTS FROM  
; FILE REFERENCE: HYPERMUTABLE CELLS  
; CURRENT APPLICATION NUMBER: US/09/708,200  
; CURRENT FILING DATE: 2000-11-07  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 934  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-708-200-13

Query Match 5.7%; Score 7; DB 4; Length 934;  
Best Local Similarity 100.0%; Pred. No. 79; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0;

QY 21 VLAQLDA 27  
| | | | |  
Db 598 VLAQLDA 604

RESULT 48  
US-09-512-250C-31  
; Sequence 31, Application US/09512250C  
; Patent No. 6518042  
; GENERAL INFORMATION:  
; APPLICANT: Borchert, Torben  
; APPLICANT: Pedersen (Executor for Lars Christiansen, deceased), Dennis  
; APPLICANT: Wind, Jesper  
; TITLE OF INVENTION: A process for Making DNA Libraries In Filamentous Fungal Cells  
; FILE REFERENCE: No. 6518042el Cloned Gene Involved in the Mismatched Repair Syst  
; TITLE OF INVENTION: Cells  
; FILE REFERENCE: 5718.200-US  
; CURRENT APPLICATION NUMBER: US/09/512,250C  
; CURRENT FILING DATE: 1999-02-24  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 31  
; LENGTH: 1010  
; TYPE: PRT  
; ORGANISM: human.p  
US-09-512-250C-31

Query Match 5.7%; Score 7; DB 4; Length 1010;  
Best Local Similarity 100.0%; Pred. No. 85; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0;

QY 21 VLAQLDA 27  
| | | | |  
Db 674 VLAQLDA 680

RESULT 49  
US-09-252-991A-28966  
; Sequence 28966, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190

; Sequence 13, Application US/09708200  
; Patent No. 6576468  
; GENERAL INFORMATION:  
; APPLICANT: Nicolaides, Nicholas C  
; APPLICANT: Grasso, Luigi  
; APPLICANT: Sasse, Philip M  
; TITLE OF INVENTION: METHODS FOR ISOLATING NOVEL ANTIMICROBIAL AGENTS FROM  
; FILE REFERENCE: HYPERMUTABLE CELLS  
; CURRENT APPLICATION NUMBER: US/09/708,200  
; CURRENT FILING DATE: 2000-11-07  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 934  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-708-200-13

Query Match 5.7%; Score 7; DB 4; Length 934;  
Best Local Similarity 100.0%; Pred. No. 79; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0;

QY 21 VLAQLDA 27  
| | | | |  
Db 598 VLAQLDA 604

RESULT 48  
US-09-512-250C-31  
; Sequence 31, Application US/09512250C  
; Patent No. 6518042  
; GENERAL INFORMATION:  
; APPLICANT: Borchert, Torben  
; APPLICANT: Pedersen (Executor for Lars Christiansen, deceased), Dennis  
; APPLICANT: Wind, Jesper  
; TITLE OF INVENTION: A process for Making DNA Libraries In Filamentous Fungal Cells  
; FILE REFERENCE: No. 6518042el Cloned Gene Involved in the Mismatched Repair Syst  
; TITLE OF INVENTION: Cells  
; FILE REFERENCE: 5718.200-US  
; CURRENT APPLICATION NUMBER: US/09/512,250C  
; CURRENT FILING DATE: 1999-02-24  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 31  
; LENGTH: 1010  
; TYPE: PRT  
; ORGANISM: human.p  
US-09-512-250C-31

Query Match 5.7%; Score 7; DB 4; Length 1010;  
Best Local Similarity 100.0%; Pred. No. 85; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0;

QY 21 VLAQLDA 27  
| | | | |  
Db 674 VLAQLDA 680

RESULT 49  
US-09-252-991A-28966  
; Sequence 28966, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 28966  
; LENGTH: 1039  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-28966

Query Match 5.7%; Score 7; DB 4; Length 1039;  
Best Local Similarity 100.0%; Pred. No. 87; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0;

QY 74 EEDHRP 80  
| | | | |  
Db 976 EEDHRP 982

RESULT 50  
US-08-747-599A-17  
; Sequence 17, Application US/08747599A  
; Patent No. 6214795  
; GENERAL INFORMATION:  
; APPLICANT: Benjamin, Howard et al.  
; TITLE OF INVENTION: Peptide Compounds Useful for Modulating  
; TITLE OF INVENTION: FGF Receptor Activity  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/747,599A  
; FILING DATE: 12-NOV-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kara, Catherine J.  
; REGISTRATION NUMBER: 41,106  
; REFERENCE/DOCKET NUMBER: PPI-029  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
US-08-747-599A-17

Query Match 4.8%; Score 6; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 17; Mismatches 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0;

QY 66 RYLLY 71  
| | | | |  
Db 2 RYLLY 7

RESULT 51  
US-08-476-405A-1  
; Sequence 1, Application US/08476405A  
; Patent No. 5776459  
; GENERAL INFORMATION:  
; APPLICANT: Vandenberg, Arthur A.

;; TITLE OF INVENTION: Method of Treatment Using TCR VBeta5 Peptides

;; NUMBER OF SEQUENCES: 27

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Connective Therapeutics, Inc.

;; STREET: 3400 West Bayshore Road

;; CITY: Palo Alto

;; STATE: California

;; COUNTRY: USA

;; ZIP: 94303

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/476,405A

;; FILING DATE:

;; CLASSIFICATION: 424

;; PRIOR APPLICATION NUMBER:

;; APPLICATION NUMBER: US 08/059,020

;; FILING DATE: 16-MAR-1993

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/735,612

;; FILING DATE: 16-JUL-1991

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/708,022

;; FILING DATE: 31-MAY-1991

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/554,529

;; FILING DATE: 19-JUL-1990

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/467,577

;; FILING DATE: 19-JAN-1990

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/382,804

;; FILING DATE: 19-JUL-1989

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Lowin, David A. 29,326

;; REGISTRATION NUMBER: 886 P15

;; REFERENCE/DOCKET NUMBER: 886 P15

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 415-843-2800

;; TELEFAX: 415-843-2899

;; INFORMATION FOR SEQ ID NO: 1:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 18 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: peptide

;; JS-08-476-405A-1

Query Match 4.9%; Score 6; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 24;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 54 VSWYQQ 59

DB 8 VSWYQQ 13

RESULT 52

JS-08-658-136-23

Sequence 23, Application US/08658136

Patent No. 6071717

GENERAL INFORMATION:

APPLICANT: KLINGER, KATHERINE W

APPLICANT: LANDES, GREGORY M

APPLICANT: BURN, TIMOTHY C

APPLICANT: CONNORS, TIMOTHY D

APPLICANT: DACKOWSKI, WILLIAM

APPLICANT: GERMINO, GREGORY

APPLICANT: QIAN, FENG

;; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE

;; NUMBER OF SEQUENCES: 58

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: GENZYME CORPORATION

;; STREET: ONE MOUNTAIN ROAD

;; CITY: FRAMINGHAM

;; STATE: MASSACHUSETTS

;; COUNTRY: USA

;; ZIP: 01701

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/658,136

;; FILING DATE:

;; CLASSIFICATION: 435

;; ATTORNEY/AGENT INFORMATION:

;; NAME: LASSEN, ELIZABETH

;; REGISTRATION NUMBER: 31,845

;; REFERENCE/DOCKET NUMBER: GEN4-17.8

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 508-872-8400

;; TELEFAX: 508-872-5415

;; INFORMATION FOR SEQ ID NO: 23:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 20 amino acids

;; TYPE: amino acid

;; TOPOLOGY: linear

;; MOLECULE TYPE: protein

;; US-08-658-136-23

Query Match 4.9%; Score 6; DB 3; Length 20;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 34 QVAQLS 39

DB 10 QVAQLS 15

RESULT 53

US-09-690-454-102

Sequence 102, Application US/09690454

Patent No. 6531447

GENERAL INFORMATION:

APPLICANT: Steven M. Ruben, et al.

TITLE OF INVENTION: 32 Human Secreted Proteins

FILE REFERENCE: P2006P1

CURRENT APPLICATION NUMBER: US/09/690,454

CURRENT FILING DATE: 2000-10-18

PRIOR APPLICATION NUMBER: 09/189,144

PRIOR FILING DATE: 1998-11-10

PRIOR APPLICATION NUMBER: 60/044,039

PRIOR FILING DATE: May 30, 1997

PRIOR APPLICATION NUMBER: 60/048,093

PRIOR FILING DATE: May 30, 1997

PRIOR APPLICATION NUMBER: 60/048,190

PRIOR FILING DATE: May 30, 1997

PRIOR APPLICATION NUMBER: 60/050,935

PRIOR FILING DATE: May 30, 1997

PRIOR APPLICATION NUMBER: 60/048,101

PRIOR FILING DATE: May 30, 1997

PRIOR APPLICATION NUMBER: 60/048,356

PRIOR FILING DATE: May 30, 1997

PRIOR APPLICATION NUMBER: 60/056,250

PRIOR FILING DATE: August 29, 1997

PRIOR APPLICATION NUMBER: 60/056,296

PRIOR FILING DATE: August 29, 1997

PRIOR APPLICATION NUMBER: 60/056,293

PRIOR FILING DATE: August 29, 1997

NUMBER OF SEQ ID NOS: 229

; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 102  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-690-454-102

Query Match 4.9%; Score 6; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 DALLVF 31  
| | | | |  
Db 8 DALLVF 13

RESULT 54  
US-08-162-102C-44  
; Sequence 44, Application US/08162102C  
; Patent No. 5762905  
; GENERAL INFORMATION:  
; APPLICANT: Burton, Dennis R.  
; APPLICANT: Barbas, III, Carlos F.  
; APPLICANT: Chanock, Robert M.  
; APPLICANT: Murphy, Brian R.  
; APPLICANT: Crowe, Jr., James E.  
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
; TITLE OF INVENTION: TO RESPIRATORY SYNCYTIAL VIRUS  
; NUMBER OF SEQUENCES: 49  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92037

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/162.102C  
; FILING DATE: 10-DEC-1993  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haile, Ph.D., Lisa A.  
; REGISTRATION NUMBER: 38,347  
; REFERENCE/DOCKET NUMBER: 07300/007001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 678-5070  
; TELEFAX: (619) 678-5099  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 53 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-162-102C-44

Query Match 4.9%; Score 6; DB 1; Length 53;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 IPDRFS 88  
| | | | |  
Db 2 IPDRFS 7

RESULT 55  
US-08-851-843A-183  
; Sequence 183, Application US/08851843A

; Patent No. 6093809  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: No. 6093809el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/851,843A  
; FILING DATE: 06-MAY-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002930US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 183:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 54 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-851-843A-183

Query Match 4.9%; Score 6; DB 3; Length 54;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 LSCITLS 43  
| | | | |  
Db 46 LSCITLS 51

RESULT 56  
US-08-974-549A-302  
; Sequence 302, Application US/08974549A  
; Patent No. 6166178  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.



APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin B.  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/974,549A  
FILING DATE: 19-NOV-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 302:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 54 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-974-549A-302

Query Match 4.9%; Score 6; DB 3; Length 54;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

38 LSCTLS 43  
|||||

Db 46 LSCTLS 51  
RESULT 57  
US-08-854-050-183  
; Sequence 183, Application US/08854050  
; Patent No. 6261836  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: No. 6261836el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/854,050  
; FILING DATE: 09-MAY-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002930US  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 183:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 54 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-854-050-183

Query Match 4.9%; Score 6; DB 3; Length 54;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 LSCTLS 43  
|||||  
Db 46 LSCTLS 51

RESULT 58  
US-09-430-323-183  
; Sequence 183, Application US/09430323  
; Patent No. 6309867  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; ; Lingner, Joachim  
; ; Nakamura, Toru  
; ; Morin, Gregg B.  
; ; Chapman, Karen B.  
; ; Harley, Calvin  
; ; Andrews, William H.  
; TITLE OF INVENTION: No. 6309867el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/430,323  
; FILING DATE: 29-Oct-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002930US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 183:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 54 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 183:  
US-09-430-323-183  
Query Match 4.9%; Score 6; DB 4; Length 54;  
Best Local Similarity 100.0%; Pred.No. 63;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 38 LSCTLS 43  
DB 46 LSCTLS 51  
RESULT 59  
US-08-765-179B-19  
; Sequence 19, Application US/08765179B  
; Patent No. 5854027  
; GENERAL INFORMATION:  
; APPLICANT: STEIPE, Boris  
; APPLICANT: STEINBACHER, Stefan  
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP  
; STREET: 655 Fifteenth Street N.W. Suite 330  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-5701  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/765,179B  
; FILING DATE: 14-JAN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP95/02626  
; FILING DATE: 06-JUL-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P 44 25 115.7  
; FILING DATE: 15-JUL-1994  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 64 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-765-179B-19  
Query Match 4.9%; Score 6; DB 2; Length 64;  
Best Local Similarity 100.0%; Pred.No. 74;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 54 VSWYQQ 59  
DB 2 VSWYQQ 7

RESULT 60  
US-08-273-146-67  
; Sequence 67, Application US/08273146  
; Patent No. 5855885  
; GENERAL INFORMATION:  
; APPLICANT: Smith, Rodger  
; APPLICANT: McCafferty, John  
; APPLICANT: Chiswell, David  
; APPLICANT: Darsley, Michael J.  
; APPLICANT: Fitzgerald, Kevin  
; APPLICANT: Kenten, John H.  
; APPLICANT: Martin, Mark T.  
; APPLICANT: Titmas, Richard C.  
; APPLICANT: Williams, Richard O.  
; TITLE OF INVENTION: The Isolation and Production of  
; TITLE OF INVENTION: Catalytic Antibodies using Phase Technology  
; NUMBER OF SEQUENCES: 71  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IGEN, Inc.  
; STREET: 1530 East Jefferson St.  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: USA  
; ZIP: 20852  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/273,146

FILING DATE: 14-JUL-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ryan, John W.

REGISTRATION NUMBER: 33,771

REFERENCE/DOCKET NUMBER: 09000

TELEPHONE: 301-984-8000

TELEFAX: 301-230-0158

INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS:

LENGTH: 67 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

IS-08-273-146-67

Query Match 4.9%; Score 6; DB 2; Length 67;  
Best Local Similarity 100.0%; Pred.No. 77;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 83 IPDRFS 88

b 14 IPDRFS 19

RESULT 61

IS-09-003-198A-17

Sequence 17, Application US/09003198A

Patent No. 6316407

GENERAL INFORMATION:

APPLICANT: Liang, Jihong

APPLICANT: Shah, Dilip Maganlal

APPLICANT: Wu, Yennie S.

APPLICANT: Rosenberger, Cindy A.

APPLICANT: Hakimi, Salim

TITLE OF INVENTION: Antifungal Polypeptide and Methods for

TITLE OF INVENTION: Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/003,198A

FILING DATE: 07-JAN-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Patterson, Melinda L.

REGISTRATION NUMBER: 33,062

REFERENCE/DOCKET NUMBER: MOET:193

TELEPHONE: (713) 787-1400

TELEFAX: (713) 787-1440

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 72 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

IS-09-003-198A-17

Query Match 4.9%; Score 6; DB 4; Length 72;  
Best Local Similarity 100.0%; Pred.No. 82;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CLSFLL 10

Db 8 CLSFLL 13

RESULT 62

US-08-476-405A-25

; Sequence 25, Application US/08476405A

; Patent No. 5776459

; GENERAL INFORMATION:

; APPLICANT: Vanderbark, Arthur A.

; TITLE OF INVENTION: Method of Treatment Using TCR Vbetas Peptides

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Connective Therapeutics, Inc.

; STREET: 3400 West Bayshore Road

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/476,405A

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/059,020

; FILING DATE: 16-MAR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/735,612

; FILING DATE: 16-JUL-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/708,022

; FILING DATE: 31-MAY-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/554,529

; FILING DATE: 19-JUL-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/467,577

; FILING DATE: 19-JAN-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/382,804

; FILING DATE: 19-JUL-1989

; ATTORNEY/AGENT INFORMATION:

; NAME: Lowin, David A.

; REGISTRATION NUMBER: 29,326

; REFERENCE/DOCKET NUMBER: 886 P15

; TELEPHONE: 415-843-2800

; TELEFAX: 415-843-2899

; INFORMATION FOR SEQ ID NO: 25:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 82 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-476-405A-25

Query Match 4.9%; Score 6; DB 1; Length 82;  
Best Local Similarity 100.0%; Pred.No. 92;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 VSWYQQ 59

Db 20 VSWYQQ 25

## RESULT 63

US-08-181-492B-27  
; Sequence 27, Application US/08181492B  
; Patent No. 5552300  
; GENERAL INFORMATION:  
; APPLICANT: Makrides, Savvas C  
; APPLICANT: Kung, Patrick C  
; TITLE OF INVENTION: T Cell Antigen Receptor V Region  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: T Cell Sciences, Inc.  
; STREET: 115 Fourth Avenue  
; CITY: Needham  
; STATE: Massachusetts  
; COUNTRY: United States of America  
; ZIP: 02194-2725  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage  
; OPERATING SYSTEM: MS-DOS 6.2  
; SOFTWARE: WordPerfect 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/181,492B  
; FILING DATE: 13-January-1994  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Yankwich, Leon R.  
; REGISTRATION NUMBER: 30,237  
; REFERENCE/DOCKET NUMBER: TCS-203-P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-345-9100  
; TELEFAX: 617-345-9111  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 92 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL:  
; ANTI-SENSE:  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; PCT-US95-00408-27

Query Match 4.9%; Score 6; DB 1; Length 92;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 VSWYQQ 59  
DB 30 VSWYQQ 35

## RESULT 64

PCT-US95-00408-27  
; Sequence 27, Application PC/TUS9500408  
; GENERAL INFORMATION:  
; APPLICANT: T Cell Sciences, Inc  
; TITLE OF INVENTION: T Cell Antigen Receptor V Region Proteins  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: T Cell Sciences, Inc.  
; STREET: 1515 Fourth Avenue  
; CITY: Needham

STATE: Massachusetts  
COUNTRY: United States of America  
ZIP: 02194-2725  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/00408  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/181,492  
FILING DATE: 13-January-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: YANKWICH, Leon R.  
REGISTRATION NUMBER: 30,237  
REFERENCE/DOCKET NUMBER: TCS-203-PCT(94,664-A)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-345-9100  
TELEFAX: 617-345-9111  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 92 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FEATURE:  
NAME/KEY:  
LOCATION:  
PCT-US95-00408-27

Query Match 4.9%; Score 6; DB 5; Length 92;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 VSWYQQ 59  
DB 30 VSWYQQ 35

## RESULT 65

US-09-732-210-818  
; Sequence 818, Application US/09732210  
; Patent No. 6573361  
; GENERAL INFORMATION:  
; APPLICANT: Bunkers, Greg J.  
; APPLICANT: Liang, Jihong  
; APPLICANT: Mittanck, Cindy A.  
; APPLICANT: Seale, Jeffrey W.  
; APPLICANT: Wu, Yonnie S.  
; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use  
; FILE REFERENCE: 38-21(15036)B  
; CURRENT APPLICATION NUMBER: US/09/732,210  
; CURRENT FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: US 60/169,513  
; PRIOR FILING DATE: 1999-12-07  
; PRIOR APPLICATION NUMBER: US 60/169,340  
; PRIOR FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 1753  
; SEQ ID NO 818  
; LENGTH: 94  
; TYPE: PRT  
; ORGANISM: Mycobacterium tuberculosis  
US-09-732-210-818

Query Match 4.9%; Score 6; DB 4; Length 94;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 60 RAGSAP 65  
b 72 RAGSAP 77

RESULT 66

S-08-488-113B-158  
Sequence 158, Application US/08488113B  
Patent No. 5744580  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,113B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 158:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 96 amino acids  
TYPE: amino acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-488-113B-158

Query Match 4.9%; Score 6; DB 1; Length 96;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 54 VSWYQQ 59  
b 32 VSWYQQ 37

RESULT 67

US-08-477-484B-158  
Sequence 158, Application US/08477484B  
Patent No. 5756699  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,484B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 158:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 96 amino acids  
TYPE: amino acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-477-484B-158

Query Match 4.9%; Score 6; DB 1; Length 96;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 54 VSWYQQ 59  
Db 32 VSWYQQ 37

RESULT 68

US-08-107-669D-22  
Sequence 22, Application US/08107669D  
Patent No. 5766886  
GENERAL INFORMATION:

APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States of America  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/107,669D  
FILING DATE: 13-AUG-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10906  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,464  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Michele A. Cimbala  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0610.1000001/MAC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/371-2540  
TELEFAX: 202/371-2540  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 96 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-107-669D-22

Query Match 4.9%; Score 6; DB 1; Length 96;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 54 VSWYQQ 59  
32 VSWYQQ 37

Db

RESULT 69  
US-08-472-788A-22  
Sequence 22, Application US/08472788A  
Patent No. 5770196  
GENERAL INFORMATION:  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Modified Antibody Variable Domains  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,788A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/082,842  
FILING DATE: 23-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10906  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,464  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Cimbala, Michele A.  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0610.1000003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/371-2600  
TELEFAX: 202/371-2540  
TELEX:  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 96 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
US-08-472-788A-22

Query Match 4.9%; Score 6; DB 1; Length 96;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 VSWYQQ 59  
32 VSWYQQ 37

Db

RESULT 70  
US-08-477-531B-22  
Sequence 22, Application US/08477531B  
Patent No. 5821123  
GENERAL INFORMATION:  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne Kessler, Goldstein and Fox P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States of America  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,531B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/107,669  
FILING DATE: 13-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10906  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,464  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Michele A. Cimbala  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0610.1000004/MAC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/371-2600

TELEFAX: 202/371-2540  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 96 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-477-531B-22

Query Match 4.9%; Score 6; DB 2; Length 96;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 54 VSWYQQ 59  
Db 32 VSWYQQ 37

## RESULT 71

US-08-646-360-158  
Sequence 158, Application US/08646360  
Patent No. 5837491

GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996  
CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 158:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 96 amino acids  
TYPE: amino acid  
STRANDEDNESS: double

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-646-360-158

Query Match 4.9%; Score 6; DB 2; Length 96;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 54 VSWYQQ 59  
Db 32 VSWYQQ 37

## RESULT 72

US-08-082-842A-22  
Sequence 22, Application US/08082842A  
Patent No. 5869619

GENERAL INFORMATION:  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Modified Antibody Variable Domains  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3934

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/082,842A  
FILING DATE: 23-JUN-1993  
CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10906  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,464  
FILING DATE: 13-DEC-1991

ATTORNEY/AGENT INFORMATION:  
NAME: Cimbala, Michele A.  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0610.1000002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/371-2600  
TELEFAX: 202/371-2540  
TELEX:

INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 96 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-082-842A-22

Query Match 4.9%; Score 6; DB 2; Length 96;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 54 VSWYQQ 59  
Db 32 VSWYQQ 37

## RESULT 73

US-08-839-765-158  
Sequence 158, Application US/08839765  
Patent No. 6146631

GENERAL INFORMATION:

APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/839,765  
FILING DATE: 15-APR-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
INFORMATION FOR SEQ ID NO: 158:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 96 amino acids  
TYPE: amino acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-839-765-158

Query Match 4.9%; Score 6; DB 3; Length 96;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 VSWYQQ 59  
DB 32 VSWYQQ 37

RESULT 74  
US-09-136-389-158  
Sequence 158, Application US/09136389  
Patent No. 6146850  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.

NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/136,389  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 158:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 96 amino acids  
TYPE: amino acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-136-389-158

Query Match 4.9%; Score 6; DB 3; Length 96;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 VSWYQQ 59  
DB 32 VSWYQQ 37

RESULT 75  
US-09-610-838-158  
Sequence 158, Application US/09610838  
Patent No. 6376217  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.



STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/610,838  
FILING DATE: 06-JUL-2000

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/136,389  
FILING DATE: 18-AUG-1998  
APPLICATION NUMBER: 08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 158:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 96 amino acids  
TYPE: amino acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
S-09-610-838-158

Query Match 4.9%; Score 6; DB 4; Length 96;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Y 54 VSWYQQ 59  
b 32 VSWYQQ 37

Search completed: February 9, 2004, 13:04:19  
Job time: 23 secs